

STIC-Biotech/ChemLib

135107

mej

From: Marvich, Maria
Sent: Friday, October 15, 2004 8:07 AM
To: STIC-Biotech/ChemLib
Subject: RE:

RECEIVED
OCT 15 2004
STIC-BIOTECH/CHEM LIB
(STIC)

SEQ ID NO 1 and SEQ ID NO 5.

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Friday, October 15, 2004 7:43 AM
To: Marvich, Maria
Subject: RE:

Good morning, now I need the SID NO for 09/911132.
MAUDE

-----Original Message-----

From: Marvich, Maria
Sent: Thursday, October 14, 2004 2:12 PM
To: STIC-Biotech/ChemLib
Subject: RE:

My apologies 09/911132
Yes, this October 5th.

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Thursday, October 14, 2004 2:11 PM
To: Marvich, Maria
Subject: RE:

Oh where you talking about Oct of this year? For this 09/011132 the status is it's a NO BIOTECH DATA.
MAUDE

-----Original Message-----

From: Marvich, Maria
Sent: Thursday, October 14, 2004 5:00 AM
To: STIC-Biotech/ChemLib
Subject:

I sent a sequence search request for 09/011132 last October 5 around 2:00. I was wondering what the status of this search was.

Thank you
Maria Bonovich Marvich
United States Patent and Trademark Office
Remsen 2B84

1636 2C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 20, 2004, 00:09:03 ; Search time 768 Seconds
(without alignments)
10088.731 Million cell updates/sec

Title: US-09-911-132A-1
Perfect score: 1476
Sequence: 1 gaattcctcatccagctga.....gcattcccgactaggggtacc 1476

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------------|---------------------|
| 1 | 1476 | 100.0 | 1476 | 6 ADI26549 | Adi26549 Bovine bi |
| 2 | 1464 | 99.2 | 1464 | 10 ADE53384 | Ades53384 Bovine al |
| 3 | 1454.2 | 98.5 | 1650 | 8 ABZ22773 | Abz22773 Calf inte |
| 4 | 1035.8 | 70.2 | 2523 | 4 AAK51495 | Aak51495 Human pol |
| 5 | 1032.6 | 70.0 | 1587 | 2 AAQ78135 | Aaq78135 Human ent |
| 6 | 1032.6 | 70.0 | 1587 | 2 AAT27384 | Aat27384 Human alk |
| 7 | 1032.6 | 70.0 | 2516 | 12 ADF45468 | Adf45468 Human vas |
| 8 | 1032.6 | 70.0 | 2516 | 12 ADO28592 | Ado28592 Human ppb |
| 9 | 1029.8 | 69.8 | 1702 | 12 ADN43057 | Adn43057 Human sec |
| 10 | 1021.6 | 69.2 | 1966 | 4 AAK52479 | Aak52479 Human pol |
| 11 | 1021.4 | 69.2 | 1491 | 2 AAQ90640 | Aaq90640 Human ent |
| 12 | 1018.2 | 69.0 | 3076 | 2 AAT27391 | Aat27391 Human igg |
| 13 | 1018.2 | 69.0 | 3127 | 2 AAT27392 | Aat27392 Human igg |
| 14 | 1008.8 | 68.3 | 2372 | 2 AAT27393 | Aat27393 Human igg |
| 15 | 1008.8 | 68.3 | 2484 | 2 AAT27386 | Aat27386 Human igg |
| 16 | 1008.8 | 68.3 | 3022 | 2 AAT27390 | Aat27390 Human igg |
| 17 | 1008.8 | 68.3 | 3147 | 2 AAT27389 | Aat27389 Human igg |
| 18 | 1006.4 | 68.2 | 1464 | 2 AAQ90639 | Aaq90639 Human ent |
| 19 | 1002.8 | 67.9 | 1597 | 10 ADH10077 | Adh10077 Human sea |
| 20 | 1002.8 | 67.9 | 1675 | 10 ADH10079 | Adh10079 Human sea |
| 21 | 1002.8 | 67.9 | 1748 | 10 ADH10087 | Adh10087 Human sea |

| | | | | | |
|----|--------|------|------|-------------|--------------------|
| 22 | 1002.8 | 67.9 | 1777 | 10 ADH10083 | Adh10083 Human sea |
| 23 | 1002.8 | 67.9 | 1915 | 10 ADH10091 | Adh10091 Human sea |
| 24 | 1002.8 | 67.9 | 1975 | 10 ADH10095 | Adh10095 Human sea |
| 25 | 1002.4 | 67.9 | 1904 | 12 ADQ80225 | Adq80225 Human gen |
| 26 | 1002.4 | 67.9 | 1918 | 10 ADH10073 | Adh10073 Human gen |
| 27 | 1002.4 | 67.9 | 7582 | 12 ADQ80226 | Adq80226 Human gen |
| 28 | 1002.2 | 67.9 | 1728 | 6 ABL49916 | AbL49916 SEAP, ins |
| 29 | 1002 | 67.9 | 1779 | 6 AAD31054 | Aad31054 Human g34 |
| 30 | 1002 | 67.9 | 2051 | 5 AAD13579 | Aad13579 Rat Mob-5 |
| 31 | 1002 | 67.9 | 2121 | 5 AAD13580 | Aad13580 Human Mob |
| 32 | 1001.4 | 67.8 | 1634 | 2 AAV42729 | Aav42729 Human pla |
| 33 | 1001.4 | 67.8 | 1697 | 12 ADQ80223 | Adq80223 Human gen |
| 34 | 1001.4 | 67.8 | 7677 | 10 ACF36695 | Acf36695 Plasmid v |
| 35 | 1000.8 | 67.8 | 1558 | 6 ABL61146 | AbL61146 SEAP repo |
| 36 | 1000.8 | 67.8 | 1560 | 6 ABK49457 | Abk49457 Human sec |
| 37 | 1000.8 | 67.8 | 1560 | 9 ACF36062 | Acf36062 Human sec |
| 38 | 1000.8 | 67.8 | 2029 | 12 ADQ80227 | Adq80227 Human gen |
| 39 | 1000.8 | 67.8 | 2645 | 12 ADM43173 | Adm43173 SEAP expr |
| 40 | 1000.8 | 67.8 | 4260 | 9 AAL62063 | Aal62063 PSP-SEAP |
| 41 | 1000.8 | 67.8 | 4260 | 9 AAL60448 | Aal60448 PSP-SEAP |
| 42 | 1000.8 | 67.8 | 4260 | 12 ADF90307 | Adf90307 PSP-SEAP |
| 43 | 1000.8 | 67.8 | 4356 | 12 ADN97132 | Adn97132 Mammalian |
| 44 | 1000.8 | 67.8 | 4677 | 8 ACC49134 | Acc49134 Cloning v |
| 45 | 1000.8 | 67.8 | 4846 | 3 AAA29133 | Aaa29133 PNF-Kappa |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | |
| ADI26549 | ADI26549 standard; DNA; 1476 BP. |
| XX | |
| XX | ADI26549; |
| AC | |
| XX | |
| DT | 22-APR-2004 (first entry) |
| XX | |
| DE | Bovine BIAP1I DNA. |
| XX | |
| KW | alkaline phosphatase; resistance gene; zeomycin; G418; heat stability; |
| KW | bovine; BIAP1I; yeast; gene; ds. |
| XX | |
| OS | Bos taurus. |
| XX | |
| PN | EP1176205-A2. |
| XX | |
| PD | 30-JAN-2002. |
| XX | |
| PF | 21-JUL-2001; 2001EP-00117822. |
| XX | |
| PR | 25-JUL-2000; 2000DE-01036491. |
| XX | |
| PA | (HOFF) ROCHE DIAGNOSTICS GMBH. |
| PA | (HOFF) HOFFMANN LA ROCHE & CO AG F. |
| XX | |
| PI | Mueller R, Thalhofer J, Geipel F, Hoelke W, Glaser S, Eckstein H; |
| PI | Kirschbaum T, Bommarius B; |
| XX | |
| DR | WPI; 2002-173123/23. |
| XX | |
| PT | Preparing eukaryotic alkaline phosphatase, useful as diagnostic reagent |
| PT | and for dephosphorylation, by recombinant expression in yeast selected |
| PT | for high gene copy number. |
| XX | |
| PS | Claim 2; SEQ ID NO 1; 23pp; German. |
| XX | |
| CC | This invention describes a novel method of preparing eukaryotic alkaline |
| CC | phosphatase in yeast cells, comprising cloning an alkaline phosphatase |
| CC | gene sequence into different vectors, transforming, and expressing and |
| CC | purifying. A first vector is used containing a resistance gene against a |
| CC | selection marker and transformants that have integrated resistance gene |
| CC | and alkaline phosphatase gene into the genome are selected by growth on |
| CC | medium containing a low concentration of selection marker. The gene copy |

applicant

CC number is increased by multiple transformation and multiple transformants
CC selected on growth medium under high selection pressure. A second vector
CC containing the alkaline phosphatase gene and a second resistance gene
CC against a second marker is introduced, its copy number increased as for
CC the first resistance gene and clones selected that have many copies of
CC the alkaline phosphatase gene and of both resistance genes, integrated
CC into the genome. The vectors used in the method are pHAP10-3 and pHAP10-
CC 3/9K. Preferred cells include methylotrophic yeast, particularly *Pichia*
CC *pastoris* and *Hansenula polymorpha* and specifically *P. pastoris* X-33
CC transformed with pHAP10-3 and pHAP10-3/9K. The amino acid sequence of
CC bovine alkaline phosphatase is known and, working back from this, an
CC optimised codon sequence was designed. This was assembled conventionally
CC from 28 synthetic oligonucleotides to give a sequence having *Eco*RI and
CC *Asp*718 recognition sites at the ends to facilitate cloning. The selection
CC markers are particularly zeomycin and G418, respectively. The alkaline
CC phosphatase is used as diagnostic reagent, as part of a conjugate and for
CC dephosphorylation of DNA. This method produces very active, glycosylated
CC alkaline phosphatase with specific activity over 3000, preferably 10000,
CC units/mg and heat stability comparable with that for commercial enzymes.
CC The expression system is resistant and stable and provides high-level
CC expression without any selection pressure. This sequence represents the
CC bovine *blalpi* gene.

XX SQ Sequence 1476 BP; 337 A; 449 C; 441 G; 249 T; 0 U; 0 Other;

Query Match 100.0%; Score 1476; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTTGGAACGCCAGGCGAGCCAG 60
Db 1 GAATTCCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTTGGAACGCCAGGCGAGCCAG 60
QY 61 GCCCTGTGTGTAGCCAGAGAGTTGACGCGCATCCAGACAGCTGCGCAAGATGTCTCTC 120
Db 61 GCCCTGTGTGTAGCCAGAGAGTTGACGCGCATCCAGACAGCTGCGCAAGATGTCTCTC 120
QY 121 TTCTTGGGGGATGGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCCTTAAGGGGAG 180
Db 121 TTCTTGGGGGATGGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCCTTAAGGGGAG 180
QY 181 ATGAATGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCCAGTCCCATACGTGGCT 240
Db 181 ATGAATGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCCAGTCCCATACGTGGCT 240
QY 241 CTGTCCAAGACATACACGCTGGACAGACAGGTGCCAGACAGCGGCACTGCCACTGCC 300
Db 241 CTGTCCAAGACATACACGCTGGACAGACAGGTGCCAGACAGCGGCACTGCCACTGCC 300
QY 301 TACCTGTGTGGGTCAAGGGCAACTACAGAACCATCGGTGTAGTGACGCCCGCTAC 360
Db 301 TACCTGTGTGGGTCAAGGGCAACTACAGAACCATCGGTGTAGTGACGCCCGCTAC 360
QY 361 AATCAGTGCAACACGACAGCTGGGAATGAGTCACTGTGTATCAACGGGGCAAGAAA 420
Db 361 AATCAGTGCAACACGACAGCTGGGAATGAGTCACTGTGTATCAACGGGGCAAGAAA 420
QY 421 GCAGGGAAGCCCGTGGAGTGTGACCAACCAAGGGTGACGATGCCCTCCCAAGCCGGG 480
Db 421 GCAGGGAAGCCCGTGGAGTGTGACCAACCAAGGGTGACGATGCCCTCCCAAGCCGGG 480
QY 481 GCCTACGGCCACACCGGTGAACCCGAACTGGTACTCAGACGCCGCACTGCTGTGATGCA 540
Db 481 GCCTACGGCCACACCGGTGAACCCGAACTGGTACTCAGACGCCGCACTGCTGTGATGCA 540
QY 541 CAGAGAATGGCTGCGCAGGACATCGCCGCAAGCTGTGTACACATGATATTGACGTG 600
Db 541 CAGAGAATGGCTGCGCAGGACATCGCCGCAAGCTGTGTGTACACATGATATTGACGTG 600
QY 601 ATCTGGGTGAGGCGCAATGTACATGTTCTCTGAGGGGAGCCCAAGCCCTGAATACCA 660
Db 601 ATCTGGGTGAGGCGCAATGTACATGTTCTCTGAGGGGAGCCCAAGCCCTGAATACCA 660

QY 661 GATGATGCCAGTGTGAATGAGTCCGGAAGGACAAAGCAGAACTGTGTGAGGAATGGCAG 720
Db 661 GATGATGCCAGTGTGAATGAGTCCGGAAGGACAAAGCAGAACTGTGTGAGGAATGGCAG 720
QY 721 GCCAAGCACAGGAGGCCAGTATGTGTGAACCGCACTGCGCTCTTACAGCGCGCGAT 780
Db 721 GCCAAGCACAGGAGGCCAGTATGTGTGAACCGCACTGCGCTCTTACAGCGCGCGAT 780
QY 781 GACTCCAGTGTACACACCTCATGGGCTCTTTGAGCCGCGACATGAGTATAATGTT 840
Db 781 GACTCCAGTGTACACACCTCATGGGCTCTTTGAGCCGCGACATGAGTATAATGTT 840
QY 841 CAGCAAGACCAACCAAGAACCCGACCTTGGCGGAGATGACGGAGGGCCCTGCAGTG 900
Db 841 CAGCAAGACCAACCAAGAACCCGACCTTGGCGGAGATGACGGAGGGCCCTGCAGTG 900
QY 901 CTGACGAGGAACCCCGGGGCTTCTACCTCTTGTGAGGGAGGCCGATTGACCAAGGT 960
Db 901 CTGACGAGGAACCCCGGGGCTTCTACCTCTTGTGAGGGAGGCCGATTGACCAAGGT 960
QY 961 CACCATGACGGCAAAAGCTTATATGGCACTGACTGAGGCGATCATGTTGACAATGCCATC 1020
Db 961 CACCATGACGGCAAAAGCTTATATGGCACTGACTGAGGCGATCATGTTGACAATGCCATC 1020
QY 1021 GCCAAGCTTAACGAGCTCACTAGCAAGTGAACAGCTGATCCTTGTCACTGACAGCAC 1080
Db 1021 GCCAAGCTTAACGAGCTCACTAGCAAGTGAACAGCTGATCCTTGTCACTGACAGCAC 1080
QY 1081 TCCCATGTCTCTTTTGGGCTTACACACTGCGTGGGACCTCATTTTCGTTGGCC 1140
Db 1081 TCCCATGTCTCTTTTGGGCTTACACACTGCGTGGGACCTCATTTTCGTTGGCC 1140
QY 1141 CCGGCAAGGCTTACAGACGAAGTCTTACACCTTCTATGGCAATGGCCAGGC 1200
Db 1141 CCGGCAAGGCTTACAGACGAAGTCTTACACCTTCTATGGCAATGGCCAGGC 1200
QY 1201 TATGCGCTTGGCGGGGCTTGAAGGCCGATGTTAATGGACACAAAGGAGAACCTCA 1260
Db 1201 TATGCGCTTGGCGGGGCTTGAAGGCCGATGTTAATGGACACAAAGGAGAACCTCA 1260
QY 1261 TACGGGACAGAGCGGCGGCTGCCCCCTGGCTAGCGAGACCAAGGGGCGAAGCGTGGC 1320
Db 1261 TACGGGACAGAGCGGCGGCTGCCCCCTGGCTAGCGAGACCAAGGGGCGAAGCGTGGC 1320
QY 1321 GTGTTGGCGGAGGCGCGGCGGCACTGTGTGACGCGGTGACGAGAGAGACCTTCGTG 1380
Db 1321 GTGTTGGCGGAGGCGCGGCGGCACTGTGTGACGCGGTGACGAGAGAGACCTTCGTG 1380
QY 1381 GCGCATCATGCGCTTTCGCGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCCAGCC 1440
Db 1381 GCGCATCATGCGCTTTCGCGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCCAGCC 1440
QY 1441 CCGGCCACCGCCACAGCATCCCGACTAGGGTACC 1476
Db 1441 CCGGCCACCGCCACAGCATCCCGACTAGGGTACC 1476

RESULT 2
ADE53384
ID ADE53384 standard; DNA; 1464 BP.

XX AC ADE53384;

XX DT 29-JAN-2004 (first entry)

XX DE Bovine alkaline phosphatase DNA.

XX DX alkaline phosphatase; mutation; immunoassay; antigen;

XX KW interference suppressor; bovine; ds; gene.

XX OS Bos taurus.

XX FH Key Location/Qualifiers

FT CDS 1. .1464
FT /*tag= a
FT /product= "alkaline phosphatase"
FT /partial
FT /note= "no start codon given"
XX
PN EP1348760-A2.
XX
PD 01-OCT-2003.
XX
PF 21-MAR-2003; 2003EP-00006426.
XX
PR 25-MAR-2002; 2002DE-01013201.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFMANN LA ROCHE & CO AG F.
XX
PI Mueller R, Thalhofer J, Geipel F, Hoelke W, Kirschbaum T;
XX
XX WPI; 2003-769844/73.
DR P-PSDB; ADE53385.
XX
XX New mutants of alkaline phosphatase (AP) where enzymatic activity is
PT reduced a hundred fold, are useful as blocking reagents in AP-based
PT immunoassays.
XX
PS Disclosure; SEQ ID NO 1; 35bp; German.
XX
CC This invention describes a novel mutant of eukaryotic alkaline
CC phosphatase where the wild-type sequence is at least 77% homologous with
CC ADE53385 and where the alkaline phosphatase activity is reduced by at
CC least 100-fold, relative to the wild type. The mutations described are
CC Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly,
CC Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for
CC Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp.
CC Conjugates of the novel mutant with antibodies are useful in alkaline
CC phosphatase-based immunoassays for antigens as interference suppressors,
CC i.e. they prevent non-specific binding of active alkaline phosphatase-
CC based conjugates to vessel walls or first antibodies, a phenomenon that
CC may result in false positive results. The mutants have almost the same
CC tertiary and quaternary structures as wild-type alkaline phosphatase, so
CC are very specific interference suppressors. This sequence encodes the
CC wild-type bovine alkaline phosphatase described in the disclosure of the
CC invention.
XX
XX Sequence 1464 BP; 334 A; 446 C; 438 G; 246 T; 0 U; 0 Other;
SQ
Query Match 99.2%; Score 1464; DB 10; Length 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 CTCATCCCACTGAGGAGGAAAAACCCGCTTCTTGAACCGCCAGGAGCCGCTT 66
DB 1 CTCATCCCACTGAGGAGGAAAAACCCGCTTCTTGAACCGCCAGGAGCCGCTT 60
QY 67 GATGTAGCCAAGAGTTGACGCCGATCCAGACAGCTGCCAAGAATGTCACTCTTCTTG 126
DB 61 GATGTAGCCAAGAGTTGACGCCGATCCAGACAGCTGCCAAGAATGTCACTCTTCTTG 120
QY 127 GGGGATGGATGGGGGTGCTTACGCTGACAGCCACTCGGATCCTAAAGGGGACAGATGAAT 186
DB 121 GGGGATGGGATGGGGGTGCTTACGCTGACAGCCACTCGGATCCTAAAGGGGACAGATGAAT 180
QY 187 GGCAACTGGGACTGAGACACCCCTGGCCATGGACCAAGTTCCCATACGTGGCTCTGTCC 246
DB 181 GGCAACTGGGACTGAGACACCCCTGGCCATGGACCAAGTTCCCATACGTGGCTCTGTCC 240
QY 247 AAGACATACACGTTGACAGACAGGTGCGACAGACGCGACAGCACTGCCACTGCTTACCTG 306
DB 241 AAGACATACACGTTGACAGACAGGTGCGACAGACGCGACAGCACTGCCACTGCTTACCTG 300
QY 307 TGTGGGGTCAAGGGCAACTACAGAACCATCGTGTAAAGTGACCGCGCCGCTACATCAG 366
DB 307 TGTGGGGTCAAGGGCAACTACAGAACCATCGTGTAAAGTGACCGCGCCGCTACATCAG 366

DB 301 TGTGGGGTCAAGGGCAACTACAGAACCATCGTGTAAAGTGACCGCGCCGCTACATCAG 360
QY 367 TGCAACACGACACGTGGGAATGAGGTCACTGTGTGATCAACCGGGCCAAAGACGAGG 426
DB 361 TGCAACACGACACGTGGGAATGAGGTCACTGTGTGATCAACCGGGCCAAAGACGAGG 420
QY 427 AAGCGCTGGAGTGTGTGACCAACCAAGGCTGACAGCATGCTCCCAAGCCGGGCTTAC 486
DB 421 AAGCGCTGGAGTGTGTGACCAACCAAGGCTGACAGCATGCTCCCAAGCCGGGCTTAC 480
QY 487 GCGCACACGGTGAACCGAACTGTACTCAGACGCCGACCTGCTGTATGCACAGAAAG 546
DB 481 GCGCACACGGTGAACCGAACTGTACTCAGACGCCGACCTGCTGTATGCACAGAAAG 540
QY 547 AATGGCTGCCAGGACATCGCCGACAGCTGCTTACAAACATGATATTTGACGTGATCCTG 606
DB 541 AATGGCTGCCAGGACATCGCCGACAGCTGCTTACAAACATGATATTTGACGTGATCCTG 600
QY 607 GGTGAGCGCGAATGTACATGTTCTTCTGAGGGGACCCAGACCTGAATACCAGATGAT 666
DB 601 GGTGAGCGCGAATGTACATGTTCTTCTGAGGGGACCCAGACCTGAATACCAGATGAT 660
QY 667 GCCAGTGTGAATGAGTCCCGAAGGACAAAGCAGAACCTGTGTGAGGAATGCGAGGCCAAG 726
DB 661 GCCAGTGTGAATGAGTCCCGAAGGACAAAGCAGAACCTGTGTGAGGAATGCGAGGCCAAG 720
QY 727 CACCAGGAGCCCACTATGTGTGAAACCGCACTGCGCTCCTTCAAGCGCGCGATGACTCC 786
DB 721 CACCAGGAGCCCACTATGTGTGAAACCGCACTGCGCTCCTTCAAGCGCGCGATGACTCC 780
QY 787 AGTGTACACACCTCATGGGCTCTTTGAGCCGCGACAGACATGAATATATGTTACAGCAA 846
DB 781 AGTGTACACACCTCATGGGCTCTTTGAGCCGCGACAGACATGAATATATGTTACAGCAA 840
QY 847 GACCACACCAAGAACCCGACCTGCGGAGATGACGAGGCGGCTGCAAGTGTGAGC 906
DB 841 GACCACACCAAGAACCCGACCTGCGGAGATGACGAGGCGGCTGCAAGTGTGAGC 900
QY 907 AGGAACCCCGGGGCTTCTACCTCTTCTGAGGAGGAGCGGCAATTGACCAAGTCAACCAT 966
DB 901 AGGAACCCCGGGGCTTCTACCTCTTCTGAGGAGGAGCGGCAATTGACCAAGTCAACCAT 960
QY 967 GACGCGAAAGCTTATATGCGACTGAGCGGATCATGTTTGACATGCCATCGCCAAAG 1026
DB 961 GACGCGAAAGCTTATATGCGACTGAGCGGATCATGTTTGACATGCCATCGCCAAAG 1020
QY 1027 GCTAACGAGCTCACTAGCGAACTGACAGCGCTGATCTTGTCACTGACAGACCACTCCCAT 1086
DB 1021 GCTAACGAGCTCACTAGCGAACTGACAGCGCTGATCTTGTCACTGACAGACCACTCCCAT 1080
QY 1087 GTCTTCTCTTTTGGTGCTACACACTGCGTGGGACCTCCATTTTGGTGGCCCCCGGC 1146
DB 1081 GTCTTCTCTTTTGGTGCTACACACTGCGTGGGACCTCCATTTTGGTGGCCCCCGGC 1140
QY 1147 AAGGCTTAGACAGCAAGTCTTACACTCCATCTTATGGCAATGGCCAGGCTATGCG 1206
DB 1141 AAGGCTTAGACAGCAAGTCTTACACTCCATCTTATGGCAATGGCCAGGCTATGCG 1200
QY 1207 CTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCACAAGCGAGAACCTCATACCGG 1266
DB 1201 CTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCACAAGCGAGAACCTCATACCGG 1260
QY 1267 CAGCAGGCGGCTGCCCCCTGGCTAGCGAGAACCCACGCGGCGAAGACGTGGCGGTTC 1326
DB 1261 CAGCAGGCGGCTGCCCCCTGGCTAGCGAGAACCCACGCGGCGAAGACGTGGCGGTTC 1320
QY 1327 GCGCGAGGCGCGCAGGCGCACCTGTGACGCGCGTGACGAGAGAACCTTCTGTGGCGCAC 1386
DB 1321 GCGCGAGGCGCGCAGGCGCACCTGTGACGCGCGTGACGAGAGAACCTTCTGTGGCGCAC 1380
QY 1387 ATCATGGCTTTTGGGGGCTGCGTGAACCTTACACCGCACTGCAATCTGACAGCCCCCGGC 1446
DB 1381 ATCATGGCTTTTGGGGGCTGCGTGAACCTTACACCGCACTGCAATCTGACAGCCCCCGGC 1440

| | | |
|----|------------------------------|------|
| QY | 1447 ACCGCCACCGCATCCCCGACTAG | 1470 |
| | | |
| Db | 1441 ACCGCCACCGCATCCCCGACTAG | 1464 |

RESULT 3
ABZ22773

ID ABZ22773 standard; DNA; 1650 BP.

AC ABZ22773;

DT 02-APR-2003 (first entry)

DE Calf intestinal alkaline phosphatase DNA sequence SEQ ID NO:26.

XX

KW Recombination; mutagenesis; sarcosine oxidase; phosphatase; human;

KM calf intestinal alkaline phosphatase.

05 Bos taurus.

PN WO2003002736-A2.

PD 09-JAN-2003.

PF 26-JUN-2002; 2002WO-EP007060.

PR 27-JUN-2001; 2001EP-00115424.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Shao Z, Kratzsch P, Schmuck R, Von Der Eltz H, Kenklies J;

DR WPI; 2003-201503/19.

PT Forming a polynucleotide sequence for optimizing biomolecules and enzymes
PT by generating a nucleic acid fragment ladder, removing the chain-
PT terminating molecules and reassembling the polynucleotide.

PS Example 2; Fig 5; 64pp; English..

CC The present invention describes a method of forming a polynucleotide
CC sequence, comprising: (a) generating a nucleic acid fragment ladder by
CC nucleic acid synthesis; (b) removing the chain-terminating molecules or
CC changing them into non-terminating molecules; and (c) reassembling the
CC polynucleotide. Also described is a method for providing mutant
CC polypeptides or proteins. The methods of forming a polynucleotide
CC sequence and providing mutant polypeptides or proteins are useful for
CC optimising biomolecules and enzymes. The present sequence represents a
CC calf intestinal alkaline phosphatase (ciap) DNA sequence, which is used
CC in an example from the present invention for the recombination of human
CC placental alkaline phosphatase (hpag) and ciap genes
XX
SQ Sequence 1650 BP, 382 A, 495 C, 483 G, 290 T, 0 U, 0 Other;

| | | | | |
|----------------------------|-------|---------------|-----------|--------------|
| Query Match | 98.5% | Score 1454.2; | DB 8; | Length 1650; |
| Best Local Similarity | 99.8% | Pred. No. 0; | | |
| Matches 1456; Conservative | 0; | Mismatches 3; | Indels 0; | Gaps 0; |

QY 10 ATCCAGCTGAGGAGGAACCCCGCCTTCTGAAccgcagcagcccaaggcccttgat 69
|||
Db 159 ATCCCAgCTAgGAGGAAAACCCCGCCTTCTGAAccgcagcagcccaaggcccttgAT 218

| | | | |
|----|-----|--|-----|
| QY | 70 | GTAGCCAAGAGTTGCAGCCGATCCAGACAGCTGCCAAGATGTCATCCTCTTCTTGGGG | 129 |
| | | | |
| Db | 219 | GTAGCCAAGAGTTGCAGCCGATCCAGACAGCTGCCAAGATGTCATCCTCTTGGGG | 278 |

QY 130 GATGGATGGGGGTGCTACCGTGACGCCACTCGGATCCTAAGGGGCATGATGGC 189
| | | | |
Db 279 GATGGATGGGGGTGCTACCGTGACGCCACTCGGATCCTAAGGGGCATGATGGC 338

OY 190 AAAC TGGG ACCT GAGACA CCCC CTGG CCAT GGACC AGTTC CCATA CTGTG TCCAA G 249
|||
Db 339 AAAC TGGG ACCT GAGACA CCCC CTGG CCAT GGACC AGTTC CCATA CTGTG TCCAA G 398

[illegible][illegible]

Qy 370 AACACGACACGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAAGCAAGGGAAG 429
|||||
Db 519 AACACGACACGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAAGCAAGGGAAG 578
|||||

QY 430 GCCGTGGAGTGTGACCAACCAGGGTGACATGCTCCCAAGCGGCGCTAACGGC 489
|||
Db 579 GCCGTGGAGTGTGACCAACCAGGGTGACATGCTCCCAAGCGGCGCTAACGGC 638

QY 490 CACACGGTGACCGAACTGGTACTCAGACGCCGACCTGCTGTGATGCACAGAAGAAT 549
|||||
Db 639 CACACGGTGAAACCGAACTGGTACTCAGACGCCGACCTGCTGTGATGCACAGAAGAAT 698
|||||

QY 550 GGCTGCCAGACATCGCCGCAAGCTGTCTACACATGATATTGACGTGATCTGGGT 609
|||||
Db 699 GAGCTGCAGGACATCGCCGCAAGCTGTCTACACATGATATTGACGTGATCTGGGT 758
|||||

QY 610 GGAGGCCGATGTACATGTTTCTGAGGGGACCCAGACCTGAATACCCAGATGATGCC 669
|||||
Db 759 GGAGGCCGATGTACATGTTTCTGAGGGGACCCAGACCTGAATACCCAGATGATGCC 818
|||||

QY 670 AGTGTGATGGAGTCCGGAAAGCAAGCAGAACCTGGTGCAGGAATGGCAGGCCAAGCAC 729

Dh 819 AGTGTGATGGAGTCCGGAAAGCAAGCAGAACCTGGTGCAGGAATGGCAGGCCAAGCAC 878

oy 730 CAGGAGCCAGTATGTGTGAACCGCACTGGCGCTCCTTCAGGCGCGCGATGACTCCAGT 789

oy 790 GTAAACACACCTCATGGGCTTTTGAGCCGGCAGACATGAAGTATTAATGTTTCAGCAAGAC 849
|||||
939 GTAAACACACCTCATGGGCTTTTGAGCCGGCAGACATGAAGTATTAATGTTTCAGCAAGAC 998

QY 850 CACACCAAGACCCGACCCCTGGCGGAGATGACGGAGGCCGCTGTGCAAGTGTGAGCAGG 909

910 AACCCCGGGCTTCTACCTTCTGTGAGGAGGCCGATTTGACCAAGTCAACCATGAC 969

970 GGCAAGCTTATATGGCACTGACTGAGCGATCATGTTGACAAATGCCATGCCAAGGCT 102

1030 AACGAGCTCACTAGCGAACTGGACACGCTGATCCTTGTCACTGCAGACCACTCCATGTC 108

QY 1090 TTCTCTTTTGGTGCTACACACTGCGTGGGACTCCATTTTCGGTTCGCCCCCGCAAG 114

1150 GCCTTAGACAGCAAGTCTCTACACCTCCATCTCTATGGCAATGGCCAGGCTATGCGCTT 120

1210 GGGGGGGCTTCAGGCCCCGATGTTAATGGCAGCACAAAGCGAGAACCTCATAACCGGCAG 126

1270 CAGGCGCGCTGCCCTAGCGAGACCCACGGGGCGAAGACTGGCGGTTCCGG 132

DB 1419 CAGGCGCGCTGCCCCCTGGCTAGCAGACCCACGGGGGCGAAGACGTGGCGTTCGCG 1478
QY 1330 CGAGGCCCGCAGGCGCACTGTGTGACGCGCGTGTGACGAGAGACCTTCGTGCGCACATC 1389
DB 1479 CGAGGCCCGCAGGCGCACTGTGTGACGCGCGTGTGACGAGAGACCTTCGTGCGCACATC 1538
QY 1390 ATGGCCTTTGCGGCGCTGCGTGAGAGCCCTACACCGACTGCAATCTGCCAGCCCCGCCACC 1449
DB 1539 ATGGCCTTTGCGGCGCTGCGTGAGAGCCCTACACCGACTGCAATCTGCCAGCCCCCTCCACC 1598
QY 1450 GCCACCAGCATCCCGACT 1468
DB 1599 GCCACCAGCATCCCGACT 1617
RESULT 4
AAK51495
ID AAK51495 standard; cDNA; 2523 BP.
XX
AC AAK51495;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 40.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR P-PSDB; AAM78362.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 1; Page 603-606; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111

CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 2523 BP; 521 A; 856 C; 713 G; 433 T; 0 U; 0 Other;
Query Match 70.2%; Score 1035.8; DB 4; Length 2523;
Best Local Similarity 81.5%; Pred. No. 8.6e-242;
Matches 1199; Conservative 0; Mismatches 272; Indels 0; Gaps 0;
QY 6 CCTCATCCCACTGAGAGAGAAAACCCGCTTCTGAAACCGCCAGGACCCAGGCCCT 65
DB 107 CGTCATCCCACTGAGAGAGAAACCCGCTTCTGAAACCGCCAGGACCTGAGGCCCT 166
QY 66 TGATGTAGCAAGAAAGTTGACAGCCGATCCAGACAGCTGCCAAGATGTCATCTTCTT 125
DB 167 GGATGCTGCCAAGAAAGCTGACAGCCCATCCAGAAAGTGCCTCAAGAACTCATCTTCT 226
QY 126 GGGGATGGGATGGGGGTGCTTACCGTGACAGCCACTCGATCCTAAAGGGCAGATGAA 185
DB 227 GGGCGATGGGTTGGGGGTGCCCCACGGTGACAGCCACAGATCCTAAAGGGCAGAGAA 286
QY 186 TGGCAAACTGGGACCTGAGACACCCCTTGCCATGGAACCAAGTCCCATAGCTGCTGTC 245
DB 287 TGGCAAACTGGGGCTTGAGACGCCCCCTTGCCATGGAACCGCTTCCCATAGCTGCTGTC 346
QY 246 CAAGACATACAACTGTGACAGACAGGTGCGACAGAGCGGACCTGCTCACTGCTACCT 305
DB 347 CAAGACATACAACTGTGACAGACAGGTGCGACAGAGCGGACCTGCTCACTGCTACCT 406
QY 306 GTGTGGGTCAAGGGCACTACTACAGAACCATGCTGTAGTGACAGCGCCGCTTACAATCA 365
DB 407 GTGCGGGTCAAGGCCAACTTCCAGACCATGCGCTTGAAGTGACAGCGCCGCTTAAACCA 466
QY 366 GTGCAACACGACACGTGGGAATGAGTCACTGTGATCAACCGGCGCAAGAAAGCAGG 425
DB 467 GTGCAACACGACACGCGGCAATGAGTCACTGTGATGAACCGGCGCAAGAAAGCAGG 526
QY 426 GAAGCCCGTGGAGATGTGTACCAACCAAGGTGCAAGCATGCTCCCAAGCCGGGCTTA 485
DB 527 AAAGTCAGTAGAGATGTGTACCAACCAAGGTGCAAGCATGCTCCCAAGCCGGCACTTA 586
QY 486 CGCGCACACGCTGAACCGAACTGTTACTAGACCGCCGACCTGCTGTGATGCACAGAA 545
DB 587 CGCACACACGCTGAACCGAACTGTTACTAGATGCTGACATGCTGCTCAGCCGCCA 646
QY 546 GAATGCTGCCAGGACATCGCCGACAGCTGCTCTCAACATGATATGACGTGATCCT 605
DB 647 GGAGGGTGCAGGACATCGCCACTGCTCATCTCAACATGACATGACGTGATCCT 706
QY 606 GGGTGAGCGCGAATGTACATGTTCTTGAGGGAGCCCAAGCCCTGAATACCAAGATGA 665
DB 707 TGGCGGAGCGCGCAAGTACATGTTTCCCATGGGGAGCCCAAGCCCTGAATACCAAGTGA 766
QY 666 TGCCAGTGTGAATGAGTCCGGAAGGACAGAACTGTGTGACAGAAATGGCAGGCCAA 725
DB 767 TGCCAGCGCAGATGGAATCAGGCTGAGCGGGAAGAACTGTGTGACAGAAATGGCTGGCAA 826
QY 726 GCACCAAGGAGCCAGTATGTGTGAACCGCACTGCGCTCCTTACAGGCGGCGGATGACTC 785
DB 827 GCACCAAGGAGCTGTATGTGTGAACCGCACTGAGCTCATGACGCGCTCCCTGAGCCA 886
QY 786 CAGTGTAAACACCTCATGAGGCTCTTTGAGCCGCGACAGACATGAATATATGTTACGA 845
DB 887 GTGTGTGACCATCTCATGAGGCTCTTTGAGCCGAGACAGAAATATGATCCACCG 946
QY 846 AGACCAACAGCAAGAACCCGACCTGCGGAGATGACGAGGCGGCGCTGCAAGTGTGAG 905
DB 947 AGACCCCACTGAAACCCCTCCTGATGAGATGACAGAGGCTGCGCTGCTGAG 1006
QY 906 CAGGAACCCCGGGGCTTACCTCTTCGTGAGAGGAGCGCGCATGACCAAGTCAACCA 965
DB 1007 CAGGAACCCCGGGGCTTACCTCTTCGTGAGAGGAGCGCGCATGACCAAGTCAACCA 1066

OY 966 TGACGCCAAAGCTTATATGGCACTGACTGAGCGCATCATGTTTGAACAATGCCATCGCCAA 1025
Db 1067 TAGAGGTGTGGCTTACACGACACTCACTGAGCGGTGTCATGTTGACGACGCCATTGAGAG 1126
OY 1026 GGCTAACGAGCTCACTAGCGAACTGACACGCTGATCCTTGTCTACTGACGACCACTCCCA 1085
Db 1127 GCGGGGCCAGCTCACACGACGAGAGACACGCTGACCCCTGTCACCGCTGACCACTCCCA 1186
OY 1086 TGTCTTCTTTTGGTGGCTACACACTGCGTGGGACCTCCATTTTGGCTGGCCCCCGG 1145
Db 1187 TGTCTTCTCTTTGGTGGCTACACCTTGGAGGAGCTCCATCTTGGGTTGGCCCCCAG 1246
OY 1146 CAAGGCTTAGACACGAAAGTCTTACACTTCCATCTCTATGGAATGGCCCAAGCTATGC 1205
Db 1247 CAAGGCTTAGGACACGAAAGCTTACACTTCCATCTCTATGGAATGGCCCGGGCTACGT 1306
OY 1206 GCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCACAAAGCGAAGAACCTCATACCG 1265
Db 1307 GTTCAACTCAGGCGTGCAGACCAAGCTGAATGAGCGAGAGCGGAGCCCGATTACCA 1366
OY 1266 GCAGCAGCGGCGCTGCGCCCTGCTAGCGAGACCCACGCGGCGAAGAGCTGGCGGTGT 1325
Db 1367 GCAGCAGCGGCGGTGCGCCCTGTCTCGAGACCCACGAGCGAAGAGCTGGCGGTGT 1426
OY 1326 CGCGCAGGCGCGCAGGCGCACCTGTGCAAGCGGCTGACAGAGAGACCTTCGTGGCGCA 1385
Db 1427 TGCGCGCGGCGCGCAGGCGCACCTGTGATGTGTGACAGAGACGACTTCGTAGCGCA 1486
OY 1386 CATCATGCGCTTTGGGGGCTGCTGAGACCCCTTACACCGACTGCAATCTGCCAGCCCCGC 1445
Db 1487 TGTCTATGCGCTTTCGCTGCTGTGTGAGGCCCTTACACGCGCTGCGACTGGCGCTCCGC 1546
OY 1446 CACCGCCACGACGATCCCCGACTAGGGTACC 1476
Db 1547 CTGCACCAACGACGCGCGCGCACCCAGTTGCC 1577

RESULT 5

AAQ78135
ID AAQ78135 standard; cDNA to mRNA; 1587 BP.

AC AAQ78135;

XX 24-JUL-1995 (first entry)

DT Human enteric alkaline phosphatase cDNA.

XX Human enteric alkaline phosphatase; homogeneous quality production;

KW clinical diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1587

FT /*tag= a

XX JP06284885-A.

XX 11-OCT-1994.

XX 02-APR-1993; 93JP-00076883.

XX 02-APR-1993; 93JP-00076883.

XX (TOYU) TOSOH CORP.

XX MPI; 1994-362592/45.

XX P-PSDB; AAR63438.

XX Recombinant human enteric alkaline phosphatase - for cheap and large

PT scale prodn. of homogeneous HIP.

PS Disclosure; Page 3-5; 9pp; Japanese.

XX AAQ78135 encodes AAR63438 human enteric alkaline phosphatase (HIP), using
CC the mutagenic primers described in AAQ78137-Q78140 the 1422, 1464 and
CC 1491 bp mutants described in AAQ90638-Q90640 were produced. Using
CC recombinant DNA techniques homogeneous quality HIP mutants could be
CC produced, avoiding the problems associated with poor quality labelled
CC enzymes in clinical diagnosis
XX
SQ Sequence 1587 BP; 317 A; 514 C; 491 G; 265 T; 0 U; 0 Other;

Query Match 70.0%; Score 1032.6; DB 2; Length 1587;
Best Local Similarity 81.4%; Pred. No. 4.5e-241;
Matches 1197; Conservative 0; Mismatches 274; Indels 0; Gaps 0;

OY 6 CTTGATCCGAGCTGAGGAGAAACCCGCTTCTTGAAACCGCAGGACGCCAGGCCCT 65
Db 57 CGTCATCCAGCTGAGAGAGAAACCCGCTTCTTGAAACCGCAGGACGCTGAGGCCCT 116
OY 66 TGATGAGCCAAAGATTGCAAGCTCCGATCCAGACAGCTGCCAAGAATGTCTCTTCTT 125
Db 117 GGAATGCTGCCAAGAAGTGCAGCCCATCCAGAAAGTGCAGCAAGACCTCATCTTCTCT 176
OY 126 GGGGATGGGATGGGGTGCCTACGGTGACAGCCACTCGATCTTAAAGGGCAGATGAA 185
Db 177 GGGGATGGGTTGGGGTGCCACGGTGACAGCCACAGGATCTTAAAGGGCAGAGAA 236
OY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCCAGTTCCCATACGTGGCTGTG 245
Db 237 TGGCAAACTGGGGCTGAGACGCCCCCTGGCCATGAGCCGCTTCCCATACCTGGCTGTG 296
OY 246 CAAGACATTAACAAGTGGACAGACAGGTGCCAGACAGCGGCAAGCACTGCCACTGCTTACT 305
Db 297 CAAGACATTAACAATGTGACAGACAGGTGCCAGACAGCGGCAAGCAAGCCAGGCTTACT 356
OY 306 GTGTGGGGTCAAGGGCACTACAGAAACCATCGGTGTAAGTGACAGCGCGGCTTACAATCA 365
Db 357 GTGCGGGTCAAGGCCAAGCTTCCAGACCATCGGCTTGAATGACAGCGCGGCTTAAACA 416
OY 366 GTGCAACACGACACGTTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAAGAACAGG 425
Db 417 GTGCAACACGACACGCGGCAATGAGTCAATCTCGGTATGAACCGGGCCAAAGAACAGG 476
OY 426 GAAGCGGTGGAGTGGTGAACCAACCAAGGTTGACATGCTCCCAAGCGGGGCTTA 485
Db 477 AAGTCAAGTAGAGTGGTGAACCAACCAAGGTTGACATGCTCCCAAGCGGGGCTTA 536
OY 486 CGCGCACACGCTGAACCGAACTGGTACTCAGACGCGCACTGGCTGTGATGACAGAA 545
Db 537 CGCACACACGCTGAACCGCACTGGTACTCAGATGCTGACATGCTGCTCAGCGGCCA 596
OY 546 GAATGGCTGCCAGGACATGCGCCGACACAGCTGGTCTTACAACATGATATTGACGTGATCT 605
Db 597 GAGGGGTGCCAGGACATGCGCCCACTGACTCATCTCCAATGACATTGACGTGATCT 656
OY 606 GGGTGAAGGCGGAATGATGTTTCTTGAAGGGGACCCAGACCCCTGAATACCAATGA 665
Db 657 TGGCGGAGGCGCAAGTATGTTTCCCATGGGACCCAGACCCCTGAATACCAATGA 716
OY 666 TGCCAGTGTGAATGAGTCCGGAAGAGACAAAGCAGAACTGTGACGAATGCGGCCAA 725
Db 717 TGCCAGCAGAAATGAAATCAGGCTGACGGAAGAACTGTGACGAATGCGGCCAA 776
OY 726 GCACCAAGGAGGCCAGTATGTGTGGAACCGGACATGCGCTCTTCAAGCGGCGGATGACTC 785
Db 777 GCACCAAGGAGGCTGTATGTGTGGAACCGGACATGCAAGCGGCTCTTCAAGCA 836
OY 786 CAGTGAACACACCTCATGGGCTCTTGAAGCGGCAAGATGAATATATGTTTACGA 845
Db 837 GTCTGTGACCATCTCATGGGCTCTTGAAGCGGCAAGATGAATATATGATCTTCCG 896
OY 846 AGACCAACCAAGGAGCCGACCTGGCGGAGATGACGAGGCGGCGCTGCAAGTCTGAG 905
Db 897 AGACCCACACTGAGCCCTCCTGATGAGATGACAGAGGCTGCGGCTGCTGAG 956

| | | | |
|----|------|---|------|
| QY | 906 | CAGGAACCCCCCGGGCTTCTACCTCTTCGTGAGGGAGGCCCATTTGACCAACGGTTCACCA | 965 |
| Db | 957 | CAGGAACCCCCCGGGCTTCTACCTCTTCGTGAGGGAGGCCCATGACCATGGTTCATCA | 1016 |
| QY | 966 | TGACGGCAAAAGCTTATATGSCACTGACTGAGGCGATCATGTTTGCAATGCCATCGCAA | 1025 |
| Db | 1017 | TGAGGGTGTGCTTACAGGACGTCACGTAGGCGGTCATGTTGACGACGCCATTGAGAG | 1076 |
| QY | 1026 | GGCTAACGAGCTCACTAGCGAACTGGACACGCTGATCCTTGTCACTGCAGACCACTCCCA | 1085 |
| Db | 1077 | GGCGGGCCAGCTCACACGAGGAGGAGGACACGCTGACCTCTGTCAACCGTGACCACTCCA | 1136 |
| QY | 1086 | TGTCCTTCTTTTGGTGGCTACACACTGCGTGGACCTTCATTTTCGGTCTGGCCCCGG | 1145 |
| Db | 1137 | TGTCCTTCTCTTTGGTGGCTACACCTTGCGAGGGAGCTTCATCTTCGGGTGGCCCCAG | 1196 |
| QY | 1146 | CAAGGCTTAGACAGCAAGTCTTACACCTTCATCTCTATGGAATGGCCAGGCTATGC | 1205 |
| Db | 1197 | CAAGGCTCAGACAGCAAGACCTTACACGTCATCCTGTACGGCAATGCCCCGGCTACGT | 1256 |
| QY | 1206 | GCTTGGCGGGGCTCGAGGCCGATGTTAATGCGAGCACAAGCGAGGAACCTCATACCG | 1265 |
| Db | 1257 | GTTCAACTCAGGCGGTGCGAACAGACGTGAATGAGAGCGAGCGGGAGCCCCGATTACCA | 1316 |
| QY | 1266 | GCAAGCAGGCGGCGGTGCCCCCTGCTAGCGAGACCCACGGGGCGAAGACGTGGCGGT | 1325 |
| Db | 1317 | GCAAGCAGGCGGCGGTGCCCCCTGTCTCGAGACCCACGGAGGCGAAGACGTGGCGGT | 1376 |
| QY | 1326 | CGCGCAGGCCCCGACAGGCGACCTGTGTACACGGCGTGCAGAGGAGACCTTCGTGGCGCA | 1385 |
| Db | 1377 | TGCGCGCGGCCCCGACAGGCGACCTGTGTGCATGTGTGCAGAGACAGACTTCGTAGCGCA | 1436 |
| QY | 1386 | CATCATGCGCTTTGCGGGCTGCGTGGAGCCCTACACCGACTGCAATCTGCAGCCCGCC | 1445 |
| Db | 1437 | TGTCATGGCCTTCGCTGCTGTCTGGAACCCCTACACGCGCTCGACCTGGCGCTCCCGC | 1496 |
| QY | 1446 | CACCGCCACCAAGCATCCCGCACTAGGGTACC | 1476 |
| Db | 1497 | CTGCACCAACCGACGCGCGCGCACCCAGTTGCC | 1527 |

| | |
|----------|--|
| RESULT 6 | |
| AAT27384 | |
| ID | AAT27384 standard; DNA; 1587 BP. |
| XX | |
| AC | AAT27384; |
| XX | |
| DT | 20-SEP-1996 (first entry) |
| XX | |
| DE | Human alkaline phosphatase coding sequence. |
| XX | |
| KW | alkaline phosphatase; label; antibody; IgG; fusion protein; chimera; |
| KW | immunoassay; ds. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | Key |
| FT | CDS |
| FT | Location/Qualifiers |
| FT | 1..1587 |
| FT | /*tag= a |
| FT | /product= "Alkaline_phosphatase" |
| XX | |
| PN | JP08070875-A. |
| XX | |
| PD | 19-MAR-1996. |
| XX | |
| PF | 05-SEP-1994; 94JP-00211035. |
| XX | |
| PR | 05-SEP-1994; 94JP-00211035. |
| XX | |
| PA | (TOYJ) TOSOH CORP. |
| XX | |
| DR | WPI; 1996-203155/21. |

DR P-PSDB; AAR91805.
XX
PT Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprises
PT AP fused downstream of antibody heavy or light chain, useful as
PT immunoassay reagent.
XX
PS Example 1; Page 10-12; 44pp; Japanese.
XX
CC The gene coding for human alkaline phosphatase is fused downstream of a
CC gene coding for either the variable and CHI regions of an antibody heavy
CC chain or an antibody light chain. Coexpression of the H- and L-chain
CC sequences, one of which is fused to the AP gene, results in production of
CC AP-labelled antibodies suitable for use in immunoassays. The present
CC sequence codes for human AP
XX
SQ Sequence 1587 BP; 317 A; 515 C; 490 G; 265 T; 0 U; 0 Other;

| | | | | |
|-----------------------|--------------|---------------------|-----------------|--------------|
| Query Match | 70.0%; | Score 1032.6; | DB 2; | Length 1587; |
| Best Local Similarity | 81.4%; | Pred. No. 4.5e-241; | | |
| Matches 1197; | Conservative | 0; | Mismatches 274; | Indels 0; |
| | | | | Gaps 0; |

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Qy      6  CCTCATCCAGCTGAGGAGGAAAAACCCCGCCTTCTGGAACCCGCCAGGCGCCAGGCCCT 65
          |||||||
Db      57  CGTCATCCCACTGAGGAGGAAACCCGGCCTTCTGGAACCCGCCAGGCGCTGAGGCCCT 116

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QY      66  TGATGTAGCCAGAAGTTGCAGCCGATCCAGACAGCTGCCAAGAATGTATCTCTTCTT  125
        |||||
Db      117  GGATGCTGCGCAGAAGCTGCAGCCCATCCAGAAGTCGCGCAAGAACCTCATCTCTTCTT  176

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Oy 126 GGGGGATGGGATGGGGGTCCCTACGGTGA CAGCCACTCGGATCCTAAAGGGCAGATGAA 185
 |||||
 Db 177 GGGCGATGGGTGGGGGTGCCACGGTGA CAGCCACGAGATCCTAAAGGGCAGAAGAA 236

[illegible]

| | | | |
|----|-----|---|-----|
| Oy | 246 | CAAGACATACAACGTTGGACAGACAGGTGCCAGACAGCGCAGGCACCTGGCCACTGCTTACTT | 305 |
| | | | |
| Db | 297 | CAAGACATACATGTGACACAGACAGGTGCCAGACAGCGCACAGCCACAGCCACGGCTTAACT | 356 |

| | | | |
|----|-----|--|-----|
| QY | 306 | GTCGTGGGGTCAAGGGCACTACGAACCATCGGTGTAAGTGACGGCCCGCTACATCA | 365 |
| | | | |
| Db | 357 | GTCGGGGGTCAAGGCCAATTCAGACCATCGGCTTGAGTGACGCCCGCTTTAACCA | 416 |

[illegible]

QY 426 GAAAGCCGTGGAGTGTGACCAACCAGGGTGACCATGCCTCCCCAGCCCGGCCCTA 485
 |||||
Db 477 AAAGTCAGTAGGAGTGTGACCAACAAGGGTGACCAAGCCTGCACCGGCACTTA 536

| | | | | | |
|----|-----|----------------------|-------------------------|-------------------|-----|
| Oy | 486 | CGCGCACACGGTGAAACCGA | ACTGGTACTCAGACGCCGACCTG | CCTGCTGATGACACAGA | 545 |
| | | | | | |
| Db | 537 | CGCACACACAGTGAACCGCA | ACTGGTACTCAGATGCTGACATG | CCTGCTCAAGCCGCCA | 596 |
| | | | | | |

QY 546 GAATGGCTGCCAGACATCGCCGCACAGCTGGTCTACAACATGGATATTGACGTGATCCT 605
597 GAGAGGGGTGCCAGACATCGCACTCAGCTCATCTCCAACATGACATTTGACGTGATCCT 656

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Oy      606 GGGTGGAGGGCCGAATGTACATGTTCTCGAGGGGACCCAGACCCTGAAATACCAATGA 665
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      657 TGGCGGAGGCCGCAAGTACATGTTTCCCATGGGGACCCAGACCCTGAATACCAAGCTGA 716

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| | | | |
|----|-----|---|-----|
| Qy | 666 | TGCCAGTGTGAATGGAGTCCGGAAGCAAGCAGAACCTGGTGCAGGAATGGCAGGCCAA | 725 |
| | | | |
| Db | 717 | TGCCAGCCAGAATGGAATCAGGCTGACGGAAGAACCTGGTGACAGGAATGGCTGGCAAA | 776 |

QY 726 GCACCAAGGAGCCAGTATGTGTGAACCGCACTGCCCTCCTTCAGGGCGGCAGTACTC 785
| | | | | | | | | | | | | | | | | | | | | |
DB 777 GCACCAAGGAGTGCCTGTATGTGTGAACCGCACTGAGCTCATGCAAGCGTCCCTTGACCA 836

QY 786 CAGTGTACACACCTCATGGGCTCTTTGAGCCGGCAGACATGAAATATGTTACGA 845
Db 837 GTCTGTGACCCATCTCATGGGCTCTTTGAGCCCGAGACAGAAATATGATCCTCCG 896
QY 846 AGACCAACCAAGAGCCCGACCTGGCGGAGATGACGAGGCGGCTGCAAGTGTAG 905
Db 897 AGACCCCACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGGCCTGTAG 956
QY 906 CAGGAACCCCCGGGCTTCTACCTCTCTGTGAGGAGGAGCGCCGATTGACCAAGTACCA 965
Db 957 CAGGAACCCCGCGGCTTCTACCTCTTGTGAGGAGGCGCGCCGCAATGATGTATCA 1016
QY 966 TGACGGCAAACTTATATGGCACTGACTGAGCGCATCATGTTGACAAATGCCATGCCAA 1025
Db 1017 TGAGGGTGTGGCTTACAGGCACTGACTGAGCGGTCATGTTGACGACGCCATTGAGAG 1076
QY 1026 GGCTAACGAGCTCACTAGGAACTGACAGCGCTGATCCTTGTCACTGACAGACCCTCCA 1085
Db 1077 GCGGGGCACTCAACGAGGAGGACACGCTGACCTCGTCAACGCTGACCACTCCCA 1136
QY 1086 TGTCTTCTTTTGGTGTGCTACACACTGCGTGGGACCTCCATTTTGGTCTGGCCCCGG 1145
Db 1137 TGTCTTCTCTTGGTGTGCTACACCTTGCAGAGGAGCTCCATCTTCGGGTGGCCCCAG 1196
QY 1146 CAAGGCTTAGACAGCAAGTCTTACCTCATCTCTATGGCAATGGCCAGGCTATGC 1205
Db 1197 CAAGGCTCAGGACAGCAAGCCTTACGTCATCTGTACGGCAATGGCCCCGGCTAGCT 1256
QY 1206 GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGCACAGCGAAGAACCTCATACCG 1265
Db 1257 GTTCAACTCAGCGCTGCGACCAAGCTGAATGAGAGCGAGCGGAGGCCGATTACCA 1316
QY 1266 GCAGCAGCGCGGCGCTGCCCCCTGGCTAGCGAGAACCCACGGGGCGAAGACGTGGCGTGT 1325
Db 1317 GCAGCAGCGCGGCGGCTGCCCCCTGTCTCCGAGACCCACGAGGCGAAGACGTGGCGTGT 1376
QY 1326 CGCGGAGGCGCGCAGGCGCACCCTGTGTGACGCGGTGACAGAGACCTTCGTGGCGCA 1385
Db 1377 TGC CGCGGCGCGCGCAGGCGCACCCTGTGTGATGTTGTGAGAGCAGACTTCGTAGCGCA 1436
QY 1386 CATCATGGCCTTTTGGCGGCTGCGTGTGAGCCCTTACACCGACTGCAATCTGCAGCCCCCGC 1445
Db 1437 TGTCAATGGCCTTTCGCTGCTGTGTGAGCCCTTACACGCGCTGTGCACTTCGCCCTCCCGC 1496
QY 1446 CACCGCCACCAAGCATCCCCGACTAGGGTACC 1476
Db 1497 CTGCACCAACGAGCGCGCGCACCCAGTTGCC 1527

RESULT 7
ADF45468
ID ADF45468 standard; DNA; 2516 BP.
XX
AC ADF45468;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human vasodilator-responsive gene #65.
XX
KW Vasodilating substance; vasodilation response gene; vasodepressor;
KW antihypertensive drug; vasodilator-responsive gene; hypotensive;
KW vasodilator; human; gene; ds.
XX
OS Homo sapiens.
XX
PN JP2003310272-A.
XX
PD 05-NOV-2003.
XX
PF 26-APR-2002; 2002JP-00126514.
XX
PR 26-APR-2002; 2002JP-00126514.
XX

PA (TANA/) TANAKA T.
PA (ASAH) ASAH KASEI KK.
PA (SUMU) SUMITOMO SEIYAKU KK.
XX
DR WPI; 2004-015357/02.
XX
PT Obtaining vasodilating substance by contacting test substance with
PT vascular smooth muscle cell, comparing change in gene expression and
PT selecting vasodilator which increases expression of vasodilation response
XX genes.
XX
PS Claim 6; SEQ ID NO 65; 98pp; Japanese.

CC The present invention relates to a method for obtaining a vasodilating
CC substance which increases expression of vasodilation response genes, and
CC obtaining a vasodepressor which increases or decreases the expression
CC level of vasodilation response genes. The method is useful for obtaining
CC vasodilating substance which increases/decreases expression of
CC vasodilation response genes. The vasodepressor substance obtained by the
CC method of the invention is useful as an antihypertensive drug. The method
CC is also useful for identifying the specific vasodilator response genes.
CC The present sequence represents a human vasodilator-responsive gene.

Seq Sequence 2516 BP; 517 A; 853 C; 712 G; 434 T; 0 U; 0 Other;

Query Match 70.0%; Score 1032.6; DB 12; Length 2516;
Best Local Similarity 81.4%; Pred. No. 5.2e-241;
Matches 1197; Conservative 0; Mismatches 274; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGGAGAAACCCCGCTTGTGAAACCGCAGGAGCCAGGCCCT 65
Db 102 CGTCATCCAGCTGAGGAGGAGAAACCCCGCTTGTGAAACCGCAGGAGCTGAGGCCCT 161
QY 66 TGATGTAGCCAAAGATTGACGCCGATCCAGACAGCTGCCAAGATGTATCTTCTT 125
Db 162 GGATGCTGCCAAGAGAGCTGACAGCCCATCCAGAGGTCGCCAAGAACCTCATCTTCT 221
QY 126 GGGGATGGGATGGGGTGCCTACGGTGACAGCCCACTCGATCTTAAAGGGCAGATGA 185
Db 222 GGGCGATGGGTTGGGGGTGCCACGGTGACAGCCCAAGATCTTAAAGGGCAGAGAA 281
QY 186 TGGCAAACTGGGACCTTGAGACACCCCTGGCCATGAGCAAGTTCCTATAGTGTCTGTC 245
Db 282 TGGCAAACTGGGGCTTGAGACGCCCTGGCCATGAGACCGCTTCCATATCTGGCTCTGTC 341
QY 246 CAAGACATACAACGTGACAGACAGGTGCCAGACGCGAGGCACTGCCACTGTACTACT 305
Db 342 CAAGACATACAATGTGACAGACAGGTGCCAGACGCGAGCCACAGCCACGCGCTTACT 401
QY 306 GTGTGGGTCGAAGGGCACTACAGAACCATCGGTGTAAAGTGACGCCCGCTCAATCA 365
Db 402 GTGCGGGTCGAAGGCCCACTTCCAGACCATCGGCTTGAAGTGACGCCCGCTTTTAA 461
QY 366 GTGCAACACGACAGTGGGAATGAGGTACGTTGTGATCAACCGGCGCAAGAACGAGG 425
Db 462 GTGCAACACGACAGCGGCAATGAGGTATCTCGTGATGAACCGGCGCAAGACGAGG 521
QY 426 GAAAGCCGTGGAGTGTGACCAACCAAGGTGACAGCATGCTCCCGAGCGGGGCTTA 485
Db 522 AAAGTCAGTAGGAGTGTGACCAACCAAGGTGACAGCAAGCTCCCGAGCGGCACTTA 581
QY 486 CGCGCACACGGGTGAACCGAACTGTACTCAGACGCGGCACTGTGCTGTGATGACAGA 545
Db 582 CGCACACACAGTGAACCGCAACTGTACTCAGATGCTGACATGCTGCTGAGCGGCCA 641
QY 546 GAATGGCTGCAGAGCATGCGCGCACAGCTGTCTACAAACATGATATGATGATGCTCT 605
Db 642 GAGGGGTGCCAGGACATCGCCACTCAGCTCATCTCCAACATGACATGACGTGATCTCT 701
QY 606 GGGTGAGGCGCGAATGTATCATGTTTCTGAGGGGAGCCCGAGACCTGAATPACCGATGA 665
Db 702 TGGCGGAGGCGCGAAGTATCATGTTTCCATGGGGAACCCAGACCTGAGTACCAGCTGA 761

QY 666 TGCCAGTGTGAATGAGTCCGGAGAGACAAGACCTGTGTGACAGAAATGGCAGGCCAA 725
DB 762 TGCCAGCCAGAAATGAATCAGGCTGACGGAGAAACCTGTGTGACAGAAATGGCAGGCCAA 821
QY 726 GCACCAGGAGCCAGTATGTGTGAACCGCATGCGCTCCTTCAGCGCGCCGATGACTC 785
DB 822 GCACCAGGAGTGTGTGTGTGTGAACCGCATGAGCTCATGACAGGCGCTCCCTGAGCCA 881
QY 786 CAGTGAACACACTCATGGGCTCTTTGAGCGGACAGACATGAAGTAATGTTACGA 845
DB 882 GTCTGTGACCCATCTCATGGGCTCTTTGAGCCGGAGACACGAATAATGAGATCCTCCG 941
QY 846 AGACCACACCAAGACCCCGACCTGGCGGAGATGACGGAGCGCGCTGCAAGTGTGAG 905
DB 942 AGACCCACACTGAGACCCCTCCTGTGATGAGATGACAGAGGCTGCGCTGCGCTGTAG 1001
QY 906 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGGAGGCGGCATTTGACCAAGGTACCA 965
DB 1002 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGGAGGCGGCATTTGACCAAGGTACCA 1061
QY 966 TGACGGCAAAAGCTTATATGACACTGACGTGAGCGATCATGTTGACAAATGCCATGCCAA 1025
DB 1062 TGAGGGTGTGGCTTACAGGAGTCACTGAGCGGTCTATGTTGACAGACGCCATTGAGAG 1121
QY 1026 GGCTAACGAGCTCACTAGCGAAGTGAACGCTGATCCTTGTCACTGACAGCACTCCCA 1085
DB 1122 GGCGGGCCAGCTTCACAGAGAGAGACACGCTGACCTGTCAACCGCTGACCACTCCCA 1181
QY 1086 TGTCTTCTCTTTTGTGGCTACACACTGCGGTGGAACCTCCATTTTCCGTTGCGCCCGG 1145
DB 1182 TGTCTTCTCTTTTGTGGCTACACACTGCGGTGGAACCTCCATTTTCCGTTGCGCCCGG 1241
QY 1146 CAAGGCTTACAGACCAAGTCTACACCTTCATCTTATGGCAATGGCCAGGCTATGC 1205
DB 1242 CAAGGCTCAGACACCAAGTCTACACCTTCATCTTATGGCAATGGCCAGGCTATGC 1301
QY 1206 GCTTGGCGGGCTCGAGCGCGGATGTTAATGGCAGCACAAAGCGAAGACCTCATACCG 1265
DB 1302 GTTCAACTCAGCGGTGCGACAGACGTGAATGAGACGAGAGCGGAGCCCGATTACCA 1361
QY 1266 GCAGCAGCGCGCTGCCCCCTGTGCTAGCGAGACCCACGGGGCGAAGAGTGGCGGTGT 1325
DB 1362 GCAGCAGCGCGGTGCCCCCTGTGCTGCGAGACCCACGAGGCGAAGAGTGGCGGTGT 1421
QY 1326 CGCGCAGGCGCGCAGCGCACCTGTGTGACCGGCTGACAGAGAGACTTCTGTGGCGCA 1385
DB 1422 TGCGCGCGCGCGCAGCGCACCTGTGTGACCGGCTGACAGAGAGACTTCTGTGGCGCA 1481
QY 1386 CATCATGGCTTTGCGGGCTGCGGTGAGCGCTTACACCGACTGCAATCTGCCAGCCCGCG 1445
DB 1482 TGTCAATGGCTTGTGCTGTGCTGTGTGAGCGCTTACACCGCGCTGCGAGCTGCGCTCCG 1541
QY 1446 CACCGCCACAGCATCCCGACTAGGGTACC 1476
DB 1542 CTGCACCAACGACGCGCGCACCCAGTTGCC 1572

RESULT 8
ADO28592
ID ADO28592 standard; cDNA; 2516 BP.

XX ADO28592;
DT 12-AUG-2004 (first entry)
XX Human PPBI encoding cDNA SEQ ID NO:21.
DE high-grade dysplasia; HGD; oesophageal adenocarcinoma;
KW neo-plastic transformation; cancer; cytostatic; gene therapy; human;
KW alkaline phosphatase intestinal precursor; PPBI; chromosome 2; gene; ss.
XX Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 46..1632
FT /*tag= a
FT /product= "PPBI"
XX PN MO200404178-A2.
XX 27-MAY-2004.
XX PF 13-NOV-2003; 2003WO-US036260.
XX PR 13-NOV-2002; 2002US-0425813P.
XX PA (GETH) GENENTECH INC.
XX PI Smith V;
XX DR WPI; 2004-420319/39.
DR P-PSDB; ADO28593.
XX
XX PT Detecting of high-grade dysplasia in cells of a mammalian tissue sample
PT comprises establishing the level of expression in the test tissue sample
PT of the genes.
XX
XX PS Claim 1; SEQ ID NO 21; 256pp; English.
XX
XX CC The present invention describes a method for detecting high-grade
CC dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
CC (1) identifying an oesophageal tissue susceptible to oesophageal
CC adenocarcinoma; (2) determining the predisposition of a mammalian tissue
CC to a neo-plastic transformation by detecting HGD in cells of the tissue;
CC and (3) detecting cancer in a patient. The method can be used in
CC detecting HGD and cancer in cells of a mammalian tissue sample. The
CC methods and compositions of the present invention can be used in treating
CC and preventing HGD and cancer, and in gene therapy. The present sequence
CC encodes human alkaline phosphatase intestinal precursor (PPBI), which is
CC used in the exemplification of the present invention. The human PPBI gene
CC is located on chromosome 2.
XX
SQ Sequence 2516 BP; 517 A; 853 C; 712 G; 434 T; 0 U; 0 Other;
Query Match 70.0%; Score 1032.6; DB 12; Length 2516;
Best Local Similarity 81.4%; Pred. No. 5.2e-241;
Matches 1197; Conservative 0; Mismatches 274; Indels 0; Gaps 0;
QY 6 CCTATCCAGCTGAGAGGAAACCCCGCTTCTGAAACCGCCAGGACCCAGGCCCT 65
DB 102 CGTCATCCAGCTGAGAGGAAACCCCGCTTCTGAAACCGCCAGGACCTGAGGCCCT 161
QY 66 TGATGAGCAAGAAGTTGACGCCGATCCAGACAGCTGCCAAGATGTCATCTCTT 125
DB 162 GGATGCTGCCAAGAAGCTGACAGCCCATCCAGAAGTCCCAAGAACCTCATCTTCT 221
QY 126 GGGGATGGGATGGGGGTGCTTACGCTGACAGCCACTCGGATCTTAAAGGGGAGATGAA 185
DB 222 GGGCGATGGGTTGGGGGTGCCACGGTGACAGCCACAGGATCTTAAAGGGGAGAGAA 281
QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGACAGTTCCATACGTGCTGTCTC 245
DB 282 TGGCAAACTGGGCGCTGAGAGCGCCCTGGCCATGAGACCGCTTCCATACGTGCTGTCTC 341
QY 246 CAAGACATCAACGTGACAGACAGGTGCGACAGAGCGCAGGCACTGCACTGCTTACT 305
DB 342 CAAGACATCAATGTGACAGACAGGTGCGACAGAGCGCAGGCACTGCACTGCTTACT 401
QY 306 GTGTGGGCTCAAGGGCACTACAGAACCATCGGTGTAAGTGAAGTGAAGCGCCGCTTACATCA 365
DB 402 GTGCGGGTCAAGGCCCACTTCCAGACCATCGGCTTGAAGTGAAGCGCCGCTTAAACCA 461
QY 366 GTGCAACACGACAGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAAGAAGCAGG 425
DB 462 GTGCAACACGACAGCGGGCAATGAGTCAATCTCCGTGATGAACCGGGCCAAAGAAGCAGG 521

| | | | |
|----|------|--|------|
| QY | 426 | GAAAGCCCGTGGAGTGGTGAACCAACCAGGGGTGACGATGCTTCCCCAGCCGGGGCTTA | 485 |
| Db | 522 | AAAGTCAGTAGGAGTGGTGAACCAACCAGGGGTGACGACGCTTGGCCAGCCGGCACCTTA | 581 |
| QY | 486 | CGCGCACACGGGTGAACCGAAACTGGTACTCAGACGCCGACCTGCTGCTATGCACAGAA | 545 |
| Db | 582 | CGCACACACAGTGAACCGCAACTGGTACTCAGATGCTGACATGCTGCTCAGCCGCCCA | 641 |
| QY | 546 | GAATGGCTGCAGGACATCGCCGACAGCTGGTCTACAACATGATATTGACGTGATCCT | 605 |
| Db | 642 | GGAGGGGTGCAGGACATCGCCACTCAGCTCATCTCCAACATGACATTGACGTGATCCT | 701 |
| QY | 606 | GGGTGGAGGCCGAATGTACATGTTTCTGAGGGGACCCGACCCCTGAATACCCAGATGA | 665 |
| Db | 702 | TGGCGGAGGCCGCAAGTACATGTTTCCCATGGGGACCCCGACCCCTGAATACCCAGCTGA | 761 |
| QY | 666 | TGCCAGTGTGAATGGAATCCGGAAGACAAGCAGAACCTGTGTGAGGAATGGCAGGCCAA | 725 |
| Db | 762 | TGCCAGCCAGATGGAATCAGGCTGGAACGGGAAGAACCTGTGTGAGGAATGGCTGGCAAA | 821 |
| QY | 726 | GCAACCAAGGAGCCCAATATGTGTGGAACCCGCACTGCCCTCTTCAAGCCGGCCGATGACTC | 785 |
| Db | 822 | GCAACCAAGGTGCTGTGTGTGTGGAACCCGCACTGAGCTCATGCAAGGCCGTCCCTGGACCA | 881 |
| QY | 786 | CAGTGTAAACACCTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTTACGCA | 845 |
| Db | 882 | GTTCTGTACCCATCTCATGGGCTCTTTGAGCCCGGAGACACGAATATAGATCCTCCG | 941 |
| QY | 846 | AGACCACACCAAGGACCCGACCTGGCCGAGATGACGAGGCCGCCCTGCMAGTCTGAG | 905 |
| Db | 942 | AGACCCACACACTGGACCCCTCCCTGATGGAGATGACAGGGCTGCCCTGCGCTGTGAG | 1001 |
| QY | 906 | CAGGAACCCCCGGGGCTTCTAATCTTCTGTGAGGAGGAGGCCGATGACCAAGTCA | 965 |
| Db | 1002 | CAGGAACCCCCGGGGCTTCTAATCTTCTGTGAGGAGGAGGCCGATGACCAAGTCA | 1061 |
| QY | 966 | TGACGGCAAAAGCTTATATGSCACTGACTGAGGCGATCATGTTGACAATGCCATGCGCAA | 1025 |
| Db | 1062 | TGAGGGTGTGCTTACGAGGACGTCACTGAGGCGGTCAATGTCAGCAGCCATTGAGAG | 1121 |
| QY | 1026 | GGCTAACGAGCTCACTAGCGAACTGACACAGCTGATCTTGTCACTGCAGACCACTCCA | 1085 |
| Db | 1122 | GGCGGGCCAGCTCACCGAGGAGAGGACACGCTGACCTGTCAACCGCTGACCACTCCA | 1181 |
| QY | 1086 | TGCTTCTCTTTTGGTGGCTACACACTGCGTGGGACCTTCATTTTCCGTCTGGCCCCCGG | 1145 |
| Db | 1182 | TGCTTCTCTTTTGGTGGCTACACCTTGCAGGGAGCTTCATCTTCCGGTTGGCCCCCAG | 1241 |
| QY | 1146 | CAAGGCTTGAACAGCAAGTCTTACACCTCCATCCTCTATGGAATGGCCAGGCTATGC | 1205 |
| Db | 1242 | CAAGGCTCAGGACAGCAAAAGCTTACACGTCCATCTGTACGGCAATGGCCCCGGGCTACGT | 1301 |
| QY | 1206 | GCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCAACAAGCAGGAACCTTCATACCG | 1265 |
| Db | 1302 | GTTCAACTCAGGCGGTGCAACGACGTGAATGAGAGGAGAGCGGAGCCCCGATTACCA | 1361 |
| QY | 1266 | GCAGCAGGCGGCGGTGCCCCCTGGCTAGCGAGACCAACGCGGGCGAAGACGTGGCGGT | 1325 |
| Db | 1362 | GCAGCAGGCGGCGGTGCCCCCTGTGTCGAGAGACCAACGAGGCGAAGACGTGGCGGT | 1421 |
| QY | 1326 | CGCGGAGGCGCGGCGCACTGTGTGACAGGCGGTGAGGAGAGACCTTGTGGCGCA | 1385 |
| Db | 1422 | TGCGCGGCGCGCGGCGCACTGTGTGATGTTGTGAGGAGAGACAGACTTGTGTAAGCA | 1481 |
| QY | 1386 | CATCATGACCTTTGGGGCTGCGTGGAGCCCTACACGACTGCAATCTGCCAGCCCCCGC | 1445 |
| Db | 1482 | TGTATGAGCCTTGCCTGCTGTCTGAGGCCCTACACGCGCTGCGACCTGGCGCTCCCGC | 1541 |
| QY | 1446 | CACCGCACCAAGCATCCCGACTAGGGTACC | 1476 |
| Db | 1542 | CTGCACCAACGACGCGCGCAACCCAGTTGCC | 1572 |

| | |
|----------|---|
| RESULT 9 | |
| ADN43057 | |
| ID | ADN43057 standard; cDNA; 1702 BP. |
| XX | |
| AC | ADN43057; |
| XX | |
| DT | 29-JUL-2004 (first entry) |
| XX | |
| DE | Human secreted protein SECP-43 cDNA. |
| XX | |
| KW | cytostatic; anorectic; immunosuppressive; gene therapy; SECP-antagonist; |
| KW | SECP-agonist; secreted protein; SECP; autoimmune disorder; obesity; |
| KW | cancer; human; SECP-43; gene; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO2004037987-A2. |
| XX | |
| PD | 06-MAY-2004. |
| XX | |
| PF | 22-OCT-2003; 2003WO-US033491. |
| XX | |
| PR | 22-OCT-2002; 2002US-0420720P. |
| PR | 07-NOV-2002; 2002US-0425207P. |
| PR | 15-NOV-2002; 2002US-0426679P. |
| PR | 19-NOV-2002; 2002US-0427871P. |
| PR | 06-JAN-2003; 2003US-0438551P. |
| PR | 17-JAN-2003; 2003US-0441144P. |
| PR | 27-JAN-2003; 2003US-0443135P. |
| XX | |
| PA | (INCY-) INCYTE CORP. |
| XX | |
| PI | Baughn MR, Becha SD, Bhatia UG, Blake JI, Burrill JD, Chawla NK; |
| PI | Chien D, Elliott VS, Emerling BM, Favero KD, Hafalia AJA; |
| PI | Harmesen BW, Ho A, Ison CH, Khare R, Lee S, Lee SY, Lu DAM; |
| PI | Marguis JP, Murage J, Nguyen DB, Ramkumar J, Richardson TW; |
| PI | Swarnakar A, Tang TY, Tran UK, Wang JT, Yue H, Zheng W; |
| XX | |
| DR | WPI; 2004-365505/34. |
| DR | P-PSDB; ADN42982. |
| PT | |
| PT | New human secreted protein (SECP) polypeptide, useful for preparing a |
| PT | composition for treating a disease associated with decreased expression |
| PT | or overexpression of functional SECP e.g., autoimmune disorders, obesity |
| PT | or cancer. |
| XX | |
| PS | Claim 5; SEQ ID NO 118; 289pp; English. |
| XX | |
| CC | The invention describes an isolated human secreted protein (SECP) |
| CC | polypeptide. Also described are: an isolated polynucleotide encoding the |
| CC | polypeptide; a recombinant polynucleotide comprising a promoter sequence |
| CC | operably linked to the polynucleotide; a cell transformed with the |
| CC | recombinant polynucleotide; a transgenic organism comprising the |
| CC | recombinant polynucleotide; a method of producing the polypeptide; an |
| CC | isolated antibody that specifically binds to the polypeptide; a method of |
| CC | detecting a target polynucleotide in a sample; a method for treating a |
| CC | disease or condition associated with decreased expression or |
| CC | overexpression of functional SECP; a method of screening a compound for |
| CC | effectiveness as an agonist or antagonist of the polypeptide or in |
| CC | altering expression of the target polynucleotide; a method of screening a |
| CC | compound that specifically binds to, or that modulates the activity of, |
| CC | the polypeptide; a method of assessing toxicity of a test compound; a |
| CC | diagnostic test for a condition or disease associated with the expression |
| CC | of SECP in a biological sample; a method of diagnosing a condition or |
| CC | disease associated with the expression of SECP in a subject; a |
| CC | composition comprising the antibody and a carrier, or the polypeptide, or |
| CC | agonist or antagonist compound and an excipient a method of preparing a |
| CC | polyclonal or monoclonal antibody; a method of detecting the polypeptide |
| CC | in a sample; a method of purifying the polypeptide; a method of |
| CC | generating an expression profile of a sample that contains |
| CC | polynucleotides; and an array comprising different nucleotide molecules |
| CC | affixed in distinct physical locations on a solid substrate, where at |
| CC | least one of the nucleotide molecules comprises a first oligonucleotide |

CC or polynucleotide sequence specifically hybridizable with at least 30
CC contiguous nucleotides of the target polynucleotide. The polypeptide is
CC useful for preparing a composition for diagnosing or treating a disease
CC or condition associated with decreased expression or overexpression of
CC functional SECP e.g. autoimmune disorders, obesity or cancer. This
CC sequence encodes a human secreted protein.

XX
SQ Sequence 1702 BP; 339 A; 562 C; 513 G; 288 T; 0 U; 0 Other;

Query Match 69.8%; Score 1029.8; DB 12; Length 1702;
Best Local Similarity 81.2%; Pred. No. 2.2e-240;
Matches 1196; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

OY 4 TTCTCATCCAGCTGAGAGAAAACCCCTTCTGAAACCGCAGAGCCAGGCC 63
DB 141 TCCCCCTGGCCAGCTGAGAGAGAAACCGGCTTCTGAAACCGCAGAGCTGAGGCC 200
OY 64 CTTGATGTAGCCAAGAAGTTGCAGCCGATCCAGACAGCTGCCAAGAATGTCATCCTCTTC 123
DB 201 CTGATGCTGCAAGAAGCTGCAGCCCATCCAGAAGTCCGCAAGAAGCTCATCCTCTTC 260
OY 124 TTGGGGGATGGGATGGGGGTGCTTACCGTGACAGCCACTCGATCCTTAAGGGGAGATG 183
DB 261 CTGGCGGATGGGTTGGGGGTGCCACGGTGACAGCCACAGGATCTTAAGGGGAGAG 320
OY 184 AATGGCAACTGGGACCTGAGACACCCCTGGCCATGAGCCAGTCCCATAGTGGCTCTG 243
DB 321 AATGGCAACTGGGGCTTGAGACGCCCTGGCCATGAGCCGCTTCCATAGCTGGCTCTG 380
OY 244 TCCAAGACATCAACGTGAGACAGACAGGTCAGACAGCGAGGCACTGCCCTTAC 303
DB 381 TCCAAGACATCAATGTGACAGACAGAGTGCAGACAGCGAGCCAGCCAGCCCTTAC 440
OY 304 CTGTGTGGGTCAGAGGCACTACAGAACCATCGGTGTAAGTGACAGCGCCGCTACAAT 363
DB 441 CTGTGGGGTCAAGGCCCACTTCCAGACCATCGGCTTGAGTCAAGCGCCGCTTAAAC 500
OY 364 CAGTGCAACACGACGTTGGGAATGAGGTCACTGTGATCAACCGGCGCAAGAAAGCA 423
DB 501 CAGTGCAACACGACGCGGCAATGAGGTCACTGTGATGAATGGGCGCAAGCAAGCA 560
OY 424 GGGAAAGCCGTGGAGTGTGACCAACCAAGGCTGAGCATGCTCCCAAGCCGGGGCC 483
DB 561 GGAAGTCAGTAGAGTGTGACCAACCAAGGCTGAGCATGCTCCCAAGCCGGGACCC 620
OY 484 TACGCGACACGCGTGAACCGAACTGTACTCAGACGCGGACCTGCTGATGCACAG 543
DB 621 TACGACACACAGTGAACCGCACTGTACTCAGATGCTGACATGCTGCTCAGCCGCG 680
OY 544 AAGATGCGTCCAGGACATCGCCGACAGCTGTCTACACATGATATTGACGTGATC 603
DB 681 CAGGAGGGGTGCCAGACATCGCCACTCAGTCTATCTCAACATGAGATTGACGTGATC 740
OY 604 CTGGGTGAGGCGCGAATGTACATGTTTCTGAGGGGAGACCCAGACCTGTAATACCCAGAT 663
DB 741 CTGGCGGAGGCGCGAATGTACATGTTTCTGAGGGGAGACCCAGACCTGTAATACCCAGCT 800
OY 664 GATGCCAGTGTGAATGAGTCCGGAAGGACAGAACTGTGTCAGGAATGGCAGGCC 723
DB 801 GATGCCAGGCAAGATGAATCAGGCTGAGCGGAAGAACTGTGTCAGGAATGGCTGCA 860
OY 724 AAGCACCAGGAGCCAGTATGTGGAACCGCACTGCGCTCTTCAAGCGGCGCATGAC 783
DB 861 AAGCACCAGGAGTGTGATGTGGAACCGCACTGAGCTCATGCAAGGCGTCCCTGAGC 920
OY 784 TCCAGTGAACACACTCATGGGCTCTTTGACCGGACAGACATGAAGTAATATGTTAG 843
DB 921 CAGTCTGTGACCCATCTCATGGGCTCTTTGACCGGAGACAGCAAGTAATGAGATCCAC 980
OY 844 CAAGACCAACCAAGAACCCGACCTGGCGGAGATGACGGAAGCGGCGCTTCAAGTCTG 903
DB 981 CGAGACCCCACTGAGACCCCTCCTGATGAGATGACAGAGGCTGCCCTGCGCTGCTG 1040

OY 904 AGCAGAACCCCGGGGCTTCTTACTCTTCTGAGAGGAGGCCCATTTGACACGCTAC 963
DB 1041 AGCAGAACCCCGGGGCTTCTTACTCTTCTGAGAGGAGGCCCATTTGACACGCTAC 1100
OY 964 CATGACGCAAGCTTATATGCACTGACTGAGGCGATCATGTTGACATGCCATCGCC 1023
DB 1101 CATGAGGTGTGCTTACAGGCACTCACTGAGGCGGTATGTCAGACGCAATTGAG 1160
OY 1024 AAGCTTAACGACTACTAGCACTGACACAGCTGATCCTTGTCACTGACAGCACTCC 1083
DB 1161 AGGCGGGCAGCTCACCAGCAGAGAGACACGCTGACCTGTCACCGCTGACCACTCC 1220
OY 1084 CATGCTTCTCTTTTGGTGTACACACTGCGTGGAACCTCCATTTTGGTCTGCCCCC 1143
DB 1221 CATGCTTCTCTTTTGGTGTACACACTGCGTGGAACCTCCATTTTGGTCTGCCCCC 1280
OY 1144 GGCAGGCTTACAGACAGCAAGTCTTACACTCCATCCTTATGCAATGGCCAGGCTAT 1203
DB 1281 AGCAAGGCTCAGGACAGCAAGCTTACACGTCATCCTGTACGCAATGGCCGCGCTAC 1340
OY 1204 GCGCTTGGCGGGGCTCGAGGCGCGATGTTAATGTCAGACACAAAGGAGAACTCATAC 1263
DB 1341 GTTTCATCACTCAGGCGTGCAGACGATGAATGAGAGGAGAGCGGAGCCCGATTAC 1400
OY 1264 CGCAGACGCGCGCGCTGCGCCCTGCTAGAGAGACCCAGCGGCGAAGACGTGCGGTG 1323
DB 1401 CAGCAGACGCGCGCGGTGCCCTGTGTCGAGACCCAGGAGCGAAGACGTGCGGTG 1460
OY 1324 TTGCGGAGGCGCGCGACGCGCATGTGTCACGCGGTGACAGAGAGACCTTGTGCGG 1383
DB 1461 TTGCGGCGGCGCGCGACGCGCATGTGTCATGTGTGACAGACAGACTTGTGAGCG 1520
OY 1384 CACATCATGCGCTTTGCGGGCTGCGGTGAGAGCCCTACACCGACTGCAATCTGCCAGCCCC 1443
DB 1521 CATGTCATGCGCTTTCGCTGCTGTGAGAGCCCTACACGCGCTGCGAATGCGGCTCCC 1580
OY 1444 GCCACCGCCACGACATCCCCGACTAGGGTACC 1476
DB 1581 GCCTGACACACGACGCGCGGACCCAGTTGCC 1613

RESULT 10
AAK52479
ID AAK52479 standard; cDNA; 1966 BP.
XX
AC AAK52479;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 2008.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
OS Homo sapiens.
PN MO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX

PA (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI; 2001-476283/51.
DR P-PSDB; AAM79346.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 1; Page 4413; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 1966 BP; 381 A; 667 C; 579 G; 339 T; 0 U; 0 Other;

Query Match 69.2%; Score 1021.6; DB 4; Length 1966;
Best Local Similarity 81.3%; Pred. No. 2.3e-238;
Matches 1197; Conservative 0; Mismatches 274; Indels 1; Gaps 1;

QY 6 CCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTTGAACCCGCGAGGCCAGCCCGCCT 65
DB 107 CGTCATCCAGCTGAGGAGGAAACCCGCTTCTTGAACCCGCGAGGCCAGCCCGCCT 166
QY 66 TGAATGAGCCAAAGATTGACAGCCGATCCAGACAGCTGCCAAGATGTCATCTCTTCT 125
DB 167 GGATGCTGCCAAGAAGCTGACGCCCATCCAGAAGTGCCAAGAACTCATCTCTCTCT 226
QY 126 GGGGATGGGATGGGGGTGCCTACGGTGACAGCCACTCGATCCTAAAGGGGAGATGA 185
DB 227 GGGCGATGGGTGGGGGTGCCACGGTGACGCCACAGGATCTAAAGGGGAGAGAA 286
QY 186 TGGCAACTGGGACCTGAGACACCCCTGGCCATGAGCCAGTCCCATACGTGGCTGTTC 245
DB 287 TGGCAACTGGGGCTGAGACGCCCCCTGGCCATGAGCCGCTTCCATACCTGGCTGTTC 346
QY 246 CAAGACATACAACGTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTACT 305
DB 347 CAAGACATACAATGTGACAGACAGGTGCCAGACAGCGCAGCCACGCGCTACTCT 406
QY 306 GTGTGGGTCAAGGGCAACTACAGAACCATCGGTGTAAGTGACGCCGCCGTACAATCA 365
DB 407 GTGCGGGTCAAGGCCAACTTCCAGACCATCGGCTTGAGTGACGCCGCCGCTTAACCA 466
QY 366 GTGCAACACGACAGCTGGAATGAGTCAAGTCTGTGATCAACGGGGCCAAGAAAGCAG 425
DB 467 GTGCAACACGACAGCGCGCAATGAGTCAATCCGTGATGAACGGGGCCAAGCAAGCAG 526
QY 426 GAAGCGCTGGGAGTGTGACCAACCAAGGCTGACATGCTCCCCAGCGGGGCTTA 485
DB 527 AAAGTCAGTAGGAGTGTGACCAACCAAGGCTGACACGCTTCCGCAAGCCGCACTTA 586
QY 486 CGCGCACACGGTGAACCGAACTGGTACTCAGACGCCGACCTGCTGTGACACAGAA 545
DB 587 CGCACACAGTGAACCGCAACTGGTACTCAGATGCTGACATGCTGCTCAGCCCGCCA 646
QY 546 GAATGCTGCCAGACATCGCCGACAGCTGTCTACAAACATGATATTGACGTGATCT 605
DB 647 GGAGGGGTGCCAGACATCGCCACTCAGCTCATCTCCAACATGACATTTGACGTGATCT 706

QY 606 GGGTGAAGCCGAATGTACATGTTTCTCTGAGGGGACCCCAAGACCCTGAATACCCAGATGA 665
DB 707 TGGCGGAGGCCCGCAAGTACATGTTTCCCATGGGGACCCCAAGACCCTGAGTACCCAGCTGA 766
QY 666 TGGCAGTGTGAATGAGTCCGGAAGACCAAGACAGAACTGGTGAGGAATGGCAGGCCAA 725
DB 767 TGGCAGCCAGAAATGAATCAGCTGACGCGGAAGAACTGGTGAGGAATGGCTGGCAAA 826
QY 726 GCACCAAGGAGCCCAATATGTGTGAACCCGACCTGCGCTCTTACAGCGCGCCGATGACTC 785
DB 827 GCACCAAGGAGCTGCTGTGTGTGTGAACCGCACTGAGCTCATGACAGCGCTCCCTGACCA 886
QY 786 CAGTGTAAACACACTCATGGGCTCTTTGAGCCCGCAGACATGAATATAATGTTCAGCA 845
DB 887 GTCTGTGACCCATCTCATGGGCTCTTTGAGCCCGCAGACAGAAATATGATTCACCG 946
QY 846 AGACCAACCAAGGACCCGACCTGGCGGAGATGACGAGCGCGCTGCAAGTGTGAG 905
DB 947 AGACCCCACTGACCTGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTGAG 1006
QY 906 CAGGAACCCCGGGGCTTCTACCTCTTCTGTGAGGAGCGCCGATTGACACCGTCAACA 965
DB 1007 CAGGAACCCCGGGCTTCTACCTCTTGTGTGAGGCGCGCCGATCGACCATGTCTATCA 1066
QY 966 TGAAGGCAAAAGCTTATATGCACTGACTGAGGCGCATGTGTTGACAAATGCCATGCCAA 1025
DB 1067 TGAGGGTGTGCTTACCAAGCACTCACTGAGGCGGTCAATGTTGACAGCGCCATGAGAG 1126
QY 1026 GAGTAAAGAGCTCACTAGCGAACTGACACAGCTGATCTTGTCACTGACAGCACTCCCA 1085
DB 1127 GGGCGGCCAAGCTCACCAAGAGAGAGACAGCTGACCTCGTACCGCTGACCACTCCCA 1186
QY 1086 TGTCTTCTCTTTGGTGCTACACACTGCGTGGACCTCCATTTCCGTCTGGCCCCGG 1145
DB 1187 TGTCTTCTCTTTGGTGCTACACCTTGCGAGGAGCTCCATCTTCGGTGGCCCCAG 1246
QY 1146 CAAAGCCTTAGACAGCAAGTCTTACACCTCCATCTCTATATGGCAATGGCCAGCTATGC 1205
DB 1247 CAAAGCTCAGACAGCAAAAGCTTACACGCTCCATCTGTATCGGCAATGGCCCCGGCTACGT 1306
QY 1206 GCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCAAAAGGAAACCTCATACCG 1265
DB 1307 GTTCAACTCAGCGGTGCAACAGAGTGAATGAGAGCAGAGCGGAGCCCGATTACCA 1366
QY 1266 GAGCAGAGC-GGCGGTGCCCCCTGGCTAGCGAGACCAAGGGGCGAAGCGTGGCGGTGT 1324
DB 1367 CCAGCAGGCGGGGGTGCCTGTGTCGCGAGACCCACGGAAGCGTGGCGGTGT 1426
QY 1325 TCGCGGAGGCCCGCAGCGCACTGTGTGACAGCGGTGACGAGAGACCTTCGTGGCGC 1384
DB 1427 TTGGCGCGGGCCCCGAGGGCACTGTGTGATGATGTGTGACGAGACAGAGCTGTAGCGC 1486
QY 1385 ACATCATGGCTTTGGGGCTGCGTGTGAGGCCCTACACCGAAGTGAATCTGCCAGCCCCG 1444
DB 1487 ATGTCTATGGCTTTCGCTGCTGTGTGAGGCCCTACAGCGGCTGCACTGGCGCTCCCG 1546
QY 1445 CCAGCGCCACAGCATCCCGAAGCTAGGGTACC 1476
DB 1547 CTTGACACCAAGCGCGCGCAACCAAGTTGCC 1578

RESULT 11
AAQ90640
ID AAQ90640 standard; cDNA to mRNA; 1491 BP.
XX
AC AAQ90640;
XX
DT 24-JUL-1995 (first entry)
XX
DE Human enteric alkaline phosphatase cDNA mutant 1491 bp.
XX
KW Human enteric alkaline phosphatase; homogeneous quality production;

KW clinical diagnosis; ds.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT mat_peptide 1..1491
FT /*tag= a
FT /note= "truncated HIP"
XX JP06284885-A.
PN
XX 11-OCT-1994.
PD
XX 02-APR-1993; 93JP-00076883.
PF
XX 02-APR-1993; 93JP-00076883.
PR 02-APR-1993; 93JP-00076883.
XX
XX (TOYJ) TOSOH CORP.
PA
XX
DR WPI; 1994-362592/45.
DR P-PSDB; AAR75700.
XX
PT Recombinant human enteric alkaline phosphatase - for cheap and large
PT scale prodn. of homogeneous HIP.
XX
PS Claim 4; Page 3-5; 9pp; Japanese.
XX
CC AAQ90640 encodes AAR75700 the human enteric alkaline phosphatase (HIP)
CC mutant 1491 bp. Using recombinant DNA techniques homogeneous quality HIP
CC mutants could be produced, avoiding the problems associated with poor
CC quality labelled enzymes in clinical diagnosis
XX
SQ Sequence 1491 BP; 309 A; 471 C; 461 G; 250 T; 0 U; 0 Other;
Query Match 69.2%; Score 1021.4; DB 2; Length 1491;
Best Local Similarity 82.1%; Pred. No. 2.3e-238;
Matches 1175; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
QY 6 CCTCATCCCACTGAGAGAGAAACCCGCTTCTGGAACCGCCAGGCAAGCCAGGCCCT 65
DB 57 CGTCATCCCACTGAGAGAGAAACCCGCTTCTGGAACCGCCAGGCAAGCCAGGCCCT 116
QY 66 TGATGTAGCCAGAAAGTTGCAAGCCGATCCAGACAGCTGCCAAGAATGTATCTTCTT 125
DB 117 GGATGCTGCAAGAGCTGCAGCCCATCCAGAGGTGCCAAGAACTCATCTCTTCTT 176
QY 126 GGGGATGGATGGGGGTGCTTACGGTGACAGCACTCGGATCTTAAAGGGCAGATGAA 185
DB 177 GGGGATGGGTGGGGGTGCCACGGTGACAGCAAGATCTTAAAGGGCAGAGAA 236
QY 186 TGGCAAACTGGAACTGAGACACCCCTGGCCATGGACCAAGTTCCCATAGTGCTGTCT 245
DB 237 TGGCAAACTGGGGCTGAGACGCCCCCTGGCCATGGACCGCTTCCCATATCTGCTGT 296
QY 246 CAAGACATCAACGTGGAACAGACAGGTGCCAGACGCGCAGGCACTGCCCTACTCT 305
DB 297 CAAGACATCAATGTGGAACAGACAGGTGCCAGACGCGCAGGCACTGCCCTACTCT 356
QY 306 GTGTGGGGTCAAGGGCACTACAGAAACCATCGGTGTAAGTGCAAGCCGCGGCTACA 365
DB 357 GTGCGGGGTCAAGGCCCACTTCCAGACCATCGGCTGAGTGCAAGCCGCGCTTTAACCA 416
QY 366 GTGCAACACGACAGTGGGAATGAGGTACGCTGTGTATCAACCGGGCCAGAAAGCAGG 425
DB 417 GTGCAACACGACAGCGGGCAATGAGGTATCTCGTGATGAACCGGGCCAGCAAGCAGG 476
QY 426 GAAGCGCGTGGAGTGTGACCAACCAAGGTCAGCATGCTCCCAAGCGGGGCGCTA 485
DB 477 AAAGTCAGTAGAGTGTGACCAACCAAGGTCAGCATGCTCCCAAGCGGGGCACTA 536
QY 486 CGCGCACACGCTGAACCGAAACTGTACTCAGAGCCGCACTGCTGCTGTGATGACAGAA 545
DB 537 CGCACACACAGTGAACCGCAACTGTGTACTCAGATGCTGACATGCTGCTGCAAGCCGCA 596

QY 546 GAATGCTGCCAGACATCGCCGACAGCTGTGTCTACAACATGATATTGACGTGATCT 605
DB 597 GGAGGGGTGCCAGACATCGCCACTCAGCTCATCTCCAACATGACATTGACGTGATCT 656
QY 606 GGGTGAAGCCCAATGTATCATGTTTCTTGAGGGGAGCCCAAGCCCTGAATACCAAGATGA 665
DB 657 TGGCGGAGGCCCAAGTACATGTTTCCCATGGGAGCCCAAGCCCTGAATACCAAGCTGA 716
QY 666 TGCCAGTGTGAATGAGTCCGGAAGCAACAGAACCTGTGTGAGGAATGGCAGGCCAA 725
DB 717 TGCCAGCCAGAAATGAATCAGGCTGACCGGAAGAACCTGTGTGAGGAATGGCTGCAAA 776
QY 726 GCACGAGGAGCCCAAGTATGTGGAACCGCACTGCGCTCTTCAGGCGCGGCGATGACTC 785
DB 777 GCACGAGGAGTCCCTGTATGTGTGAACCGCACTGAGCTCATGTCAAGGCGCTCCGAGCCA 836
QY 786 CAGTGTACACACCTCATGGGCTCTTGAGCCGAGACATGAATATATGTTACGA 845
DB 837 GTCTGTACCCATCTCATGGGCTCTTGAGCCCGAGACACGAATATGAGATCTCCG 896
QY 846 AGACCAACCAAGGACCCGACCTTGCGGAGATGACGAGCGCGCCCTGCAAGTGTGAG 905
DB 897 AGACCCCACTGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTGAG 956
QY 906 CAGGAACCCCGGGGCTTCTACTCTTCTGTGAGGAGGAGCGCGCATTTGACCAAGGTACCA 965
DB 957 CAGGAACCCCGCGGCTTCTACTCTTGTGTGAGGAGGCGCGCATTTGACCAAGGTACCA 1016
QY 966 TGACGCAAAAGTTATATGCACTGAGGCGATCATGTTTGAACAATGCCATCGCCAA 1025
DB 1017 TGAGGCTGTGCTTACAGGCACTGAGGCGGTATGATGACAGCCATTGAGAG 1076
QY 1026 GGCTAACGAGCTCACTAGCGAATGAGACAGCGTGATCTTGTGACTGACAGCACTCCCA 1085
DB 1077 GCGGGGCCAGCTCACAGGAGGAGACAGCGTGACCTCGTCAACCGCTGACCACTCCCA 1136
QY 1086 TGTCTTCTTTTGTGCTTACACTGCGTGGACCTCCATTTTCCGCTGCGCCCGG 1145
DB 1137 TGTCTTCTTTTGTGCTTACACTGCGTGGAGGAGCTCCATTTTCCGCTGCGCCCGAG 1196
QY 1146 CAAGGCTTGAACAGCAAGTCTTACACTTCCATCTTATGGAATGGCCCAAGCTATGC 1205
DB 1197 CAAGGCTGAGACAGCAAAAGCTTACACTTCTGTACGGCAATGGCCCGGCTACGT 1256
QY 1206 GCTTGGCGGGCTCGAGGCCGATTTAATGGCAGCAACGCGAAGAACCTCATACCG 1265
DB 1257 GTTCACTCAGGCGGTGCGACCAAGAGTGAATGAGCGAGAGCGGAGCCCGATTACCA 1316
QY 1266 GCAGCAGGCGCGCTGCCCCCTGGCTAGCGAGACCCAGGGGCGAAGACGTGGCGGT 1325
DB 1317 GCAGCAGGCGCGGTGCCCCCTGTCTGCTCGAGACCCAGGAGCGGAGAGCGGTGT 1376
QY 1326 CGCGGAGGCGCGCAGGCGCACTGTGTGACAGGCGTGCAGGAGAGACCTTGTGCGCA 1385
DB 1377 TGCGGCGGCGCGCAGGCGCACTGTGTGATGCTGTGACAGGAGCAGACTTGTGCGCA 1436
QY 1386 CATCATGCGCTTTGCGGGCTGCGTGAGCCCTACACCGACTGCAATCTGCC 1436
DB 1437 TGTCTATGCGCTTGTGCTGCTGTGAGCCCTACACGCGCTGCGAAGCTGCG 1487
RESULT 12
AAT27391
ID AAT27391 standard; DNA; 3076 BP.
XX
AC AAT27391;
XX
DT 23-SEP-1996 (first entry)
XX
DE Human IgG CH1-hinge-CH2 region-alkaline phosphatase fusion pXPD.
XX
KW alkaline phosphatase; label; antibody; IgG; H-chain; constant region;

| | | |
|------|---|---|
| KW | immunoglobulin gamma; fusion protein; chimera; immunoassay; E.coli; | |
| KW | xanthine-guanine phosphoribosyl transferase; ds. | |
| XX | | |
| OS | Homo sapiens. | |
| OS | Escherichia coli. | |
| OS | Synthetic. | |
| XX | | |
| FH | Key | Location/Qualifiers |
| FT | exon | 212..503 |
| FT | | /*tag= a |
| FT | | /note= "precise start position is unclear" |
| FT | exon | 892..936 |
| FT | | /*tag= b |
| FT | exon | 1055..2538 |
| FT | | /*tag= c |
| FT | | /note= "end position corresponds to termination codon; nucleotides 1111..2532 are derived from the alkaline phosphatase gene" |
| FT | CDS | 2618..3076 |
| FT | | /*tag= d |
| FT | | /product= "Ecogpt" |
| FT | | /note= "E.coli xanthine-guanine phosphoribosyl transferase gene" |
| XX | | |
| PN | JP08070875-A. | |
| XX | | |
| PD | 19-MAR-1996. | |
| XX | | |
| PF | 05-SEP-1994; 94JP-00211035. | |
| XX | | |
| PR | 05-SEP-1994; 94JP-00211035. | |
| XX | | |
| PA | (TOYJ) TOSOH CORP. | |
| XX | | |
| DR | WPI; 1996-203155/21. | |
| P-DR | P-PSDB; AAW03139, AAR91812. | |
| XX | | |
| PT | Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprises AP fused downstream of antibody heavy or light chain, useful as immunoassay reagent. | |
| PT | | |
| XX | | |
| PS | Example 1; Page 32-36; 44pp; Japanese. | |
| XX | | |
| CC | The gene coding for human alkaline phosphatase is fused downstream of a gene coding for either the variable and CH1 regions of an antibody heavy chain or an antibody light chain. Coexpression of the H- and L-chain sequences, one of which is fused to the AP gene, results in production of AP-labelled antibodies suitable for use in immunoassays. The present sequence is an insert from plasmid pXPD coding for human IgG heavy chain constant region sequences (CH1-hinge- CH2) fused to a partial AP-coding region; the insert also encodes the xanthine-guanine phosphoribosyl transferase from E.coli | |
| CC | | |
| XX | | |
| SQ | Sequence 3076 BP; 652 A; 993 C; 873 G; 558 T; 0 U; 0 Other; | |
| | Query Match 69.0%; Score 1018.2; DB 2; Length 3076; | |
| | Best Local Similarity 82.2%; Pred. No. 1.7e-237; | |
| | Matches 1170; Conservative 0; Mismatches 253; Indels 0; Gaps 0; | |
| QY | 6 CCTCATCCCAAGTGTGAGAGGAAAAACCCCGCTTCTGGAACCGCGAGGAGCCAGGCCCT 65 | |
| Db | 1110 CGTCATCCCAAGTGTGAGAGGAGAAACCCGCTTCTGGAACCGCGAGGAGCTGAGGCCCT 1169 | |
| QY | 66 TGATGTAGCCAAGAAGTTGCAGCCGATCCAGACAGCTGCCAAGAATGTCTCTTCTT 125 | |
| Db | 1170 GGAATCTGCAAGAAGCTGCAGCCATCCAGAAGTGCAGCAAGAACTCATCTCTTCTT 1229 | |
| QY | 126 GGGGGATGGATGGGGTGCTTACGCTGACAGCCACTCGGATCCTAAAGGGGAGATGAA 185 | |
| Db | 1230 GGGCGATGGGTTGGGGGTGCCACGGTGAACAGCACAGATCTTAAAGGGGAGAGAA 1289 | |
| QY | 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCCAGTTCCCATACGTGGCTGTTC 245 | |

| | | |
|----|--|--|
| Db | 1290 TGGCAAACTGGGCTGAGACGCCCCCTGGCCATGAGCCGCTTCCATACCTGGCTGTTC 1349 | |
| QY | 246 CAAGACATACAACGTGACAGACAGGTGCCAGACAGCGCAGCACTGCGCACTGCTTACTT 305 | |
| Db | 1350 CAAGACATACAATGTGACAGACAGGTGCCAGACAGCGCAGCACTGCGCACTGCTTACTT 1409 | |
| QY | 306 GTGTGGGCTCAAGGGCAACTACAGAACCATCGGTGTAAGTGACAGCCGCGCTTACAATCA 365 | |
| Db | 1410 GTGCGGGGTCAAGGCCCACTTCCAGACCATCGGCTTGAGTGACAGCCGCGCTTAAACA 1469 | |
| QY | 366 GTGCAACACGACACCGTGGGAATGAGGTCACGCTCTGTGATCAACCGGGCCAAAGAACAGG 425 | |
| Db | 1470 GTGCAACACGACACCGGGCAATGAGGTCACTCTCGTGATGAACCGGGCCAAAGAACAGG 1529 | |
| QY | 426 GAAGCCGTGGAGTGTGACCAACCAAGGCTGACATGCTCCCGCAGCCGCGGCTTA 485 | |
| Db | 1530 AAAGTCAGTAGAGTGTGACCAACCAAGGCTGACACGCGGTGACACGCTCGCAGCCGCACTTA 1589 | |
| QY | 486 CGCGCACACGCGTGAACCGGAACTGCTACTCAGACGCGGACCTGCTGATGACAGAA 545 | |
| Db | 1590 CGCACACACAGTGAACCGCACTGCTACTCAGATGCTGACATGCTGCTCAGCCGCGCA 1649 | |
| QY | 546 GAATGGCTGCCAGGACATCGCCGACACAGCTGCTTACAACATGATATTGACGTGATCCT 605 | |
| Db | 1650 GAGGGGTGCCAGGACATCGCCACTCAGCTCATCTCCAACATGACATGACGTGATCCT 1709 | |
| QY | 606 GGGTGAAGGCCGAATGTACATGTTTCTGAGGGGACCCAGACCCCTGAATACCGAGATGA 665 | |
| Db | 1710 TGGCGGAGGCCGCAAGTACATGTTTCCATGGGGACCCAGACCCCTGAGTACCGACTGA 1769 | |
| QY | 666 TGCCAGTGTGAATGAGTCCGGAAAGGACAAAGCAACTGTGTCAAGGAATGGCAGGCCAA 725 | |
| Db | 1770 TGCCAGCCAGAAATGAATCAGGCTGACCGGAAACCTGTGTCAAGGAATGGCTGGCAAA 1829 | |
| QY | 726 GCACCAAGGAGCCCAAGTATGTGTGAAACCGCACTGCGCTCTTCAGGCGCGCGATGACTC 785 | |
| Db | 1830 GCACCAAGGATGCTGTGATGTGTGAAACCGCACTGAGCTCATGACGGCGTCCCTGAGCCA 1889 | |
| QY | 786 CAGTGTAAACACACTCATGAGCTCTTTGAGCCGCGCAGACATGAAGTATATGTTTACAGCA 845 | |
| Db | 1890 GTCTGTGACCCATCTCATGAGGCTCTTTGAGCCGCGGAGACACGAATATGAGATCTCTCG 1949 | |
| QY | 846 AGACCACACCAAGACCCGACCTGGCGGAGATGACGGAAGCGGCCCTGCAAGTGTGAG 905 | |
| Db | 1950 AGACCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTGAG 2009 | |
| QY | 906 CAGGAACCCCGGGGCTTCTACTCTTCTGTGAGGAGGCGCGCATTGACCAAGCTTACCA 965 | |
| Db | 2010 CAGGAACCCCGGGGCTTCTACTCTTGTGTGAGGCGCGCGCATGACCAAGCTTATCA 2069 | |
| QY | 966 TGACGGCAAAAGCTTATATGCACTGACTGAGGCGCATGTGTTGACAAATGCCATGCGCAA 1025 | |
| Db | 2070 TGAGGGTGTGCTTACAGGCAAGTCACTGAGGCGGTATGTTGACAGCGCAATTGAGAG 2129 | |
| QY | 1026 GACTTAAGAGCTCACTAGCGAACTGACACAGCTGATCTTGTCACTGACAGCACTCCCA 1085 | |
| Db | 2130 GAGCGGCACAGCTCACAGCGAGAGAGACACGCTGACCTCGTCAACGCTGACCACTCCCA 2189 | |
| QY | 1086 TGTCTTCTTTTGTGTGCTACACACTGCGTGGGACTTCCATTTTCGCTGTGGCCCCGG 1145 | |
| Db | 2190 TGTCTTCTCTTTGTGTGCTACACCTTGCAGAGGAGCTCCATCTTCGGGTGGCCCCAG 2249 | |
| QY | 1146 CAAGCCTTAGACAGCAAGTCTTACACCTCCATCTCTATGGCAATGGCCAGGCTATGC 1205 | |
| Db | 2250 CAAGCCTCAGACAGCAAGCTTACACGTCATCTCTGTAAGGCAATGGCCCGGCTACGT 2309 | |
| QY | 1206 GCTTGGCGGGGCTCAGAGGCCCGATGTTAATGGGACACAAAGCGAGGAACCTTCATACCG 1265 | |
| Db | 2310 GTTCAACTCAGGCGGTGGAACAGAGTGAATGAGAGCGAGAGCGGAGCCCGGATTAACA 2369 | |
| QY | 1266 GCAGCAGGCGGCGCTGCCCCCTGGCTAGCGAGACCCACGGGGCGGAAGACGTGCGGTGT 1325 | |
| Db | 2370 GCAGCAGGCGGCGGTGCCCTGTGTGTGTCGAGACCCACGAGGCGGAAGACGTGCGGTGT 2429 | |


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Qy      1326  CGCGCGAGGCCCCGACGCGACTGTGTGCACGGCGGTGCAGAGAGACCTTCGTGGCGCA 1383
          |||||
Db      2430  TCGCGCGCGCCCGCAGCGCGCACTGTGTGCATGTGTGTGCAGAGACGAGCTTCGTAGCGCA 2489
          |||||

Qy      1386  CATCATGGCCTTTGCGGCGTGCCTGAGCCCTACACCGACTGC 1428
          |||||
Db      2490  TGTTCATGGCCTTCGCTGCTGTGTGAGCCCTACACGCGCTGC 2532
          |||||

RESULT 13
AAT27392
ID      AAT27392 standard; DNA; 3127 BP.
XX
AC      AAT27392;
XX
DT      23-SEP-1996 (first entry)
XX
DE      Human Igg CH1-hinge-CH2 region-alkaline phosphatase fusion pXPE.
XX
KW      alkaline phosphatase; label; antibody; IgG; H-chain; constant region;
KW      immunoglobulin gamma; fusion protein; chimera; immunoassay; E.coli;
KW      xanthine-guanine phosphoribosyl transferase; ds.
XX
OS      Homo sapiens.
OS      Escherichia coli.
OS      Synthetic.
XX

Key      Location/Qualifiers
FH      exon                212..503
FT      /*tag= a
          /note= "precise start position is unclear"
FT      exon                892..936
FT      /*tag= b
          /note= "2589
FT      exon                1055..2589
FT      /*tag= c
          /note= "end position corresponds to termination codon;
FT      CDS                nucleotides 1162..2583 are derived from the alkaline
          phosphatase gene"
          2669..3127
          /*tag= d
          /product= "Ecogpt"
          /note= "E.coli xanthine-guanine phosphoribosyl
          transferase gene"
XX
PN      JP08070875-A.
XX
PD      19-MAR-1996.
XX
PF      05-SEP-1994;      94JP-00211035.
XX
PR      05-SEP-1994;      94JP-00211035.
XX
PA      (TOYJ ) TOSOH CORP.
XX
DR      WPI; 1996-203155/21.
DR      P-PSDB; AAW03141, AAR91812.
XX
PT      Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprises
PT      AP fused downstream of antibody heavy or light chain, useful as
PT      immunoassay reagent.
XX
PS      Example 1; Page 36-40; 44pp; Japanese.
XX

The gene coding for human alkaline phosphatase is fused downstream of a
CC gene coding for either the variable and CH1 regions of an antibody heavy
CC chain or an antibody light chain. Coexpression of the H- and L-chain
CC sequences, one of which is fused to the AP gene, results in production of
CC AP-labelled antibodies suitable for use in immunoassays. The present
CC sequence is an insert from plasmid pXPE coding for human IgG heavy chain
CC constant region sequences (CH1-hinge-CH2) fused to a partial AP-coding
CC region; the insert also encodes the xanthine-guanine phosphoribosyl
CC transferase from E.coli

```

| XX | Sequence | 3127 BP; 656 A; 1002 C; 900 G; 569 T; 0 U; 0 Other; |
|----------------------------|--|---|
| Query Match | 69.0%; | Score 1018.2; DB 2; Length 3127; |
| Best Local Similarity | 82.2%; | Pred. No. 1.8e-237; |
| Matches 1170; Conservative | 0; Mismatches 253; Indels 0; Gaps 0; | |
| QY | 6 CCTCATCCAGCTGAGAGGAGAAAACCCGCTTCTGGAAACCGCAGGCGCCAGGCCCT | 65 |
| Db | 1161 CGTCATCCAGCTGAGAGGAGAGAAACCCGCTTCTGGAAACCGCAGGCGCCAGGCCCT | 1220 |
| QY | 66 TGATGTAGCCAAAGAGTTGACGCCGATCCAGACAGCTGCGCAAGATGTCATCTTCTT | 125 |
| Db | 1221 GGATGCTGCCAAGAGAGTGCAGGCCCATCCAGAGGTGCGCAAGAACTCATCTTCTT | 1280 |
| QY | 126 GGGGGATGGATGGGGGTGCCCTACGGTGAACAGCCACTCGATCCTAAAGGGGAGATGAA | 185 |
| Db | 1281 GGGCGATGGGTGGGGGTGCCCAAGGTGACAGCCACAGGATCCTAAAGGGGAGAGAA | 1340 |
| QY | 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGSAACCAAGTTCCCATACGTGGCTGTG | 245 |
| Db | 1341 TGGCAAACTGGGGCTGAGACGCCCTGGCCATGSAACCGCTTCCCATACCTGGCTGTG | 1400 |
| QY | 246 CAAGACATACAACGTGGAACAGACAGGTGCCAGACGCGCAGGCACTGCGCATGCTTACT | 305 |
| Db | 1401 CAAGACATACAATGTGGACAGACAGGTGCCAGACGCGCAGGCACTGCGCATGCTTACT | 1460 |
| QY | 306 GTGTGGGTCAAGGCACTACAGAACCATCGGTGAAGTGACAGCGCCGCTTACAATCA | 365 |
| Db | 1461 GTGCGGGGTCAAGGCCCAACTTCCAGACCATCGGCTTGAAGTGACAGCGCCGCTTAA | 1520 |
| QY | 366 GTGCAACACGACACGTGGGAATGAGGTCAAGTCTGTGATCAACCGGGCCAAAGAACAG | 425 |
| Db | 1521 GTGCAACACGACACGCGGCAATGAGTCAATCTCGTATGAACCGGGCCAAAGAACAG | 1580 |
| QY | 426 GAAGGCGGTGGAGTGTGTGACCAACCAAGGTGACAGCATGCTCCCCAGCGGGCTTA | 485 |
| Db | 1581 AAAGTCAGTAGAGTGTGTGACCAACCAAGGTGACAGCATGCTCCCCAGCGGGCTTA | 1640 |
| QY | 486 CGGCACACCGGTGAACCGAACTGTACTCAGACGCCGACCTGCTGTATGCAAGAA | 545 |
| Db | 1641 CGCACACACAGTGAACCGCAACTGTACTCAGATGTGACATGCTGCTGACGCCGCA | 1700 |
| QY | 546 GAATGCTGCCAGGACATCGCCGACAGCTGTGCTTACAACATGGATATTGACGTGATCCT | 605 |
| Db | 1701 GGAGGGTGCAGGACATCGCCACTCAGCTCATCTCCAACATGACATTTGACGTGATCCT | 1760 |
| QY | 606 GGGTGGAGGCCGAATGTACATGTTTCTGAGGGGACCCAGACCCCTGAATACCAGATGA | 665 |
| Db | 1761 TGGCGGAGGCCGCAATGATGTTTCCCATGGGGACCCAGACCCCTGAATACCAGTGA | 1820 |
| QY | 666 TGCCAGTGTGAATGAGTCCGGAAGGACAAAGCAACCACTGTGTGAGGAATGGAGGCCAA | 725 |
| Db | 1821 TGCCAGCCAGAAATGAATCAGGCTGGAACGGGAAGAACTGTGTGAGGAATGGCTGCAAA | 1880 |
| QY | 726 GCACCAAGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCCTCAGGGCGCGATGACTC | 785 |
| Db | 1881 GCACCAAGGAGTGTGTGTGTGTGAACCGCACTGAGCTCATGCAAGGCGTCCCTGAGCCA | 1940 |
| QY | 786 CAGTGTAAACACACTCATGGGCTCTTTGAGCCGCGACAGCATGAAGTATTAATGTTCA | 845 |
| Db | 1941 GTCTGTGACCCATCTCATGGGCTCTTTGAGCCGCGAGACAGAAATATGAGATCTTCCG | 2000 |
| QY | 846 AGACCAACCAAGAACCCGACCCCTGGCGGAGATGAACGAGCGCGCTGCAAGTGTGAG | 905 |
| Db | 2001 AGACCCCAACCTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTGAG | 2060 |
| QY | 906 CAGGAACCCCGGGGCTTCTACCTCTTCTGTGAGAGGAGCGCGCATTTGAACCGGTCA | 965 |
| Db | 2061 CAGGAACCCCGCGGCTTCTACCTCTTGTGTGAGGCGCGCGCATGCAACCATGTCTATCA | 2120 |
| QY | 966 TGACGGCAAAAGCTTATATGGCACTGACTGAGCGCATGTGTTGACAATGCGCAAC | 1025 |

Db 2121 TGAAGGTGTGCTTACAGGACAGTCACTGAGGCGGTCACTGTTGACAGACGCCATTGAGAG 2180
QY 1026 GGCTAACGAGCTCACTAGCGAACTGGAACAAGCTGATCCTTGTCACTGACAGACCACTCCCA 1085
Db 2181 GCGGGCCAGCTCACACAGAGAGACAGCTGACCTCGTCACTGACCGCTGACCACTCCCA 2240
QY 1086 TGTCTTCTTTTGTGTGCTACACACTGCGTGGAGACCTCCATTTTCGGTCTGCCCCCGG 1145
Db 2241 TGTCTTCTCCTTTGTGTGCTACACCTTGCAGAGGAGCTCCATCTTCGGGTGCCCCCAG 2300
QY 1146 CAAGGCTTGAACAGACAGCAAGTCCCTACACCTCCATCCTCTATGGCAATGGCCCCAGGCTATGC 1205
Db 2301 CAAGGCTCAGGACAGCAAGCAAGCTTACACCTCCATCCTGTATCGGCAATGGCCCCGGCTACGT 2360
QY 1206 GCTTGGCGGGGGCTCGAGGCCCCGATGTTAATGGCAGCACAAAGCGAGGAACCTCATACCG 1265
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QY 1266 GCAGCAGCGCGCGCTGCCCCCTGCTAGCGAGACCCACGCGGGCGAAGAGCTGGCGGTGT 1325
Db 2421 GCAGCAGCGCGCGGTGCCCCCTGTCTGTCCAGACCCACGAGGCGAAGAGCTGGCGGTGT 2480
QY 1326 CGCGCGAGCGCGCGAGCGCACCTGTGTCAACGCGGTGACAGAGAGACCTTGTGTGCGCA 1385
Db 2481 TCGCGCGCGCGCGCGAGCGCACCTGTGTGATGTGTGACAGAGACAGCTTGTGTGCGCA 2540
QY 1386 CATCATGGCCTTTGCGGCTGCGTGAAGCCCTACACCGACTGC 1428
Db 2541 TGTCAATGGCCTTCGCTGCTGTGTGAGCCCTACACGCGCTGC 2583

RESULT 14
AAT27393
ID AAT27393 standard; DNA; 2372 BP.
AC AAT27393;
XX 23-SEP-1996 (first entry)
DT Human IgG CHI-hinge-linker-alkaline phosphatase fusion pCH1P1.
DE
XX
KW alkaline phosphatase; label; antibody; IgG; H-chain; constant region;
KW immunoglobulin gamma; fusion protein; chimera; immunoassay; ds.
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT exon 212..503
FT /tag= a
FT /note= "precise start position is unclear"
FT exon 892..2372
FT /tag= b
FT /transl_except= pos:948..950, aa:Ser
FT /transl_except= pos:951..953, aa:Thr
FT /note= "end position corresponds to termination codon;
FT nucleotides 906..956 encode a 17 amino acid linker and
FT nucleotides 957..2366 are derived from the alkaline
FT phosphatase gene"
XX
PN JP08070875-A.
XX
PD 19-MAR-1996.
XX
PF 05-SEP-1994; 94JP-00211035.
XX
PR 05-SEP-1994; 94JP-00211035.
XX
PA (TOYO) TOSOH CORP.
XX
XX
DR WPI; 1996-203155/21.
DR P-PSDB; AAW03141.
XX

PT Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprises
PT AP fused downstream of antibody heavy or light chain, useful as
PT immunoassay reagent.
XX
PS Example 1; Page 40-43; 44pp; Japanese.
XX
CC The gene coding for human alkaline phosphatase is fused downstream of a
CC gene coding for either the variable and CHI regions of an antibody heavy
CC chain or an antibody light chain. Coexpression of the H- and L-chain
CC sequences, one of which is fused to the AP gene, results in production of
CC AP-labelled antibodies suitable for use in immunoassays. The present
CC sequence is an insert from plasmid pCH1P-1 coding for human IgG heavy
CC chain constant region sequences (CHI-hinge) fused to a partial AP-coding
CC region via a 17 amino acid linker
XX
SQ Sequence 2372 BP; 481 A; 781 C; 710 G; 400 T; 0 U; 0 Other;

Query Match 68.3%; Score 1008.8; DB 2; Length 2372;
Best Local Similarity 82.2%; Pred. No. 3.1e-235;
Matches 1160; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

QY 17 CTGAGGAGGAAACCCCGCTTCTGGAACCGCCAGGACGCCAGGCCCTTGATGTAACCA 76
Db 955 CTGAGGAGGAAACCCCGCTTCTGGAACCGCCAGGACGCTGAGGCCCTGATGTGCCA 1014
QY 77 AGAAGTTGACGCCGATCCAGACAGCTGCCAAGAAATGTCATCTTCTTGGGGGATGGGA 136
Db 1015 AGAAGCTGACGCCCATCCAGAAAGGTGCGCAAGAACTCATCTTCTTGGCGATGGGT 1074
QY 137 TGGGGGTGCTTACGGTGACAGCCACTCGGATCTTAAAGGGGAGATGAGCAAACTGG 196
Db 1075 TGGGGGTGCCCCACGGTGACAGCCAGAGATCTTAAAGGGGAGATGAGCAAACTGG 1134
QY 197 GACCTGAGACACCCCTGGCCATGAGACCACTGATCCCATACGTGGCTGTGCCAAGACATACA 256
Db 1135 GGCCTGAGACGCCCCCTGGCCATGAGACCGCTTCCCATACCTGGCTGTGCCAAGACATACA 1194
QY 257 ACGTGGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTACCTGTGTGGGTCA 316
Db 1195 ATGTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTGTGTGGGTCA 1254
QY 317 AGGCACTACAGAACCATCGGTGTAAGTGACAGCGCGCCGCTACAATCAGTGCAACACGA 376
Db 1255 AGGCCAATTCAGACCATCGGCTTGAGTGACGCGCGCTTTAAACAGTGCAACACGA 1314
QY 377 CACGTGGGAATGAGGTCAAGTCTGTGATCAACCGGGCCAAAGAACAGGAGCGGTGG 436
Db 1315 CACGCGCAATGAGGTCAATCTCGTGATGAACCGGGCCAAAGAACAGGAGTCAAGTAG 1374
QY 437 GAGTGTGACCAACCAAGGTGACAGATGCTTCCCAAGCGGGGCTTACCGGCACACAGG 496
Db 1375 GAGTGTGACCAACCAAGGTGACAGATGCTTCCCAAGCGGGGCTTACCGGCACACAGG 1434
QY 497 TGAACCGAACTGTACTCAGACGCGCACTGCTGATGACACAGAAATGGCTGCC 556
Db 1435 TGAACCGCACTGTACTCAGATGCTGACATGCTGCTCAGCCCCGACAGAGGGGTGCC 1494
QY 557 AGGACATGCGCGCACAGCTGCTTACACATGATATTTGACGTGATCCTGGTGGAGGCC 616
Db 1495 AGGACATGCGCACATGCTATCTCCAACATGACATTTGACGTGATCCTGGCGGAGGCC 1554
QY 617 GAATGTACATGTTTCTGAGGGGAGACCCAGACCTGAATACCCAGATGATGCAAGTGTGA 676
Db 1555 GCAAGTACATGTTTCTGAGGGGAGACCCAGACCTGAATACCCAGATGATGCAAGTGTGA 1614
QY 677 ATGAGTCCGGAAGCAAGCAAGAACTGTGTCAGGAATGGCAGGCAAGCAAGGAG 736
Db 1615 ATGGAATCAGGCTGAGCGGAAGAACTGTGTCAGGAATGGCTGCAAGCAAGGAGT 1674
QY 737 CCCAGTATGTGTGAACCGCACTGCGCTCTCAGGGCGCGATGACTCAAGTGAACAC 796
Db 1675 CCGTGTATGTGTGAACCGCACTGAGCTCATGACAGCGGTCCCTGACCAAGTCTGTGAACC 1734

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OM nucleic - nucleic search, using sw model

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(without alignment)
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Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------------------------|
| 1 | 1462 | 99.1 | 1798 | 4 | US-09-305-681-1 Sequence 1, Appli |
| 2 | 1338.2 | 90.7 | 2460 | 4 | US-09-305-681-3 Sequence 3, Appli |
| 3 | 1327 | 89.9 | 2542 | 4 | US-09-305-681-5 Sequence 5, Appli |
| 4 | 1002.4 | 67.9 | 1956 | 3 | US-08-867-352-20 Sequence 20, Appli |
| 5 | 1000.8 | 67.8 | 4989 | 4 | US-09-693-011-12 Sequence 12, Appli |
| 6 | 1000.8 | 67.8 | 5083 | 4 | US-09-693-011-11 Sequence 11, Appli |
| 7 | 1000.8 | 67.8 | 5928 | 4 | US-09-932-581-25 Sequence 25, Appli |
| 8 | 1000.8 | 67.8 | 6314 | 4 | US-09-693-011-10 Sequence 10, Appli |
| 9 | 1000.8 | 67.8 | 6408 | 4 | US-09-693-011-9 Sequence 9, Appli |
| 10 | 1000.8 | 67.8 | 7076 | 4 | US-09-837-863-20 Sequence 20, Appli |
| 11 | 1000.8 | 67.8 | 7076 | 4 | US-09-837-863-21 Sequence 21, Appli |
| 12 | 1000.8 | 67.8 | 7092 | 4 | US-09-837-863-19 Sequence 19, Appli |
| 13 | 1000.8 | 67.8 | 7092 | 4 | US-09-837-863-22 Sequence 22, Appli |
| 14 | 1000.8 | 67.8 | 7573 | 4 | US-09-837-863-27 Sequence 27, Appli |
| 15 | 1000.4 | 67.8 | 4951 | 2 | US-08-752-307B-1 Sequence 1, Appli |
| 16 | 1000.4 | 67.8 | 4951 | 3 | US-09-707-802-1 Sequence 1, Appli |
| 17 | 1000.4 | 67.8 | 4951 | 3 | US-09-991-326-1 Sequence 1, Appli |
| 18 | 999.2 | 67.7 | 13910 | 3 | US-09-263-933-1 Sequence 1, Appli |
| 19 | 999.2 | 67.7 | 13910 | 3 | US-09-263-933-8 Sequence 8, Appli |
| 20 | 999.2 | 67.7 | 13910 | 3 | US-09-263-933-15 Sequence 15, Appli |
| 21 | 999.2 | 67.7 | 13910 | 4 | US-09-919-901-1 Sequence 1, Appli |
| 22 | 999.2 | 67.7 | 13910 | 4 | US-09-919-901-8 Sequence 8, Appli |
| 23 | 999.2 | 67.7 | 13910 | 4 | US-09-919-901-15 Sequence 15, Appli |
| 24 | 999.2 | 67.7 | 13910 | 4 | US-10-191-966-1 Sequence 1, Appli |
| 25 | 999.2 | 67.7 | 13910 | 4 | US-10-191-966-8 Sequence 8, Appli |
| 26 | 999.2 | 67.7 | 13910 | 4 | US-10-191-966-15 Sequence 15, Appli |
| 27 | 982.2 | 66.5 | 8299 | 1 | US-08-462-014-2 Sequence 2, Appli |

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| 28 | 982.2 | 66.5 | 8299 | 3 | US-08-923-137-3 | Sequence 3, Appli |
| 29 | 982.2 | 66.5 | 8299 | 3 | US-08-973-334-5 | Sequence 5, Appli |
| 30 | 982.2 | 66.5 | 8299 | 3 | US-09-563-869A-5 | Sequence 5, Appli |
| 31 | 978.6 | 66.3 | 1467 | 3 | US-09-330-317B-17 | Sequence 17, Appli |
| 32 | 978.6 | 66.3 | 1467 | 4 | US-09-808-589A-17 | Sequence 17, Appli |
| 33 | 262.8 | 17.8 | 5399 | 1 | US-08-368-071-9 | Sequence 9, Appli |
| 34 | 262.8 | 17.8 | 5399 | 1 | US-08-458-181-9 | Sequence 9, Appli |
| 35 | 262.8 | 17.8 | 5399 | 5 | PCT-US93-02172-9 | Sequence 9, Appli |
| 36 | 139.4 | 9.4 | 5293 | 4 | US-09-900-708-1 | Sequence 1, Appli |
| 37 | 134.8 | 9.1 | 884 | 4 | US-09-270-767-11859 | Sequence 11859, A |
| 38 | 120.8 | 8.2 | 220 | 3 | US-09-263-933-22 | Sequence 22, Appli |
| 39 | 120.8 | 8.2 | 220 | 4 | US-09-919-901-22 | Sequence 22, Appli |
| 40 | 120.8 | 8.2 | 220 | 4 | US-10-191-966-22 | Sequence 22, Appli |
| 41 | 114.8 | 7.8 | 1074 | 4 | US-09-270-767-13264 | Sequence 13264, A |
| 42 | 92.2 | 6.2 | 709 | 4 | US-09-270-767-1586 | Sequence 1586, Ap |
| 43 | 92.2 | 6.2 | 709 | 4 | US-09-270-767-16868 | Sequence 16868, A |
| 44 | 76.8 | 5.2 | 200 | 4 | US-09-900-708-4 | Sequence 4, Appli |
| 45 | 67.4 | 4.6 | 1368 | 2 | US-08-738-172-3 | Sequence 3, Appli |

ALIGNMENTS

RESULT 1
US-09-305-681-1
; Sequence 1, Application US/09305681
; Patent No. 6406899
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Highly active alkaline phosphatase
; NUMBER OF SEQUENCES: 54
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/305,681
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1798 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; US-09-305-681-1

Query Match 99.1%; Score 1462; DB 4; Length 1798;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 6 | CCTCATCCAGCTGAGAGGAAACCCGCTTCTGGAACCGCCAGCCAGGCCCT | 65 |
| DB | 107 | CCTCATCCAGCTGAGAGGAAACCCGCTTCTGGAACCGCCAGCCAGGCCCT | 166 |
| QY | 66 | TGATGTAGCCAGAGAGTTGACGCCGATCCAGACAGCTGCCAAGATGTCATCTT | 125 |
| DB | 167 | TGATGTAGCCAGAGAGTTGACGCCGATCCAGACAGCTGCCAAGATGTCATCTT | 226 |
| QY | 126 | GGGGATGGATGGGGGTGCTTACGGTGAACAGCCACTGGATCTTAAAGGGCAGATGAA | 185 |
| DB | 227 | GGGGATGGATGGGGGTGCTTACGGTGAACAGCCACTGGATCTTAAAGGGCAGATGAA | 286 |
| QY | 186 | TGGCAACTGGAGCTGAGACACCCCTGGCCATGAGACCAAGTCCATACGTGGCTGTG | 245 |
| DB | 287 | TGGCAACTGGAGCTGAGACACCCCTGGCCATGAGACCAAGTCCATACGTGGCTGTG | 346 |
| QY | 246 | CAAGACATACAGCTGAGACAGAGGTGCCAGACAGCGCAGGCACTGCACTGCTACCT | 305 |
| DB | 347 | CAAGACATACAGCTGAGACAGAGGTGCCAGACAGCGCAGGCACTGCACTGCTACCT | 406 |

| | | | |
|----|------|--|------|
| QY | 306 | GTGTGGGGTCAAGGGCACTTACAGAACCATCGGTGTAAGTGAAGCCGCCGCTTACAATCA | 365 |
| Db | 407 | GTGTGGGGTCAAGGGCAACTACAGAACCATCGGTGTAAGTGAAGCCGCCGCTTACAATCA | 466 |
| QY | 366 | GTGCAACACGACACGTGGGAATGAGGTCAAGTCTGTGATCAACGGGCCAAGAAAGCAGG | 425 |
| Db | 467 | GTGCAACACGACACGTGGGAATGAGGTCAAGTCTGTGATCAACGGGCCAAGAAAGCAGG | 526 |
| QY | 426 | GAAGGCCGTGGAGTGTGACCAACCAAGGGTGCAGCATGCTCCCCAGCCGGGGCTTA | 485 |
| Db | 527 | GAAGGCCGTGGAGTGTGTGACCAACCAAGGGTGCAGCATGCTCCCCAGCCGGGGCTTA | 586 |
| QY | 486 | CGCGCACACGGTGAAACCGAAACTGGTACTCAGACGCCGACCTGCTGTATGCACAGAA | 545 |
| Db | 587 | CGCGCACACGGTGAAACCGAAACTGGTACTCAGACGCCGACCTGCTGTATGCACAGAA | 646 |
| QY | 546 | GAATGGCTGCCAGGACATCGCCGCAAGCTGCTTACAACAATGGAATATTGACGTGATCCT | 605 |
| Db | 647 | GAATGGCTGCCAGGACATCGCCGCAAGCTGCTTACAACAATGGAATATTGACGTGATCCT | 706 |
| QY | 606 | GGGTGGAGGCCGAATGTACATGTTTCTGTAGGGGAGCCCGCAGACCTGTAATACCAAGATGA | 665 |
| Db | 707 | GGGTGGAGGCCGAATGTACATGTTTCTGTAGGGGAGCCCGCAGACCTGTAATACCAAGATGA | 766 |
| QY | 666 | TGCCAGTGTGAATGAGTCCGGAAGGACAAAGCAGAAACCTGGTGCAGGAATGGCAGGCCAA | 725 |
| Db | 767 | TGCCAGTGTGAATGAGTCCGGAAGGACAAAGCAGAAACCTGGTGCAGGAATGGCAGGCCAA | 826 |
| QY | 726 | GCACCAAGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCTTCAAGCGGCCGATGACTC | 785 |
| Db | 827 | GCACCAAGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCTTCAAGCGGCCGATGACTC | 886 |
| QY | 786 | CAGTGTAAACACACTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTCAAGCA | 845 |
| Db | 887 | CAGTGTAAACACACTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTCAAGCA | 946 |
| QY | 846 | AGACCAACACCAAGGACCCGACCCCTGGCGGAGATGACGAGGGCGCCCTGCAGTGTGAG | 905 |
| Db | 947 | AGACCAACACCAAGGACCCGACCCCTGGCGGAGATGACGAGGGCGCCCTGCAGTGTGAG | 1006 |
| QY | 906 | CAGGAAACCCCGGGGCTTCTAATTCTTGTGAGGAGGAGCGGCATTGACCAAGTCAACCA | 965 |
| Db | 1007 | CAGGAAACCCCGGGGCTTCTAATTCTTGTGAGGAGGAGCGGCATTGACCAAGTCAACCA | 1066 |
| QY | 966 | TGACGGCAAAAGCTTATATGGCACTGACGTAGCGATCATGTTTGACAATGCCATCGCCAA | 1025 |
| Db | 1067 | TGACGGCAAAAGCTTATATGGCACTGACGTAGCGATCATGTTTGACAATGCCATCGCCAA | 1126 |
| QY | 1026 | GGCTTAACGAGCTCACTAGCCAACTGGACACGCTGATCTCTTGTCACTGCAGACCACTCCCA | 1085 |
| Db | 1127 | GGCTTAACGAGCTCACTAGCCAACTGGACACGCTGATCTCTTGTCACTGCAGACCACTCCCA | 1186 |
| QY | 1086 | TGTCCTTCTTTTGTGTGCTACACACTGCGTGGGACCTCCATTTTCGCTGCGCCCGG | 1145 |
| Db | 1187 | TGTCCTTCTTTTGTGTGCTACACACTGCGTGGGACCTCCATTTTCGCTGCGCCCGG | 1246 |
| QY | 1146 | CAAGCCTTAGACAGCAAGTCTTACACTCTCCATCTCTAATGGCAATGGCCAGGCTATGC | 1205 |
| Db | 1247 | CAAGCCTTAGACAGCAAGTCTTACACTCTCCATCTCTAATGGCAATGGCCAGGCTATGC | 1306 |
| QY | 1206 | GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGCACAAAGGAAACCTCATATCCG | 1265 |
| Db | 1307 | GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGCACAAAGGAAACCTCATATCCG | 1366 |
| QY | 1266 | GCAGCAGGCGGCGGTGCCCTGTGCTAGCGAGACCAACCGGGCGAAAGACGTGGCGGTGTT | 1325 |
| Db | 1367 | GCAGCAGGCGGCGGTGCCCTGTGCTAGCGAGACCAACCGGGCGAAAGACGTGGCGGTGTT | 1426 |
| QY | 1326 | CGCGCGAGGCCCGCAGCGCACTGTGTGACGCGCGTGCAGAGGAGAACCTTCTGTGCGCA | 1385 |
| Db | 1427 | CGCGCGAGGCCCGCAGCGCACTGTGTGACGCGCGTGCAGAGGAGAACCTTCTGTGCGCA | 1486 |
| QY | 1386 | CATCATGGCCTTTGCGGGCTGTGAGACCTTACACCGCATGTCAATCTGCCAGCCCCCGC | 1445 |

Db 1487 CATCATGGCCTTTGGGGGTGCGTGAGGCCCTACACGACTGCAATCTGCCAGCCCCCGC 1546

QY 1446 CACCGCCACCAGCATCCCCGAC 1467

Db 1547 CACCGCCACCAGCATCCCCGAC 1568

RESULT 2

US-09-305-681-3
; Sequence 3, Application US/09305681

GENERAL INFORMATION:

APPLICANT: Highly active alkaline phosphatase
TITLE OF INVENTION: Highly active alkaline phosphatase

```

; NUMBER OF SEQUENCES: 54
; COMPUTER READABLE FORM:
;

```

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;
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
ORDERING SYSTEM: 800-800-4400

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
: :
: CURRENT APPLICATION DATA

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CORRENI APPLICATION DATA:
APPLICATION NUMBER:  US/09/305,681
FILING DATE:

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CLASSIFICATION: INFORMATION FOR SEO ID NO: 3

SEQUENCE CHARACTERISTICS:
LENGTH: 2460 base pairs

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; TYPE: nucleotide
; STRANDEDNESS: single strand
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; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA

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US-09-305-681-3

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|----------------------------|--------|----------------|-----------|--------------|
| Query Match | 90.7%; | Score 1338.2; | DB 4; | Length 2460; |
| Best Local Similarity | 94.4%; | Pred. No. 0; | | |
| Matches 1388; Conservative | 0; | Mismatches 83; | Indels 0; | Gaps 0; |

| | | | | |
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| OY | | 6 | CCTCATCCCAAGCTGAGAGGAAAAACCCCCCTTCTTGAAACCGGCAGGCCAGCCCAGGCCCT | 65 |
| Db | | 122 | CTTCATCCCAAGTTGAGAGGAAGAACCCCGCCTTCTTGAAACCGGCAGGCCAGGCCAGGCCCT | 181 |
| OY | | 66 | TGATGTAGCCAAGAAGTTGCAGCCGATCCAGACAGCTGCAAGATGTATCTTCTT | 125 |
| Db | | 182 | TGATGTGCTAAGAAGCTGCAGCCCATCCAGAAAGCCGCAAGATGTATCTTCTT | 241 |
| OY | | 126 | GGGGGATGGGATGGGGGTGCCCTACGGTGACAGCCACTCCGATCCTAAGGGGAGATGAA | 185 |
| Db | | 242 | GGGAGATGGGATGGGGGTGCCCTACGGTGACAGCCACTCCGATCTGAAGGGGAGATGAA | 301 |
| OY | | 186 | TGGCAAACCTGGGACCTGAGACAACCCCTGGCCATGACCACTTCCCATACGTGGCTCTGTC | 245 |
| Db | | 302 | TGACAAAGCTGGGACCTGAGACAACCCCTGGCCATGACCACTTCCCATACGTGGCTCTGTC | 361 |
| OY | | 246 | CAAGACATAACAAGTGCACAGAGTGCACAGCGCAGGCACTGCCACTGCCCTACT | 305 |
| Db | | 362 | CAAGACATAACAAGTGCACAGAGTGCACAGCGCAGGCACTGCCACTGCCCTACT | 421 |
| OY | | 306 | GTTGGGGTCAAGGGCACTACAGAACCATCGGTGTAAGTGCAGCCGCCGCTACAATCA | 365 |
| Db | | 422 | GTTGGGGTCAAGGGCACTACAGAACCATCGGTGTAAGTGCAGCCGCCGCTACAATCA | 481 |
| OY | | 366 | GTCAACACGACACGTTGGGAATGAGGTCAAGTCTGTGATCAACC GGCCAAAGAAAGCAGG | 425 |
| Db | | 482 | GTCAACACGACACGTTGGGAATGAGGTCAAGTCTGTGATGAAACGGGCCAAGAAAGCAGG | 541 |
| OY | | 426 | GAAAGCCGTGGAGTGTGTGACCAACCACAGGGTGCAGATGCTCCCAAGCCGGGGCTTA | 485 |
| Db | | 542 | GAAAGCCGTGGAGTGTGTGACCAACCACAGGGTGCAGATGCTCCCAAGCCGGGGCTTA | 601 |
| OY | | 486 | CGCGCACACGGGTGAACCGAAACTGTACTCAGACCGCCGCACTGCTGTGATGCACAGAA | 545 |
| Db | | 602 | TGCACACACGGGTGAACCGGTGACTGTACTCAGACCGCCGCACTGCTGTGATGCACAGAC | 661 |

| | | | | | | |
|----|------|-----|---------------------------|---------------------------------------|------------------------------|-----|
| QY | 546 | GAA | TGGCTGCCAGGACATCGCCGCA | CAGCTG | GTCTACAACATGATATTGACGTGATCCT | 605 |
| Db | 662 | GTA | TGGCTGCCAGGACATCGCCACACA | CACTGGTCAACAACATGATATTGACGTGATCCT | 721 | |
| QY | 606 | GCG | TGAGGCGCCGAATGTACATGTTTCT | TGAGGGGACCCGAGACCTTGAATACCAGATGA | 665 | |
| Db | 722 | GGG | TGAGGAGGCCGAAGTACATGTTTCT | TGAGGGGACCCGAGACCTTGAATACCAGAGCA | 781 | |
| QY | 666 | TG | CAAGTGTGATGAGTCCGGAAAGACA | AGCAGAACCTGGTGCAGGAATGGCAGGCCAA | 725 | |
| Db | 782 | TG | CAAGTGTGATGAGTCCGGAAAGACA | AGCAGGAATCTGGTGCAGGAATGGCAGGCCAA | 841 | |
| QY | 726 | GCA | CCAGGGAGCCCAAGTATGTGTGAA | CCGCACTGCGCTCTTCAGGCGGCCGATGATC | 785 | |
| Db | 842 | GCA | CCAGGGAGCCCAAGTATGTGTGAA | CCGCAAGAGCTCTTCAGGCGGCCAATGATC | 901 | |
| QY | 786 | CAG | TGTAAACACACCTCATGGGCTTTTG | AGCCGCGACAGACATGAAGTATATGTTACGA | 845 | |
| Db | 902 | CAG | TGTAAACACATCTCATGGGCTTTTG | AGCCGCGACAGACATGAAGTATATGTTACGA | 961 | |
| QY | 846 | AGA | CCACACCAAGGACCCGACCTTGG | CGGAGATGACGGAGGCGCCCTGCAAGTGTGAG | 905 | |
| Db | 962 | AGA | CCACACCAAGGACCCGACCTTGG | CGGAGATGACGGAGGCGCCCTGCAAGTGTGAG | 1021 | |
| QY | 906 | CAG | GAACCCCCCGGGCTTCTACTCTT | CGTGAGGGAGGCGGCATTGACCAAGGTACCA | 965 | |
| Db | 1022 | CAG | GAACCCCCCGGGCTTCTACTCTT | CGTGAGGGAGGCGGCATTGACCAAGGTACCA | 1081 | |
| QY | 966 | TGA | CGCAAAAGCTTATATGGCACTGAC | TGAGCGCATGTTGACATGCCATCGCCAA | 1025 | |
| Db | 1082 | TGA | TAGCAAAAGCTTATATGGCGCTG | ACGTGAGCGGTATGTTGACATGCCATCGCCAA | 1141 | |
| QY | 1026 | GG | CTAACGAGCTCACTAGCAACTGGA | CACGCTGATCCTTGTCACTGCAGACCCTCCA | 1085 | |
| Db | 1142 | GG | CTAACGAGCTCACTAGCAACTGGA | CACGCTGATCCTTGTCACTGCAGACCCTCCA | 1201 | |
| QY | 1086 | TGT | CTTCTTTTGGTGGCTACACACTG | CGTGGGACCTTCATTTTCGGTCTGGCCCCCGG | 1145 | |
| Db | 1202 | TGT | CTTCTTTTGGTGGCTACACACTG | CGTGGGACCTTCATTTTCGGTCTGGCCCCCGG | 1261 | |
| QY | 1146 | CAA | GCCCTTAGACAGCAAGTCTTACA | CACTCCATCCTTAATGGCAATGGCCAGGCTATGC | 1205 | |
| Db | 1262 | CAA | GCCCTTAGACAGCAAGTCTTACA | CACTCCATCCTTAATGGCAATGGCCCTGGCTACGT | 1321 | |
| QY | 1206 | GCT | TGGCGGGGCTCGAGCCCGATGTT | AATGGCAGCAACAAGGAAACCTCATACCG | 1265 | |
| Db | 1322 | GCT | TGGTGGGGGCTCAAGGCCGATGTT | AATGACAGCATTAAGGAGAACCCCTCATACCG | 1381 | |
| QY | 1266 | GCA | GCAAGCGCGCCGTGCCCCCTGG | CTAGCGAGACCCACGGGGGCGAAGACGTGGCGGTGTT | 1325 | |
| Db | 1382 | GCA | GCAAGCGCGCGCTGCCCCCTGT | AGCGAGACCCACGGGGGCGAAGACGTGGCGGTGTT | 1441 | |
| QY | 1326 | CG | CGGAGGCCCCGACGGCGCACTG | GTGACGCGGTGCGAGAGACCTTGTGCGCA | 1385 | |
| Db | 1442 | CG | CGGAGGCCCCGACGGCGCACTG | GTGACGCGGTGCGAGAGACCTTGTGCGCA | 1501 | |
| QY | 1386 | CAT | CATGCGCTTTGCGGGCTGCGT | GGAGCCCTACACCGACTGCAATCTGCCAGCCCCGC | 1445 | |
| Db | 1502 | CGT | CATGCGCTTTGCGGGCTGCGT | GGAGCCCTACACCGACTGCAATCTGCCAGCCCCGC | 1561 | |
| QY | 1446 | CA | CGCCACCAAGCATCCCCGACTA | GGGTACC 1476 | | |
| Db | 1562 | TGG | CTCTCCGACGCCGCGCACTT | GCGGCC 1592 | | |

RESULT 3
US-09-305-681-5
; Sequence 5, Application US/09305681
; Patent No. 6406899
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Highly active alkaline phosphatase

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; NUMBER OF SEQUENCES: 54
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/305,681
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2542 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
;
US-09-305-681-5

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| Query Match | 89.9% | Score 1327 | DB 4 | Length 2542 |
|-----------------------|--------------|---|---------------|-------------|
| Best Local Similarity | 93.9% | Pred. No. 0 | | |
| Matches 1381 | Conservative | 0 | Mismatches 90 | Indels 0 |
| | | | Gaps | 0 |
| QY | 6 | CCTCATCCCGAGTGAAGAAACCCCGCTTCTGAAACCCGACGAGCCCGCCCT | 65 | |
| Db | 121 | CTTCATCCCGAGTGAAGAAAGAACCCCGCTTCTGAAACCCGACGAGCCCGCCCT | 180 | |
| QY | 66 | TGATGTAGCCAAAGATTGCAAGCCGATCCAGACAGCTGCCAAGAATGTCATCTTCTT | 125 | |
| Db | 181 | TGATGTAGCCAAAGATTGCAAGCCGATCCAGACAGCTGCCAAGAATGTCATCTTCTT | 240 | |
| QY | 126 | GGGGGATGGATGGGGTGCTTACGGGTGACAGCCACTCGATCTTAAAGGGCAGATGAA | 185 | |
| Db | 241 | GGGGGATGGATGGGGTGCTTACGGGTGACAGCCACTCGATCTTAAAGGGCAGATGAA | 300 | |
| QY | 186 | TGGCAAACTGGAGCTGAGACACCCCTGGCCATGACCACTTCCCATACGTGCTCTGC | 245 | |
| Db | 301 | TGTTAAGCTGGAGCTGAGACACCCCTGGCCATGACCACTTCCCATACGTGCTCTGC | 360 | |
| QY | 246 | CAAGACATACAACTGGACAGACAGGTGCCAGACAGCCAGGCACTGCCACTGCTTACT | 305 | |
| Db | 361 | CAAGACATACAACTGGACAGACAGGTGCCAGACAGCCAGGCACTGCCACTGCTTACT | 420 | |
| QY | 306 | GTGTGGGTCAAGGGCACTACAGAAACCATCGTGTAAAGTGACGCCGCCGCTACATCA | 365 | |
| Db | 421 | GTGTGGGTCAAGGGCACTACAGAAACCATCGTGTAAAGTGACGCCGCCGCTACATCA | 480 | |
| QY | 366 | GTGCAACACGACACCTGGGAATGAGTCACTGTGTATCAACCGGGCCAAGAAAGCAG | 425 | |
| Db | 481 | GTGCAACACGACACCTGGGAATGAGTCACTGTGTATCAACCGGGCCAAGAAAGCAG | 540 | |
| QY | 426 | GAAAGCCGTGGAGTGTGTACCAACCAAGGCTGACATGCTTCCCAAGCCGGGGCTTA | 485 | |
| Db | 541 | AAAGTCAGTGGAGTGTGTACCAACCTCAGGGTGCATGCTTCCCAAGCCGGGGCTTA | 600 | |
| QY | 486 | CGCGCACACGGTGAACCGAAACTGTACTCAGACGCGCACTGCTGTATGACAGAA | 545 | |
| Db | 601 | TGCACACACGGTGAACCGAAACTGTACTCAGATGCGGACCTGCTGCCGATGACAGAC | 660 | |
| QY | 546 | GAATGCTGCCAGACATCGCCGACACAGCTGTGTACAACATGATATTGACGTATCT | 605 | |
| Db | 661 | GTATGCTGCCAGACATCGCCACACAACTGTGTACAACATGATATTGACGTATCT | 720 | |
| QY | 606 | GGGTGAGGCCGAATGTACATGTTCTCTGAGGGGACCCCGATCTGAATACCAATACGA | 665 | |
| Db | 721 | GGGTGAGGCCGAATGTACATGTTCTCTGAGGGGACCCCGATCTGAATACCAATACGA | 780 | |
| QY | 666 | TGCCAGTGTGAATGAAGTCCGGAAGACAAGCAGAACTGTGTAGGAATGGCAGGCCAA | 725 | |
| Db | 781 | TGTCAATCAGACTGAAGTCCGGAAGACAAGCAGAACTGTGTAGGAATGGCAGGCCAA | 840 | |
| QY | 726 | GCACCAAGGAGCCAGTATGTGTGAACCGCACTGCGCTCTTACAGCGGCCGATGACTC | 785 | |

Db 841 GCACGAGGAGCCAGTATGTGTGAACCGCACGGAGCTCCTTCAGGACCAATGACCC 900
Qy 786 CAGTGTAAACACCTCATGGGCTCTTTGAGCCGGCAGACATGATATATGTTACGA 845
Db 901 CAGTGTAAACACCTCATGGGCTCTTTGAGCCGGCAGACATGATATATGTTACGA 960
Qy 846 AGACCAACCAAGAGACCCGAGCCCTGGCGAGATGACGAGGCGGCCCTGCAAGTGTGAG 905
Db 961 AGACCCCAACAGAGACCCGAGCCCTGGAGAGATGACGAGGCGGCCCTGCAAGTGTGAG 1020
Qy 906 CAGGAACCCCGGGGCTTCTACCTCTTCGTGAGGAGGAGCGCCGATTGACCAAGTACCA 965
Db 1021 CAGGAACCCCGAGGGCTTCTACCTCTTCGTGAGGAGGAGCGCCGATTGACCAAGTACCA 1080
Qy 966 TGACGCAAAAGCTTATATGAGCACTGAGCGGATCATGTTGACAAATGCCATGCCAA 1025
Db 1081 TGAAGGCAAAAGCTTATATGAGCACTGAGTATACAGTCAATGTTGACAAATGCCATGCCAA 1140
Qy 1026 GGCTTAACGAGCTCACTAGCGAAGTGAACAGCTGATCCTTGTCACTGACAGCACTCCCA 1085
Db 1141 GGCTTAACGAGCTCACTAGCGAAGTGAACAGCTGATCCTTGTCACTGACAGCACTCCCA 1200
Qy 1086 TGTCTTCTCTTTGGTGTACACACTGCGTGGAGACCTCCATTTTCGCTGGCCCCCG 1145
Db 1201 TGTCTTCTCTTTGGTGTACACACTGCGTGGAGACCTCCATTTTCGCTGGCCCCCG 1260
Qy 1146 CAAGGCTTAGACAGCAAGTCTTACCTCCATCCTCTATGGCAATGGCCAGGCTATGC 1205
Db 1261 CAAGGCTTAGACAGCAAGTCTTACCTCCATCCTCTATGGCAATGGCCAGGCTATGC 1320
Qy 1206 GCTTGCGGGGGCTCGAGGCGCCGATTTAATGGACACAGCGAAGCAACCTCATACCG 1265
Db 1321 GCTTGCGGGGGCTTAAAGGCCCGATGTTAATGACAGCATTAAGCGAAGCAACCTCATACCG 1380
Qy 1266 GCAGCAGGCGGCGCTGCCCCCTGGCTAGCGAGAACCCAGGGGGCGAAGCCTGGCGGT 1325
Db 1381 GCAGCAGGCGGCGCTGCCCCCTGGCTAGCGAGAACCCAGGGGGCGAAGCCTGGCGGT 1440
Qy 1326 CGCGGAGGCGCGCAGGCGCACCTGTGACAGGCGGTGACAGGAGACCTTCTGGCGCA 1385
Db 1441 CGCGGAGGCGCGCAGGCGCACCTGTGACAGGCGGTGACAGGAGACCTTCTGGCGCA 1500
Qy 1386 CATCATGACCTTTGCGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCCAGCCCCGC 1445
Db 1501 CGTCATGGCTTTGCGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCCAGCCCCGC 1560
Qy 1446 CACGCGACACGATCCCCGACTAGGTAAC 1476
Db 1561 TGGCTCTCCGACGCGCGCACCTGGCGGCC 1591

RESULT 4
US-08-867-352-20
; Sequence 20, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multicistronic expression units and their use
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,352
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,847
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:

LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: pS02-SEAP (Berger et al., 1988)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1560
OTHER INFORMATION: /note= "human SEAP gene; flanked
OTHER INFORMATION: by 5'-EcoRI and 3'-HindIII restriction cleavage
OTHER INFORMATION: sites"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 94..1560
OTHER INFORMATION: /product= "mature protein"
PUBLICATION INFORMATION:
AUTHORS: Berger, J.
AUTHORS: Hauber, J.
AUTHORS: Hauber, R.
AUTHORS: Geiger, R.
AUTHORS: Cullen, B. R.
JOURNAL: Gene
VOLUME: 66
PAGES: 1-10
DATE: 1988
PUBLICATION INFORMATION:
AUTHORS: Millan, J. L.
JOURNAL: J. Biol. Chem.
VOLUME: 261
PAGES: 3112-3115
DATE: 1986
US-08-867-352-20

Query Match 67.9%; Score 1002.4; DB 3; Length 1956;
Best Local Similarity 80.2%; Pred. No. 2.3e-242;
Matches 1177; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

Qy 6 CCTCATCCAGCTGAGGAGGAAAAACCCCGCTTCTGGAACCGCCAGGCAAGCCAGGCCCT 65
Db 93 CATCATCCAGTTGAGGAGGAGAAACCCGACTTCTGGAACCGCCAGGCAAGCCAGGCCCT 152
Qy 66 TGATGTAGCCAAAGATTGCAAGCCGATCCAGACAGCTGCCAAGATGTCTCTTCTT 125
Db 153 GGGTCCGCCAAGAGCTGCAAGCTGCAACAGACAGCGCCCAAGAACCTCATCTTCT 212
Qy 126 GGGGATGGATGGGGGTGCTTACGCTGACAGCACTCGGATCTTAAAGGGCAGATGA 185
Db 213 GGGCGATGGATGGGGGTGCTTACGCTGACAGCACTCGGATCTTAAAGGGCAGATGA 272
Qy 186 TGGCAAACTGGACCTGAGACACCCCTGGCCATGAGCCAGTCCCATACGTGCTGTG 245
Db 273 GGACAAACCTGGGCTGAGATACCCCTGGCCATGAGCCGCTTCCCATATGTGCTGTG 332
Qy 246 CAAGACATACACGTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCCACT 305
Db 333 CAAGACATACATGTAGACAAACATGTGCCAGACAGTGAAGCCACAGCCAGGCTACT 392
Qy 306 GTGTGGGTCAAGGGCACTACAGAACCATCGGTGTAAGTGCAGCGCGCGCTTACATCA 365
Db 393 GTGCGGGTCAAGGGCACTTCCAGACCATGTGCTTGAAGTGCAGCGCGCGCTTAAACA 452
Qy 366 GTGCAACAGACACGTGGAATGAGTCAAGTCAAGTCAACCGGGCCAAGAAAGCAGG 425
Db 453 GTGCAACAGACACGTGGAATGAGTCAAGTCAAGTCAACCGGGCCAAGAAAGCAGG 512
Qy 426 GAAGCGGTGAGTGTGACCAACCAAGGCTGACATGCTCCCAAGCGCGGCTTA 485
Db 513 GAAGTCAAGTGTGTAACCAACCAAGGCTGACATGCTCCCAAGCGCGGCTTA 572

Db 1854 GCGCCAGGCTGCCGGTATGTGTGAACCGCACTGAGCTCATGCAAGCTTCCCTGGACCC 1913
QY 786 CAGTGTAAACACCTCATGAGGCTCTTTGAGCCGGCAGACATGAATATATGTTACAGCA 845
Db 1914 GTCTGTGAACCATCTCATGAGGTTCTTTGAGCCTGAGACATGAATAACAGATCCACCG 1973
QY 846 AGACCACCAAGAACCCGACCCCTGGCGAGATGACGAGGCGGCCCTGCAAGTGTGAG 905
Db 1974 AGACTCCACACTGGAACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTAG 2033
QY 906 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGAGCGCAATTGACCACGTCAACA 965
Db 2034 CAGGAACCCCGGGGCTTCTTCTCTTGTGAGGAGGTGTGCGATCGACCATGTGATCA 2093
QY 966 TGACGGCAAAAGCTTATATGCACTGAGGCGGATCATGTTTGAACAATGCCATGCCAA 1025
Db 2094 TGAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGACGCCATTGAGAG 2153
QY 1026 GGCTAACGAGCTCACTAGCGAATGAGACGCTGATCCTTGTCACTGACAGACCACTCCA 1085
Db 2154 GCGCGGCAGCTCAACGAGGAGGACACGCTGAGCCTCGTCACTGCGACCACTCCCA 2213
QY 1086 TGTCTTCTCTTTTGGTGTACACACTGCGTGGGACCTTCCATTTTGGTCTGGCCCCCG 1145
Db 2214 CGTCTTCTCTTGGAGGCTACCCCTGCGAGGAGCTCCATCTTGGGGCTGGCCCCCTGG 2273
QY 1146 CAAGCCTTGAACAGCAAGTCCCTACCTTCCATCCTATGGAATGGCCAGGCTATGC 1205
Db 2274 CAAGCCCGGAGCAGGAAGGCTTACCGGTCTCTATACGGAACGGTCCAGGCTATGT 2333
QY 1206 GCTTGGCGGGGCTCGAGCCCGATGTTAATGGACACAAAGCGAAGAACCTCATACCG 1265
Db 2334 GCTCAAGAGAGGGCGCCCGCGGATGTTACCGAGAGCGAGCGGGAGCCCCGAGTATCG 2393
QY 1266 GCAGCAGCGCGCCGTGCCCCCTGGCTAGCGAGAACCCACGGGGCGAAGACGTGGCGGT 1325
Db 2394 GCAGCAGTCAAGCAGTGCCTCCCTGGACGAAGAACCACGACGGCGGAGACGTGGCGGT 2453
QY 1326 CGCGCAGAGCCCGCAGAGCGCACCTGTGTACAGCGCGTGAGAGAGACCTTGTGGCGCA 1385
Db 2454 CGCGCGCGGCGCCGACGCGCACCTGTGTCAAGCGGTGAGAGAGACCTTCATAGCGCA 2513
QY 1386 CATCATGAGCCTTTGCGGGCTGCGTGAGGCCCTTACACCGACTGCAATCTGCAGCCCCCG 1445
Db 2514 CGTCATGAGCCTTTCGCGCCTGCTGTGAGCCCTTACACCGCCTGTGCACTTGGCCCCCG 2573
QY 1446 CACCGCCACAGCATCCCCGACTAGGGT 1473
Db 2574 CCGCACCAACGACGCGCGCGCACCCGGGT 2601

RESULT 6
US-09-693-011-11
; Sequence 11, Application us/09693011
; Patent No. 6632978
; GENERAL INFORMATION:
; APPLICANT: Kaelin, Edgar
; APPLICANT: Luyten, Marcel
; APPLICANT: Zierwes, Hans-Gunter
; TITLE OF INVENTION: Transgenic Animals For Studying
; FILE REFERENCE: 4-31176A
; CURRENT APPLICATION NUMBER: US/09/693,011
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 5083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA CONSTRUCT
US-09-693-011-11

Query Match 67.8%; Score 1000.8; DB 4; Length 5083;
Best Local Similarity 80.1%; Pred. No. 8e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;
QY 6 CCTCATCCAGCTGAGAGGAAAAACCCGCTTCTGGAACCGCCAGCAGCCCGCCCT 65
Db 1134 CATCATCCAGTTGAGAGGAGAAACCCGACTTCTGGAACCGCCAGCAGCCCGCCCT 1193
QY 66 TGATGTAGCCAAAGATTGACCGCGATCCAGACAGCTGCCAAGAATGTATCTTCTT 125
Db 1194 GGTGTCCGCCAAGAGCTGACGCTTGACAGACAGCGCCCAAGAACCTCATCTTCT 1253
QY 126 GGGGATGGATGGGGGTGCTACCGGTGACAGCCACTCGGATCTTAAAGGGCAGATGA 185
Db 1254 GGGCGATGGATGGGGGTGTCTACGGTGAACAGCTGCCAGGATCTTAAAGGGCAGAA 1313
QY 186 TGGCAACTGGGACCTGAGACACCCCTGGCCATGACCAATTCCATACGTGCTGTG 245
Db 1314 GGACAACTGGGCGCTGAGATACCCCTGGCCATGAGCGGCTTCCATATGTGCTGTG 1373
QY 246 CAAGACATACAAGCTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTAC 305
Db 1374 CAAGACATACAATGTAGCAAAACATGTGCCAGACAGTGAAGCCACAGCCAGGCTAC 1433
QY 306 GTGTGGGTCAAGGGCACTACAGAACCATCGGTGTAACTGCAAGCCCGCCCTTACA 365
Db 1434 GTGCGGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAAGTGCAAGCCCGCCCTT 1493
QY 366 GTGCAACACGACAGTGGGAATGAGTCAAGTCAAGTCAACCGGGCCAAAGACAGG 425
Db 1494 GTGCAACACGACAGCGGCAAGAGTCAATCTCGTGTATGATCGGGCCAAAGACAGG 1553
QY 426 GAAGCCGTGGAGTGTGACCAACCAAGGTGACAGATGCTCCCGAGCGGGCTTAC 485
Db 1554 GAAGTCAGTGGAGTGTGACCAACCAAGGTGACAGATGCAAGCTCCCGAGCGGCACT 1613
QY 486 CGGCACACGGTGAACCGAACTGTACTCAGACGCGGACCTGCTGTATGACAGAA 545
Db 1614 CGCCACACGGTGAACCGCACTGTACTCGAGCGCGGACGCTGCTCGGCGGCCA 1673
QY 546 GAATGCTGCCAGACATCGCCCGCACAGCTGCTTACATCATGATATTGACGTATCT 605
Db 1674 GGAAGGGGTGCCAGACATCGCTTACGAGCTCATCTTCAACATGGAATTGACGTATCT 1733
QY 606 GGGTGAAGCCGAATGTATGTTTCTTGAAGGGGACCCCAAGACCTGAAATCCAGATGA 665
Db 1734 AGGTGAAGCCGAAGTATGTGTTTGCATGGGAACCCAGACCTGAGTACCCAGATGA 1793
QY 666 TGCCAGTGTGATGAGTCCGGAAGACAAAGACAGAACTGTGACGAATGGAGCCAA 725
Db 1794 CTACAGCCAAAGTGGACCAAGCTGACGGAAGAACTGTGACGAATGGCTGGCGAA 1853
QY 726 GCACCAAGGAGCCCAATGTGTGAACCGCACTGCGCTCTTCAAGCGCGCGATGACTC 785
Db 1854 GCGCCAGGGTCCCGGTATGTGGAACCGCACTGAGCTCATGCAAGCTTCCCTGAGCC 1913
QY 786 CAGTGTAAACACCTCATGAGGCTCTTTGAGCCGAGACATGAAGTATATGTTACGA 845
Db 1914 GTCTGTAGCCCATCTCATGAGGTTCTTTGAGCCTGAGACATGAATATGATCCACCG 1973
QY 846 AGACCACCAAGAACCCGACCCCTGGCGAGATGACGAGGCGGCCCTGCAAGTGTGAG 905
Db 1974 AGACTCCACACTGGAACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCTGTAG 2033
QY 906 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGCGCATTTGACCAAGCTCACCA 965
Db 2034 CAGGAACCCCGGGGCTTCTCTCTTGTGAGGAGGTGTGCGATCGACCATGTATCA 2093
QY 966 TGACGCAAAAGCTTATGCACTGACTGAGCGGATCATGTTTGAACAATGCCATGCCAA 1025
Db 2094 TGAAGCAGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGAGCGCATTTGAGAG 2153

| | | | |
|----|------|--|------|
| QY | 1206 | GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGCACAGCGAGAAACCTCATATCCG | 1265 |
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| QY | 1266 | GCAGCAGCGCGCGCTGCCCTGAGCTAGCGAGACCAACGGGGCGAAGACGTGCGGT | 1325 |
| | | | |
| Db | 1618 | GCAGCAGTCAGCAGTGCCTCTGACGAAAGAACCCACGCAAGCAGACGTGGCGGT | 1677 |
| QY | 1326 | CGCGCGAGGCCCGCAGGCGCACTGTGTACACGCGGTGACAGAGAGACCTTCGTGCGCA | 1385 |
| | | | |
| Db | 1678 | CGCGCGCGGGCCCCGACGCGCACTGTTCACGCGGTGACAGAGCAGACCTTCATAGCGCA | 1737 |
| QY | 1386 | CATCATGGCCTTTGCGGGCTGCCTGGAGGCCCTACACCGCATCTGCATCTGCCAGCCCCGC | 1445 |
| | | | |
| Db | 1738 | CGTCATGGCCTTCGCCCGCTGCTGGAGGCCCTACACCGCCTTGCGAACCCTGGCGCCCCCGC | 1797 |
| QY | 1446 | CACCGCCACCAAGCATCCCCGACTAGGGT | 1473 |
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RESULT 8

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US-09-693-011-10
; Sequence 10, Application US/09693011
; Patent No. 6632978
; GENERAL INFORMATION:
; APPLICANT: Kaslin, Edgar
; APPLICANT: Luyten, Marcel
; APPLICANT: Zermes, Hans-Gunter
; TITLE OF INVENTION: Transgenic Animals For Studying
; TITLE OF INVENTION: Regulation Of Genes
; FILE REFERENCE: 4-31176A
; CURRENT APPLICATION NUMBER: US/09/693,011
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6314
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TARGETING SEQUENCE
US-09-693-011-10

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| Query Match | 67.8%; | Score 1000.8; | DB 4; | Length 6314; |
| Best Local Similarity | 80.1%; | Pred. No. 8.6e-242; | | |
| Matches 1176; Conservative | 0; | Mismatches 292; | Indels 0; | Gaps 0; |

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| Dd | 1147 | CATCATCCCAAGTTGAGGAGGAAACCCGGACTTCTGAAACCGAGGCAGCCGAGGCCCT | 1206 |
| OY | 66 | TGATGTAGCCAAGAATTGCAAGCCGATCCAGACAGCTGCCAAGAATGTCATCCTCTT | 125 |
| Dd | 1207 | GGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCATCTTCT | 1266 |
| OY | 126 | GGGGGATGGGATGGGGTGCTACGGTGACAGCCACTCGSATCTAAAGGGCAGATGAA | 185 |
| Dd | 1267 | GGCGGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGATCTAAAAAGGCAGAGAA | 1326 |
| OY | 186 | TGGCAAACCTGGGACCTGAGACAACCCCTGGCCATGGAACCAATTCCATACGTGGCTGTTC | 245 |
| Dd | 1327 | GGAACAACCTGGGGCCTGAGATACCCCCTGGCCATGGAACCGCTTCCCATATGTGGCTGTTC | 1386 |
| OY | 246 | CAAGACATTAACAACGTGGACAGACAGGTGCCAGACAGCGCACAGCACTGCCACTGCTACT | 305 |
| Dd | 1387 | CAAGACATTAACAATGTAGACAACAACATGTGCCAGACAGTGGAGCCACAGCCACGGCCTACT | 1446 |
| OY | 306 | GTTGTGGGGTCAAGGGCAACTACAGAACCATCGGTGTAAGTGACCGCCCGCTACAATCA | 365 |
| Dd | 1447 | GTTCCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCCGCTTTAACCA | 1506 |

| | | | |
|----|------|---|------|
| QY | 366 | GTGCAACACGACACGTGGGAATGAGTCACGTCTGTGATCAACCGGGGCCAAGAAAGCAGG | 425 |
| Db | 1507 | GTGCAACACGACACGCGGCAACGAGTCACTCTCGTGATGAATCGGGCCAAAGAAAGCAGG | 1566 |
| QY | 426 | GAAAGCCGTGGAGTGTGTGACCACACGAGGTGCAGCATGCTCTCCAGCGGGGCTTA | 485 |
| Db | 1567 | GAAGTCAGTGGAGTGTGTAAACCAACACAGAGTGCACACGCTCTGCGCAGCGGCACCTA | 1626 |
| QY | 486 | CGCGCACACGGTGAACCGAAACTGTACTCAGACGCGGACCTGCTGTGATGCACAGAA | 545 |
| Db | 1627 | CGCCCAACACGGTGAACCGCAACTGTACTCGGACGCGGACGCTGCTGCGCCCGCCA | 1686 |
| QY | 546 | GAATGCTGCCAGGACATCGCCGACACGCTGTCTACAACATGATATTGAAGTGATCCT | 605 |
| Db | 1687 | GGAAGGGTGCAGGACATCGCTACGCAAGCTCATCTCCAACATGGACATTGACGTGATCCT | 1746 |
| QY | 606 | GGGTGGAGGCCGAATGTACATGTTTCTCTGAGGGGACCCCAAGACCTGATATCCAGATGA | 665 |
| Db | 1747 | AGGTGAGGCCGAAGTATCATGTTTCCGATGGGAACCCAGACCTGAGTATCCAGATGA | 1806 |
| QY | 666 | TGCCAGTGTGAATGAGTCCGGAAGACAAGCAGAACTGTGTGAGGAATGGCAGGCCAA | 725 |
| Db | 1807 | CTACAGCCAAAGTGGGACCAAGCTGACGCGGAAGAAATGTGTGAGGAATGGTGGCAA | 1866 |
| QY | 726 | GCACAGGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCCTTCAGGCGGCGATGACTC | 785 |
| Db | 1867 | GCGCCAGGGTGCCCGGTATGTGTGAACCGCACTGAGCTCATGACAGGCTTCCCTGGAACC | 1926 |
| QY | 786 | CAGTGTAAACACACCTCATGGGCTCTTTGAGCGCGCAGACATGAAGTATTAATGTCAGCA | 845 |
| Db | 1927 | GTCTGTGACCCATCTCATGGGTCTCTTGAGCCTGGAGACATGAATAAGATCCACCG | 1986 |
| QY | 846 | AGACCAACACCAAGGACCCGACCTGGCGGAGATGACGGAAGCGGCCCTGCAAGTCTGAG | 905 |
| Db | 1987 | AGACTCCACACTGGACCCCTCCTGATGGAGATGACAGAGGCTGCCCTGCGCTGTGAG | 2046 |
| QY | 906 | CAGGAACCCCCGGGGCTTCACTCTTCGTGAGGGAAGCCGCATTTGACCAACGGTCAACA | 965 |
| Db | 2047 | CAGGAACCCCCGGGCTTCTCTCTTCGTGAGGGTGTCCGATCGAACCATGGTCACTCA | 2106 |
| QY | 966 | TGACGGCAAAAGCTTATATGCACTGACTGAGGCGATCATGTTTGACAATGCCATCGCCAA | 1025 |
| Db | 2107 | TGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTTGACGACGCCATTTGAGAG | 2166 |
| QY | 1026 | GGCTAACGAGCTCACTAGCGAACTGGACACGCTGATCTTGTCACTGCAGACCACTCCCA | 1085 |
| Db | 2167 | GGCGGGCCAGCTCACCAAGGAGAGGACACGCTGAGCTCTGCACTGCCAGCACTCCCA | 2226 |
| QY | 1086 | TGTTCTTCTTTTGTGGCTACACTGCTGGACCTCATTTTGGTCTGGCCCCCGG | 1145 |
| Db | 2227 | CGTCTTCTCTTCGGAGGCTACCCCTGCGAGGAGCTCCATCTTCGGGCTGGCCCCCTGG | 2286 |
| QY | 1146 | CAAGGCTTAGACAGCAAGTCTTACACCTCCATCTCTATATGGCAATGSGCCCAAGCTATGC | 1205 |
| Db | 2287 | CAAGGCTCCGGGACAGGAAGGCTTACACGGTCTCTCTATACGGAACGGTCCAGGCTATGT | 2346 |
| QY | 1206 | GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGCACAAGCGAGGAACCTCTATACCG | 1265 |
| Db | 2347 | GCTCAAGGACGGCGCCCGGCGGATGTTACCGAGAGGAGAGCGGGAGCCCCGAGTATCG | 2406 |
| QY | 1266 | GCAAGAGCGCGCGCTGCGCTGGCTAGCGAGACCAAGGGGGCGAAGACGTGGCGGTGT | 1325 |
| Db | 2407 | GCAAGAGTCAAGAGTGCCTCTGGACGAAGAGACCACGCAAGCGAGGACGTGGCGGTGT | 2466 |
| QY | 1326 | CGCGGAGGCGCCGACAGGCGCACTGTGCAAGCGGCTGCAAGAGAGACCTTCGTGGCGCA | 1385 |
| Db | 2467 | CGCGGCGGCGCCGACAGGCGCACTGTGTTCAAGGCTGCAAGAGACCACTTCATAGCGCA | 2526 |
| QY | 1386 | CATCATGGCCTTTGCGGGCTGGTGGAGGCCCTACACCGACTGCAATCTGCCAGGCCCGGC | 1445 |
| Db | 2527 | CGTCATGGCCTTTCGCGGCTGTGAGGCCCTTACACCGGCTGCACTGGCGGCCCGCGC | 2586 |
| QY | 1446 | CACCGCCACCAAGCATCCCCCACTAGGGT | 1473 |

Db 2587 CGGCACCACCGCCGCCGACCCGGGT 2614

RESULT 9
US-09-693-011-9

; Sequence 9, Application US/09693011
; Patent No. 6632978
; GENERAL INFORMATION:
; APPLICANT: Kaslin, Edgar
; APPLICANT: Luyten, Marcel
; APPLICANT: Zewes, Hans-Gunter
; TITLE OF INVENTION: Transgenic Animals For Studying
; TITLE OF INVENTION: Regulation Of Genes
; FILE REFERENCE: 4-31176A
; CURRENT APPLICATION NUMBER: US/09/693,011
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6408
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TARGETING SEQUENCE
US-09-693-011-9

Query Match 67.8%; Score 1000.8; DB 4; Length 6408;
Best Local Similarity 80.1%; Pred. No. 8.7e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 6 CCTCATCCCACTGAGGAGGAAACCCCGCTTCTGGAACCGCCAGCGACCCGAGCCCT 65
Db 1147 CATCATCCCACTGAGGAGGAAACCCCGACTTCTGGAACCGCCAGCGACCCGAGCCCT 1206
QY 66 TGATGTAGCCAGAAATTGTCAGCCGATCCAGACAGCTGCCAAGATGTCATCTTCTT 125
Db 1207 GGGTGCCGCAAGAGCTGCAGCTGCACAGACCGCCAAAGCACTCATCTTCTTCT 1266
QY 126 GGGGATGGATGGGGGTGCTTACGGTGACAGCACTCGGATCTTAAAGGGCAGATGAA 185
Db 1267 GGGGATGGATGGGGGTGCTTACGGTGACAGCTCGGATCTTAAAGGGCAGATGAA 1326
QY 186 TGGCAAACTGGGACTGAGACACCCCTGGCCATGGACCAAGTCCCATAGCTGCTGTG 245
Db 1327 GGACAACTGGGGCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGCTGTG 1386
QY 246 CAAGACATACAACTGGAACAGACAGGTGCCAGACGGCAGGCACTGCCCTACCT 305
Db 1387 CAAGACATACAACTGGAACAAACATGTGCCAGACAGTGGACCAAGCCACGGCCTTACT 1446
QY 306 GTGTGGGTCAAGGGCACTACAGAACCATGGGTGTAAGTGCAGCCGGCCGCTACAATCA 365
Db 1447 GTGCGGGTCAAGGGCACTTCCAGACCATTTGGCTGAGTGCAGCCGGCCGCTTAAACA 1506
QY 366 GTGCAACACGACAGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAGAAAGCAGG 425
Db 1507 GTGCAACACGACAGCGGGCAACGAGGTCAATCTCGTATGAATCGGGCCAGAAAGCAGG 1566
QY 426 GAAGGCGGTGGGATGGTGACCAACCAAGGCTGACATGCTCCCGAGCGGGGCTTA 485
Db 1567 GAAGTCAAGTGGGATGGTGAACCAACCAAGTGCAGACCGCTCGCCAGCGGCACTTA 1626
QY 486 CGGCACACCGGTGAACCGAACTGTACTCAAGCGCCGACCTGCTGTGATGCACAGAA 545
Db 1627 CGGCACACCGGTGAACCGCAACTGTACTCGGACCGCCGACGTGCTGCTGCGCCCA 1686
QY 546 GAATGGCTGCCAGGACATCGCCGACAGCTGGTCTACAAACATGATGATATTGACGTGATCT 605
Db 1687 GGAGGGGTGCCAGGACATCGCTACGACGCTCATCTCAACATGACATGACATGATGATCT 1746
QY 606 GGGTGAGGCGCGAATGTACATGTTCTTGAGGGGACCCAGACCCCTGAATACCCAGATGA 665

Db 1747 AGGTGAGGCGGAAAGTACATGTTTCGATGGGAACCCAGACCTTGAGTACCAGATGA 1806
QY 666 TGCCAGTGTGATGAGTCCGGAAGGACAAAGCAACCTGTGTGACGAATGGCAGGCCAA 725
Db 1807 CTACAGCCAAAGTGGGACGAGCTGGAACGGAAGATCTGGTGACGAATGGCTGGCAA 1866
QY 726 GCACCAAGGACCCAGTATGTGTGAACCGCACTGCGCTCTTCAAGCGGCCGATGACTC 785
Db 1867 GCGCCAGGGTGGCCGGTATGTGTGAACCGCACTGAGCTCATGAGGCTTCCCTGAGACC 1926
QY 786 CAGTGTACACACCTCATGAGGCTCTTTGAGCCCGGACAGACATGAAGTAAATGTTACGA 845
Db 1927 GTCTGTAGCCATCTCATGAGTCTTTGAGCCTGAGACATGAATACGAGATCCACCG 1986
QY 846 AGACCACACCAAGGACCCGACCTGGCGAGATGACGGAGCGGCCCTGCAAGTCTGAG 905
Db 1987 AGACTCCACACTGGAACCCCTCGATGAGATGACAGAGGCTGCCCTGCGCTGCTGAG 2046
QY 906 CAGGAACCCCGGGCTTCTACCTCTTGTGAGGAGGAGCGCCATGACCAAGTCAACA 965
Db 2047 CAGGAACCCCGGGCTTCTTCTTGTGAGGAGGAGTGTGCAATGACCATGTCATCA 2106
QY 966 TGACGCAACCTTATATGCACTGAGCGGATCATGTTTGAACATGCCATCGCCAA 1025
Db 2107 TGAAGCAGGCTTACCGGGCACTGACATGACATGATGTTGACGACGCCATTGAGAG 2166
QY 1026 GGCTAACGAGCTCACTAGCAACTGGAACGCTGATCCTTGTCTACTGACAGCACTCCA 1085
Db 2167 GCGGGCCAGCTCAACGAGGAGGAGACAGCTGAGCCTCTGCTACTGCGGACCACTCCA 2226
QY 1086 TGTCTTCTTTTGTGGCTACACACTGCTGGGACCTTCATTTTGGTCTGGCCCCGG 1145
Db 2227 GGTCTTCTCTTGGAGGCTACCCCTGAGGAGGAGCTCCATCTTGGGCTGGCCCCGG 2286
QY 1146 CAAGCCTTGAACAGCAAGTCTTACCTCATCTCTATGCAATGGCCCAAGGCTATGC 1205
Db 2287 CAAGCCTTGAACAGCAAGGCTTACCTCATCTCTATGCAATGGCCCAAGGCTATGT 2346
QY 1206 GCTTGGCGGGCTCGAGGCCGATGTAATGGACAGCAACAAGCGAGAACCTCATACCG 1265
Db 2347 GCTCAAGACGCGCGCCCGGATGTTACCGAGAGGAGCGGAGCCCGAGATATCG 2406
QY 1266 GCAGCAGCGCGCTGCCCCCTGGCTAGCGAGACCCACGGGGCGAAGACGTGGCGTGT 1325
Db 2407 GCAGCAGTACAGTGTCCCTGACGAGAGAACCCACGACGGCGAGACGTGGCGTGT 2466
QY 1326 CGCGGAGCGCGGACGCGCACTGTGTGACGGCGTGACGAGAGACCTTGTGCGCA 1385
Db 2467 CGCGGCGCGCGGACGCGCACTGTGTGACGGCGTGACGAGAGACCTTGTGAGCGCA 2526
QY 1386 CATCATGGCTTTGCGGGCTGCGTGAGCCCTTACCGCACTGCAATGTGCCAGCCCCCGC 1445
Db 2527 GGTATGGCTTTCGCGGCTGCTGAGCCCTTACCGCTGCACTGTGGCGCCCCCGC 2586
QY 1446 CACCGCACACGATCCCGCACTAGGT 1473
Db 2587 CGGCACCACGACCGCGGCACTGGGT 2614

RESULT 10

US-09-837-863-20
; Sequence 20, Application US/09837863
; Patent No. 6468754
; GENERAL INFORMATION:
; APPLICANT: Greene, Amy
; APPLICANT: Zhou, Hua
; APPLICANT: Thode, Slike
; APPLICANT: Jarnigan, Kurt
; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
; TITLE OF INVENTION: of an Integrated DNA Sequence
; FILE REFERENCE: 025.1US
; CURRENT APPLICATION NUMBER: US/09/837,863
; CURRENT FILING DATE: 2001-04-17

; PRIOR APPLICATION NUMBER: US 60/198,498
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 7076
; TYPE: DNA
; ORGANISM: vector
US-09-837-863-20

Query Match 67.8%; Score 1000.8; DB 4; Length 7076;
Best Local Similarity 80.1%; Pred. No. 9e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGAGAAAACCCGCTTCTGGAACCGCAGAGCCAGGCCCT 65
DB 1349 CATCATCCCAAGTTGAGAGAGAACCCGACTTCTGGAACCGCAGAGCCAGGCCCT 1408
QY 66 TGATGTAGCCAAGAAGTTGCAGCCGATCCAGACAGCTGCCAAGAATGTCATCTTCTT 125
DB 1409 GGGTCCCGCAAGAAGCTGCAGCCTGCACAGACAGCCGCAAGAACTTCATCTTCTT 1468
QY 126 GGGGATGGATGGGGGTGCTTACCGTGAACAGCCACTCGGATCTTAAAGGGCAGATGAA 185
DB 1469 GGGCGATGGATGGGGGTGCTTACCGTGAACAGCTGCCAGGATCTTAAAGGGCAGAGAA 1528
QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGACCAATTCCATACGTGGCTCTGTC 245
DB 1529 GGACAAACTGGGGCTTGAGATACCCCTGGCCATGAGACCCGCTTCCATATGTGGCTCTGTC 1588
QY 246 CAAGACATACAACGTGAGACAGAGTGCAGACAGCGCAGGCACTGCCACTGCCCTACCT 305
DB 1589 CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGAAGCACAAGCCAGCCTACCT 1648
QY 306 GTGTGGGTCAAGGGCACTACAGAACCATCGTGTAGTGAAGCCGCGCCGTACAATCA 365
DB 1649 GTGCGGGGTCAAGGGCACTTCCAGAACCATTTGGCTTGAAGTGAAGCCGCGCCGTACAATCA 1708
QY 366 GTGCAACACGACAGCTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAAGAACAGG 425
DB 1709 GTGCAACACGACAGCGGGCAACGAGGTCAATCTCCGTGATGAATCGGGCCAAAGAACAGG 1768
QY 426 GAAGCGCTGGGAGTGTGACCAACCAAGGGGTGACAGATGCTTCCCAAGCGGGGCTTA 485
DB 1769 GAAGTCAAGTGGGAGTGTAAACCAACAGAGTGAAGCAGCGCTTCCAGCGGCACTTA 1828
QY 486 CGCGCACAGGTGAACCGAACTGTACTCAGACGCGGACCTGCTGTATGCACAGAA 545
DB 1829 CGCCACACAGGTGAACCGCAACTGTACTCGAGCGCGGACGTGCTGCTCGCGCGCA 1888
QY 546 GAATGCTGCAGGACATCGCGCAGCAGCTGTCTACAACATGATATTGACGTGATCT 605
DB 1889 GGAAGGGTGCAGGACATCGCTACGAGCTCATCTCAACATGACATTTGACGTGATCT 1948
QY 606 GGGTGAAGCCGAATGTACATGTTTCTGAGGGGAGCCCAAGCCCTGAATACCCAGATGA 665
DB 1949 AGGTGAAGCCGAAGTACATGTTTCCGATGGGAACCCCAAGCCCTGAATACCCAGATGA 2008
QY 666 TGCCAATGTGAATGAGTCCCGAAGACAAAGCAAGAACCTGTGTCAAGGAATGGCAGGCCAA 725
DB 2009 CTACAGCCCAAGGTGGGACCAAGGCTGGAAGGGAAGATCTGTGTCAAGGAATGGCTGGCGAA 2068
QY 726 GCACAGAGGAGCCCAAGTATGTGGAACCGCACTGCGCTCTTCAAGCGCGCGGATGACTC 785
DB 2069 GCGCCAGGGTCCCGGTATGTGGAACCGCACTGAGCTCATGTCAAGGCTTCCCTGAGCCC 2128
QY 786 CAGTGTAAACACACTCATGGGCTCTTTGAGCCGCGCAGACATGAAGTATATGTTACGA 845
DB 2129 GTCTGTGAACCATCTCATGGGTCTTTTGAAGCCTGAAGACATGAATAACGAGATCCACCG 2188
QY 846 AGACCAACCAAGAGACCGCACTGGCGGAGATGACGAGGCGGCGCTGCAAGTGTGAG 905
DB 2189 AGACTCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCCTGTGAG 2248

QY 906 CAGAACCCCCGGGCTTCTACCTCTTCTGTGAGGAGGCCGATTGACCAAGGTACCA 965
DB 2249 CAGAACCCCCGGGCTTCTTCTCTTCTGTGAGGGGTGCTGCATGCACCATGTGTATCA 2308
QY 966 TGACCGCAAAAGCTTATATGCACTGACTGAGGCGCATGTTTGACAAATGCCATGCCAA 1025
DB 2309 TGAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTTCAGACGCGCATTGAGAG 2368
QY 1026 GGCTAACGAGCTCACTAGCAACTGACACGCTGATCTGTCACTGCAGACCACTCCA 1085
DB 2369 GGGGAGCAGCTCACGAGAGAGACACGCTGAGCTTGTCACTGCCAGCACTCCA 2428
QY 1086 TGCTTCTCTTTTGTGCTTACACACTGCGTGGACCTTCAATTTTGGTCTGCGCCCGG 1145
DB 2429 CGTCTTCTCTTGGAGGCTTACCCCTGCGAGGAGCTTCAATCTTGGGCTGCGCCCTGG 2488
QY 1146 CAAGCCTTAGACAGCAAGTCTTACACCTCCATCCTCTATGGCAATGCCCAGGCTATGC 1205
DB 2489 CAAGGCCCGGACAGAGAGGCTTACACGCTCCTCTATACGGAACGCTCAGGCTATGT 2548
QY 1206 GCTTGGCGGGGCTCGAGGCCGATGTTATGCAAGCACAAGCGAGAACCTCTATACCG 1265
DB 2549 GCTCAAGGACGCGCGCCCGCGGATGTTACCGAGACGAGAGCGGAGCCCGCACTATCG 2608
QY 1266 GCAGCAGGCGCGCTGCTGCTGCTAGCGAGACCCAGGGGGCGAAGACGTGGGGTGT 1325
DB 2609 GCAGCAGTACAGAGTCCCTTGACGAAAGAACCCAGAGGCGAGACGTGGCGGTGT 2668
QY 1326 CGCGGAGGCGCGCAGCGCACTGTGTGACGCGGTGACAGAGAGACCTTGTGGCGCA 1385
DB 2669 CGCGCGGCGCGCAGCGCACTGTGTGACGCGGTGACAGAGACGACCTTATAGCGCA 2728
QY 1386 CATCATGGCCTTTCGCGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCCAGCCCCGC 1445
DB 2729 CGTCATGGCCTTTCGCGCCTGCTGAGCCCTACACCGCCTGCACTGGCGCCCCCGC 2788
QY 1446 CACCGCACCAAGCATCCCGACTAGGT 1473
DB 2789 CGGCACCAACGACGCGCGCAACCGGGT 2816

RESULT 11
US-09-837-863-21
; Sequence 21, Application US/09837863
; Patent No. 6468754
; GENERAL INFORMATION:
; APPLICANT: Greene, Amy
; APPLICANT: Zhou, Hua
; APPLICANT: Thode, Silke
; APPLICANT: Jarnigan, Kurt
; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
; TITLE OF INVENTION: of an Integrated DNA Sequence
; FILE REFERENCE: 025.1US
; CURRENT APPLICATION NUMBER: US/09/837,863
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/198,498
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 7076
; TYPE: DNA
; ORGANISM: vector
US-09-837-863-21

Query Match 67.8%; Score 1000.8; DB 4; Length 7076;
Best Local Similarity 80.1%; Pred. No. 9e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGAGAAAACCCGCTTCTGGAACCGCAGAGCCAGGCCCT 65
DB 1349 CATCATCCCAAGTTGAGAGAGAACCCGACTTCTGGAACCGCAGAGCCAGGCCCT 1408

| | | | |
|----|------|--|------|
| QY | 66 | TCATGTAGCCAAAGAGTTGCAGCCCGATCCAGACAGCTTGCCAAAGATGTCACTCTTCTT | 125 |
| Db | 1409 | GGGTGCCGCCAAGAGCTGCAGCCTGCACAGACAGCCGCCAAGAACTTCATCATTTCTT | 1468 |
| QY | 126 | GGGGGATGGATGGGGTGCTACGGTGACAGCCCACTCGGATCTTAAAGGGCAGATGAA | 185 |
| Db | 1469 | GGCGATGGATGGGGGTGTCTACGTGACAGCTGCCAGATCTTAAAGGGCAGAGA | 1528 |
| QY | 186 | TGGCAAACTGGACCTGAGACACCCCTGGCCATGGACCAAGTTCCCATACGTGGCTGT | 245 |
| Db | 1529 | GGACAAACTGGGGCCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGCTGT | 1588 |
| QY | 246 | CAAGACATACACGTTGACAGACAGGTGCCAGACAGCCGACGCACTGCCACTGCTTACT | 305 |
| Db | 1589 | CAAGACATACATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCAGGCTTACT | 1648 |
| QY | 306 | GTGTGGGTCAAAGGGCAACTACAGAACCATCGGTGTAAGTGACGCCGCCGCTACATCA | 365 |
| Db | 1649 | GTGCGGGTCAAGGGCAACTTCCAGACCATTTGGCTTGAAGTGACGCCGCCGCTTAA | 1708 |
| QY | 366 | GTGCAACACGACACGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAAGACAG | 425 |
| Db | 1709 | GTGCAACACGACACGCGGCAACGAGTCACTCCGTGATGAATCGGGCCAAAGACAG | 1768 |
| QY | 426 | GAAAGCCGTGGGAGTGTGACCAACACAGGCTGCAGCATGCTCCCGACGCCGGGCT | 485 |
| Db | 1769 | GAAGTAGTGGAGTGTGTAACCAACACAGAGTGACAGCGCTCGCCAGCCGGCACT | 1828 |
| QY | 486 | CGCGCACACGGTGAAACCGAACTGGTACTCAGACGCCCACTGCTGTATGCAGAA | 545 |
| Db | 1829 | CGCCACACCGTGAAACCGCACTGTACTCGAGCGCCGACGTGCTCGGCCGCCA | 1888 |
| QY | 546 | GAATGCTGCAGACATCGCCGACAGCTGTCTACACATGATATTGACGTATCT | 605 |
| Db | 1889 | GGAGGGGTGCAGACATCGCTACGACGTCACTCCAAATGACATTGACGTATCT | 1948 |
| QY | 606 | GGGTGAGCCGAATGTACATGTTTCTGAGGGGACCCCAAGCCTGAATACCAATGA | 665 |
| Db | 1949 | AGGTGAGGCCGAAGTACATGTTTCCGATGGGAACCCAGACCTGAGTACCCAGATGA | 2008 |
| QY | 666 | TGCCAGTGTGATGAGTCCGGAAGGACAGCAACCTGCTGCAGGAATGGCAGGCCAA | 725 |
| Db | 2009 | CTACAGCCAAAGTTGGACACAGGCTGACCGGAAGAAATCTGCTGACGAATGGCTGG | 2068 |
| QY | 726 | GCAACGAGGAGCCCACTATGTGTGAAACCGCACTGCGCTCTTCAAGCGGCCGATGCT | 785 |
| Db | 2069 | GCGCAGGGTGCCCGGTATGTGTGAAACCGCACTGAGCTCATGCAGGCTTCCCTGACC | 2128 |
| QY | 786 | CAGTGTAAACACACTCATGGGCTCTTTGAGCCCGCAGACATGAATATATGTTCAGCA | 845 |
| Db | 2129 | GTCTGTGACCCATCTCATGGGTCTTTGAGCCTGAGACATGAATACGAGATCCACG | 2188 |
| QY | 846 | AGACCAACCAAGGACCCGACCCCTGGCGGAGATGACGAGGCGGCCCTGCAAGTGTGAG | 905 |
| Db | 2189 | AGACTCCACACTGACCCCTCTCTGATGGAGATGACAGAGGCTGCCCTGCGCTGTGAG | 2248 |
| QY | 906 | CAGGAACCCCCCGGGCTTCTACTCTTCTGTGAGGAGGCGCATTGACCAACGCTACCA | 965 |
| Db | 2249 | CAGGAACCCCCCGGCTTCTCTCTTCTGTGAGGAGGTGCATGCAACATGTTCATCA | 2308 |
| QY | 966 | TGACGCAAAAGCTTATATGCACTGACTGAGGCGATCATGTTGACAATGCCATGCGCAA | 1025 |
| Db | 2309 | TGAAAGCAGGCTTACCGGGCACTGACTGAGACGATCATGTTGCACGACGCCATGAGAG | 2368 |
| QY | 1026 | GGCTAACGAGCTCACTAGCGAATGGAACAGCTGATCCTGTCTACTGCAGACCACTCCCA | 1085 |
| Db | 2369 | GGCGGGCCAGCTCACGACGAGAGGAGACACGCTGAGCTCGTCACTGCCGACCACTCCCA | 2428 |
| QY | 1086 | TGTCTTCTTTTGGTGGCTACACTGCGTGGGACCTTCATTTTCCGTCTGGCCCCCGG | 1145 |
| Db | 2429 | CGTCTTCTCTTCGAGGCTACCCCTGCGAGGGAGCTTCATCTTCCGGCTGGCCCCCTGG | 2488 |

| | | | |
|----|------|---|------|
| QY | 1146 | CAAGGCCTTAGACAGCAGAATCCTTACACCCTCCATCCTCTATGGCAATGCCCCAAGCTATGC | 1205 |
| Db | 2489 | CAAGGCCCGGACAGGAAGGECTTACACGGTCCTCTATAACGAAACGGTCCAGGCTATGT | 2548 |
| QY | 1206 | GCTTGCGGGGCTCGAGGCCCGATGTTAATGGCAGCACAAGCGAGGAACTCTATACCG | 1265 |
| Db | 2549 | GCTCAAGAGACGGCGCCCGGCGCGATGTTACCGAGAGCAGAGCGGGAGCCCCGAGTATCG | 2608 |
| QY | 1266 | GCAGCAGCGCGCCGTGCCCCCTGTAGCGAGACCACGGGGGCGAAGACTGCGGTGT | 1325 |
| Db | 2609 | GCAGCAGTCAGCAGTGCCTTGACGAAAGAGACCACGACGCGAGGACGTGGCGGT | 2668 |
| QY | 1326 | CGCGCGAGGCCCGCAGCGCACCTGTGTACACGCGGTGCAGAGGAGACCTTGTGCGCA | 1385 |
| Db | 2669 | CGCGCGCGGCCCGCAGCGCACCTGTGTACGCGGTGCAGAGCAGACCTTATAGCGCA | 2728 |
| QY | 1386 | CATCATGSCCTTTGGCGSGCTGCTGGAGGCCCTAACCCGACTGCATCTGCGACCCCCC | 1445 |
| Db | 2729 | CGTCATGGCCTTCGCGCCCTGCTGTGAGCCCTTAACCGCCTGCGACCTGGCGCCCCCGC | 2788 |
| QY | 1446 | CACCGCCACCAAGCATCCCCTGAGGT | 1473 |
| Db | 2789 | CGGCACCAACCGACCGCCGCGCACCCGGGT | 2816 |

```

RESULT 12
US-09-837-863-19
; Sequence 19, Application US/09837863
; Patent No. 6468754
; GENERAL INFORMATION:
; APPLICANT: Greene, Amy
; APPLICANT: Zhou, Hua
; APPLICANT: Thode, Silke
; APPLICANT: Jarnigan, Kurt
; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
; TITLE OF INVENTION: of an Integrated DNA Sequence
; FILE REFERENCE: 025.1US
; CURRENT APPLICATION NUMBER: US/09/837,863
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/198,498
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 7092
; TYPE: DNA
; ORGANISM: vector
US-09-837-863-19

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| Query Match | Best Local Similarity | Matches 1176; | Score 67.84; | DB 4; | Pred. No. 9e-242; | Mismatches 0; | Indels 292; | Gaps 0; | Length 7092; |
|-------------|-----------------------|-------------------------|--|-------|-------------------|---------------|-------------|---------|--------------|
| QY | 6 | CCTCATCCAGCTGAGAGGAAAA | CCCCCGCCTTCTGAAACCGCCAGGCAGCCGAGCCCT | 65 | | | | | |
| Db | 1349 | CATCATCCAGCTTGAGAGGAGAA | CCCCGACTTCTGAAACCGCAGGCAGCCGAGCCCT | 1408 | | | | | |
| QY | 66 | TGATGTAGCCAAGAGTTG | CAGCCGATCCAGACAGCTGCCAAGAATGTCATCCTCTT | 125 | | | | | |
| Db | 1409 | GGGTGCCGCCAAGAGCTG | CAGCCTGCACAGACAGCCGCCAAGAACTCATCTTCT | 1468 | | | | | |
| QY | 126 | GGGGGATGGGATGGGGGT | CCTACGGTGACAGCCACTCGATCCTAAAGGGGCGATGAA | 185 | | | | | |
| Db | 1469 | GGGCGATGGGATGGGGGT | CTTACGGTGACAGCTGCCAAGATCCTAAAGGGCGAGAAGAA | 1528 | | | | | |
| QY | 186 | TGGCAAACTGGGACCTG | AGACACCCCTGGGCCATGGACCAAGTTCCCATACGTGGCTCTGTC | 245 | | | | | |
| Db | 1529 | GGACAAACTGGGGCTTG | AGATACCCCTGGGCCATGGAACCCGCTTCCCATATGTGGCTCTGTC | 1588 | | | | | |
| QY | 246 | CAAGACATACAACGTGGA | CAGACAGAGTGCCAGACAGCGCAGGCACTGCCCATGCTTA | 305 | | | | | |
| Db | 1589 | CAAGACATACAATGTAGA | CAAAACATGTGCCAGACAGTGAGCCACAGCCACCGGCTTA | 1648 | | | | | |

Db 1889 GGAGGGGTGCCAGGACATCGCTACGACGCTCATCTCCAACATGAGACATGACATGACGTGATCCT 1948
QY 606 GGGTGGAGGCCGGAATGTACATGTTTCTCTGAGGGGACCCAGAGCCCTGAATATCCAGATGA 665
Db 1949 AGGTGAGGCGCGAAGTACATGTTTCCGATGGGAACCCAGACCCTGAGTACCCAGATGA 2008
QY 666 TGCCAGTGTGAATGAGTCCGGAAGGACAAAGCACTGTGTGAGGAATGGCAGGGCCAA 725
Db 2009 CTACAGCCAAAGGTGGACCAAGCTGAGCGGGAAGATCTGTGAGGAATGGTGGCGAA 2068
QY 726 GCACCAGGAGCCCAATGTGTGGAACCGCACTGCGCTCCTTCAAGCGCGCGATGACTC 785
Db 2069 GCGCCAGGGTCCCGGTATGTGTGAACCGCACTGAGCTCATGCAAGCTTCCCTGGAACC 2128
QY 786 CAGTGTAAACACCTCATGGGCTCTTTGAGCCGCGAGACATGAAGTATAATGTTACGA 845
Db 2129 GTCTGTGACCCATCTCATGGGTCTCTTGAAGCTGAGAGACATGAATATACGATCCACCG 2188
QY 846 AGACCACACCAAGGACCCGACCTTGCGGAGATGACGAGCGCGCCCTGCAAGTGTAG 905
Db 2189 AGACTCCACACTGGACCCCTCCTGTATGAGATGACAGAGGCTGCCCTGCGCTGTAG 2248
QY 906 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGCGCCGATTGACCAAGTACCA 965
Db 2249 CAGGAACCCCGGGGCTTCTCTCTTGTGAGGAGGCTGCGATGACCAATGTCATCA 2308
QY 966 TGACGGCAAAAGCTTATATGCGACTGACTGAGCGATCATGTTTGACAAATGCCATGCCAA 1025
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QY 1026 GGCTAACGAGCTCACTAGCGAAGTGAACGCTGATCCTTGTCACTGACAGCACTCCCA 1085
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QY 1086 TGTCTTCTCTTTGGTGGCTACACACTGCGTGGGACCTCCATTTTGGGTGGCCCCGG 1145
Db 2429 CGTCTTCTCTTCCGAGGCTACCCCTGCGAGGAGCTCCATCTTCCGGGTGGCCCCGG 2488
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Db 2489 CAAGGCCCGGAGACGAAAGGCTTACACGCTCTCTATACGMAACGGTCCAGGCTATGT 2548
QY 1206 GCTTGGCGGGGCTCGAGGCGCCGATGTTAATGGCAGACAAAGCGGGAAGAGTGGCGTGT 1265
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QY 1266 GCAGCAGGCGGCGTCCCTGCTAGCGAGACCCACGGGGCGAAGAGTGGCGTGT 1325
Db 2609 GCAGCAGTACAGAGTCCCCCTGAGCAGAGAGACCCACGAGGCGAGCGTGGCGTGT 2668
QY 1326 CGCGCAGGCGCGCAGAGCGCACCTGTGTGACGCGCGTGCAGAGAGAGACCTTTCGTGGCA 1385
Db 2669 CGCGCGCGCGCGCAGAGCGCACCTGTGTGACGCGCGTGCAGAGAGAGACCTTTCATAGCGCA 2728
QY 1386 CATCATGGCTTTGGGGGCTGCGTGAGCCCTTACACCGACTGCAATCTGCGAGCCCGCGC 1445
Db 2729 CGTCATGGCTTTCGCGCGCTGCTGAGCCCTTACACCGCTGCGAGCTGGCGCCCGCGC 2788
QY 1446 CACCGCCACCAAGCATCCCGACTAGGGT 1473
Db 2789 CGGCACCAACGACGCGCGCACCCGGGT 2816

RESULT 14
US-09-837-863-27

; Sequence 27, Application US/09837863

; Patent No. 6468754

; GENERAL INFORMATION:

; APPLICANT: Greene, Amy

; APPLICANT: Zhou, Hua

; APPLICANT: Thode, Silke

; APPLICANT: Jarnigan, Kurt

; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
; FILE REFERENCE: of an Integrated DNA Sequence
; CURRENT APPLICATION NUMBER: US/09/837,863
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/198,498
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 7573
; TYPE: DNA
; ORGANISM: vector
; US-09-837-863-27

Query Match 67.8%; Score 1000.8; DB 4; Length 7573;
Best Local Similarity 80.1%; Pred. No. 9.2e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 6 CCTATCCCAAGTGAAGGAGGAAAACCCCGCTTCTGGAACCGCCAGGACCCAGGCCCT 65
Db 1349 CATCATCCCAAGTGAAGGAGGAAAACCCCGACTTCTGGAACCGCCAGGACCCAGGCCCT 1408
QY 66 TGATGTAGCCAGAAAGTTGACAGCCGATCCAGACAGCTGCCAAGAATGTCTTCTT 125
Db 1409 GGGTCCGCGCAAGAAAGCTGACAGCTGACAGACAGACCGCCAAAGAACTTATCTTCT 1468
QY 126 GGGGATGGATGGGGGTGCGCTACAGGTGACAGCACTCGATCTTAAAGGGCAGATGA 185
Db 1469 GGGCATGGATGGGGGTGCTCTACAGGTGACAGCTGCCAGATCTTAAAGGGCAGAA 1528
QY 186 TGGCAACTGGGACCTGAGACACCCCTGGCCATGGAACCAAGTTCCTATAGTGGCTGTG 245
Db 1529 GGACAACTGGGGCTGAGATACCCCTGGCCATGGAACCGCTTCCATATGTGGCTGTG 1588
QY 246 CAAGACATACAAAGTGAAGAGAGAGAGTGGCAGACAGCGGCACTGCTTACCT 305
Db 1589 CAAGACATACAAAGTGAAGAAACATGTGCCAGACAGTGAAGCCACAGCCAGGCTTACCT 1648
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Db 1649 GTGCGGGGTGAAGGGCACTTCCAGAACCACTGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1708
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Db 1709 GTGCAACACGACAGCGGCAAGAGTCACTCCGTGATGAATGGGCGCAAGAAAGCAGG 1768
QY 426 GAAGCGGTGGAGTGTGACCAACCAAGGTCAGCATGCTCCCGAGCGGGGCTTA 485
Db 1769 GAAGTCAAGTGGAGTGTGTAACCAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1828
QY 486 CGCGCACAGGTGAACCGAACTGTCTACAGCGCGGACCTGCTGCTGATGACAGAA 545
Db 1829 CGCCACACAGGTGAACCGAACTGTCTGAGCGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1888
QY 546 GAATGCTGCGAGACATGCGCGCACAGCTGTCTACAAACATGATATGACGTGATCCT 605
Db 1889 GGAGGGTGCAGAGACATGCTACGCACTCATCTCAACATGACATGACATGACATGACATGACATG 1948
QY 606 GGGTGAAGCGGAATGTACATGTTTCTGAGGGGACCCAGACCTGTAATACCCAGATGA 665
Db 1949 AGGTGAGGCGGAAAGTACATGTTTCCGATGGGAACCCAGACCCGAGTACCCAGATGA 2008
QY 666 TGCCAGTGTGAATGAGTCCGGAAGGACAAAGCACTGTGTGAGGAATGGCAGGGCCAA 725
Db 2009 CTACAGCCAAAGTGGACCAAGCTGAGCGGGAAGATCTGTGAGGAATGGTGGCGAA 2068
QY 726 GCACCAGGAGCCCAATGTGTGGAACCGCACTGCGCTCCTTCAAGCGCGGATGACTC 785
Db 2069 GCGCCAGGGTCCCGGTATGTGTGAACCGCACTGAGCTCATGCAAGCTTCCCTGGAACC 2128
QY 786 CAGTGTAAACACCTCATGGGCTCTTTGAGCCGCGAGACATGAAGTATAATGTTACGA 845

Db 2129 GTCTGTGACCCATCTCATGGGTCTTTTGAGCCTTGAGACATGAATAACGAGATCCACCG 2188
QY 846 AGACCACACCAAGAGACCCGACCTGGCGGAGATGACGAGCGGCCCTGCAAGTGTGAG 905
Db 2189 AGACTCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTGAG 2248
QY 906 CAGGAACCCCCCGGGGCTTCTACCTCTTCGTGAGGAGGAGCGCGCATTGACCAAGTACCA 965
Db 2249 CAGGAACCCCCCGGGGCTTCTCTCTTCGTGAGGAGGTGTGCGCATCGACCATGGTCATCA 2308
QY 966 TGAACGCAAAAGCTTATATGGCACTGACAGCGCATCATGTTTGAACAATGCCATCGCCAA 1025
Db 2309 TGAAGCAGGGGCTTACCGGGCACTGACGAGACGATCATGTTTGAACGACCATTTGAGAG 2368
QY 1026 GGCTAACGAGCTCACTAGCGAAGTGGACACCGCTGATCCTTGTCACTGCAGACCACTCCCA 1085
Db 2369 GGGGGGCAAGCTCACACGAGAGAGACACGCTGAGCCTGTCACCTGCCAACCACTCCCA 2428
QY 1086 TGTCTTCTCTTTTGGTGGCTACACACTGCGTGGGACCTTCATTTTGGTCTGGCCCCCGG 1145
Db 2429 CGTCTTCTCTTCGGAGGCTACCCCTTGCGAGGAGGAGCTTCATCTTCGGGCTGGCCCCCTGG 2488
QY 1146 CAAGCCTTGAACAGCAAGTCTCAACCTTCATCCTCTATGGCAATGGCCAGGCTATGC 1205
Db 2489 CAAGCCCCGGGACAGAGAGGCTTACACGCTCCTCTATACGGAACGCTCCAGGCTATGT 2548
QY 1206 GCTTGGCGGGGCTCGAGGCCGATGTTAATGGACACACAAGGAGGAACCTCATACCG 1265
Db 2549 GCTCAAGACGCGCGCGCGCGCGCGGATGTTACCGAGAGCGAGAGCGGAGCCCCGAGTATCG 2608
QY 1266 GCAAGAGCGCGCGCTGCCCCCTGGCTAGCCGAGACCCACGCGGCGGAAGACGTGGCGGT 1325
Db 2609 GCAGCAGTCAAGCAGTGCCTCCCTGGACGAAGAAGACCCACGACGCGGACGACGTGGCGGT 2668
QY 1326 CGCGGAGGCGCGCGCAGGCGCACCTGGTGACAGCGCGTGACAGAGAGAACCTTCGTGGCGCA 1385
Db 2669 CGCGCGCGCGCGCGCAGGCGCACCTGGTGACAGCGCGTGACAGAGAACCTTCATAGCGCA 2728
QY 1386 CATCATGGCCTTTGCGGGCTGCGTGAGACCTTACACCGCATGCAATCTGCCAGCCCCCGC 1445
Db 2729 CGTCATGGCCTTCGCGCGCTGCTGGAACCTTACACCGCCTGCGACCTTGGCGCCCCCGC 2788
QY 1446 CACGCGCACCAAGCATCCCCGACTAGGGT 1473
Db 2789 CGGCAACCAACGACGCGCGCGCACCGGGT 2816

RESULT 15

US-08-752-307B-1

; Sequence 1, Application US/08752307B

; Patent No. 5952171

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A.

; APPLICANT: Gearing, David P.

; APPLICANT: Levinson, Douglas A.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING GENES

; TITLE OF INVENTION: ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/752,307B

; FILING DATE: 19-NOV-1996

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/020001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-752-307B-1

Query Match

Best Local Similarity 67.8%; Score 1000.4; DB 2; Length 4951;

Matches 1175; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 8 TCATCCAGCTGAGAGAGAAAACCCGCTTCTGGAACCGCAGGAGCCGACCTTG 67
Db 1314 TCATCCAGTTGAGAGAGAGAACCCGACTTCTGGAACCGCAGGAGCCGACCTTG 1373
QY 68 ATGTAGCCAAGATTGACGCCGATCCAGACAGCTGCCAAGATGTATCTTCTTG 127
Db 1374 GTGCCGCAAGAGCTGACGCTGCACAGACAGCGCCCAAGAACCTCATCTTCTTG 1433
QY 128 GGGATGGATGGGGGTGCTTACCGGTGACAGCCACTCCGATCTTAAAGGGGAGATG 187
Db 1434 GCGATGGATGGGGGTGCTTACCGGTGACAGCTCCAGAGATCTTAAAGGGGAGATG 1493
QY 188 GCAAACTGGGACCTGAGACACCCCTGGCCATGACAGTTCCTATACGTGCTGTCCA 247
Db 1494 ACAAACTGGGCTGAGATACCCCTGGCCATGACCGCTTCCATATGTGCTGTCCA 1553
QY 248 AGACATCAACGTGACAGACAGAGTGCCAGACAGCGGACGACTGCTTACCTGT 307
Db 1554 AGACATCAATGTAGACAAACATGTGCCAGACAGTGAGCCACAGCCAGCGCTTACCTGT 1613
QY 308 GTGGGTCAAGGGCACTACAGAACCATCGGTGTAAGTGACGCGCGGCTCAATCACT 367
Db 1614 GCGGGGTCAAGGGCACTTCCAGACCATTTGGCTGAGTGACGCGCGGCTTAAACCAT 1673
QY 368 GCAACACGACGCTGGGATGAGGTACGCTGTGTATCAACCGGGGCAAGAACGAGGA 427
Db 1674 GCAACACGACACGCGGCAACGAGGTATCTCCGTATGATCGGGCCAGAAAGCAGGA 1733
QY 428 AGCGCTGGGAGTGTGACCAACCAACGAGGTGACAGTCCCTCCCAAGCGGGGCTACG 487
Db 1734 AGTCAGTGGAGTGTGACCAACCAACGAGGTGACAGTCCCTCCCAAGCGGGGCTACG 1793
QY 488 CGCACACGCTGAACCGAACTGTACTCAGACGCGGACCTGCTGTGATGACAGAGA 547
Db 1794 CCCACACGCTGAACCGCACTGTACTCGAGCGGACGCTGCTGCTGCGCGGCAAG 1853
QY 548 ATGGCTGCAGACATCGCCGACAGCTGTGCTTCAACATGATGATGACGATGCTTGG 607
Db 1854 AGGGGTGCAGACATCGCTTACGAGCTCATCTCAACATGACATGACGATGATCTTAG 1913
QY 608 GTGAGGCGGATGTATGTTTCTCTGAGGGGACCCAGACCTGATATACCAATGATG 667
Db 1914 GTGAGGCGGAGATGATGTTTCTCGATGGGAGCCCAAGACCTGATACCAAGATGACT 1973
QY 668 CCACTGTGATGAGTCCGGAAGAGACAGACAGAACTGTGACAGATGGCAGGCAAGC 727
Db 1974 ACAGCCAAGGTGGAGCAGGCTGACGAGGAAGATCTGTGCAAGATGGCTGCGCAAGC 2033
QY 728 ACCAGGAGCCAGTATGTGTGGAACCGCACTGCGCTCTTCAAGGCGGCGGATGACTCCA 787

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Db      2034 GCCAGGGTGCCCGGTATGTGTGAACCGCACTGAGCTCATGACGGCTTCCCTGAGCCCGT 2093
QY      788 GTGTACACACTTCATGGGCTCTTTGAGCCGCGACACATGAAGTATATGTTCAGCAAG 847
Db      2094 CTGTGACCCCATCTCATGGGTCTCTTTGAGCCTTGAGACATGAATATACGATCCACCGAG 2153
QY      848 ACCACACCAAGGACCCGACCCCTGGCGGAGATGACGGAGCGGCCCTGCAAGTGTAGCA 907
Db      2154 ACTCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGGCCTGTGAGCA 2213
QY      908 GGAACCCCGCGGCTTCTACCTCTTCTGTGAGGAGGCGCCGATTTGACCAAGGTCAACCATG 967
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QY      968 ACGCAAAAGCTTATGCGCACTGACTGAGCGCATCATGTTGACAATGCCATCGCCAAG 1027
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Db      2334 CGGGCCAGCTCACCAAGGAGGAGGACACGCTGAGCCTCGTCACTGCCGACCACTCCACG 2393
QY      1088 TCTTCTCTTTTGGTGGCTACACACTGCGTGGGACCTCCATTTTCGGTCTGGCCCCGGCA 1147
Db      2394 TCTTCTCTTGGAGGCTACCCCTGCGAGGAGCTCCATCTTGGGCTGGCCCCCTGGCA 2453
QY      1148 AGGCTTAGACAGCAAGTCTCTACACCTTCATCTTATGGAATGCGCCAGGCTATGCGC 1207
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QY      1268 AGCAGCGCGCTGCTGCTGCTAGCGAGACCCACGGGGCGAAGACGTGGCGGTTCG 1327
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QY      1328 CGCGAGGCGCGAGGCGCACCTGTGTCACGCGGTGACAGAGGAGACCTTGTGCGCACA 1387
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QY      1388 TCATGGCCTTTGCGGGCTGCGTGAGGCGCTTACACCGACTGCAATCTGCCAGCCCCGCA 1447
Db      2694 TCATGGCCTTGCCTGCGCTGCGTGAAGCCCTTACACCGCCTGCGACCTGGCGCCCCCGCG 2753
QY      1448 CCGCACCAAGCATCCCGACTAGGCT 1473
Db      2754 GCACCAACGACGCGCGCAACCGGCT 2779
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Search completed: October 19, 2004, 17:37:52
Job time : 146.5 secB

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Db 181 ATGAATGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCCAGTTCCCATACGTGGCT 240
Qy 241 CTGTCCAAGACATACACGCTGGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCC 300
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Db 301 TACCTGTGTGGGTCAAGGGCAACTACAGAAACCATCGGTGTAAGTGACAGCCGCCGCTAC 360
Qy 361 AATCAGTGCAACACGACACGCTGGGAATGAGGTCACGCTGTGTATCAACCCGGGCCAAGAAA 420
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Qy 421 GCAGGGAAGGCCCTGGGAGTGGTACCAACCAAGGGTGACAGATGCCCTCCCAAGCCGGG 480
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Qy 481 GCCTACGGGCACACGCTGAACCCGAACTGCTACTCAGACGCCGCACTGCTGCTGATGCA 540
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Qy 601 ATCCTGGGTGAGGCCGAATGTACTGTTTCTTGAGGGGACCCGACACCTGATATACCA 660
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Qy 661 GATGATGCCAGTGTGAATGAGTCCGGAAGGACAAAGCAGAACCTGTGCAAGGAATGGCAG 720
Db 661 GATGATGCCAGTGTGAATGAGTCCGGAAGGACAAAGCAGAACCTGTGCAAGGAATGGCAG 720
Qy 721 GCCAAGCACAGGGAGGCCAGTATGTGGAAACCGCACTGCGCTCTTCAGGCGGCCGAT 780
Db 721 GCCAAGCACAGGGAGGCCAGTATGTGGAAACCGCACTGCGCTCTTCAGGCGGCCGAT 780
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Db 841 CAGCAAGACCAACCAAGGACCCGACCTGGCGGAGATGACGGAGCGGCCCTGCAAGTG 900
Qy 901 CTGAGCAGGAACCCCGGGGCTTTACTCTTCTGAGGAGGAGCGCCGATTTGACCAAGGT 960
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Qy 961 CACCATGACGGCAAGCTTATATGGCACTGACTGAGGCGATCATGTTTGACAATGCCATC 1020
Db 961 CACCATGACGGCAAGCTTATATGGCACTGACTGAGGCGATCATGTTTGACAATGCCATC 1020
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RESULT 2
US-10-395-790A-1
; Sequence 1, Application US/10395790A
; Publication No. US20040072316A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase
; FILE REFERENCE: RDID 02028US
; CURRENT APPLICATION NUMBER: US/10/395,790A
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Bovine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1464)
; OTHER INFORMATION:
US-10-395-790A-1

Query Match 99.2%; Score 1464; DB 16; Length 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CTCATCCCAAGTGAAGGAAAAACCCCGCTTCTGGAACCGCCAGGAGCCCGCCCTT 66
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Qy 67 GATGTAGCCAAAGATTGACGCGGATCCAGACAGCTGCAAGAAATGTCATCTTCTTG 126
Db 61 GATGTAGCCAAAGATTGACGCGGATCCAGACAGCTGCAAGAAATGTCATCTTCTTG 120
Qy 127 GGGGATGGATGGGGTGGCTTACGGTGAACGCACTCGGATCCTTAAAGGGCAGATGAAT 186
Db 121 GGGGATGGATGGGGTGGCTTACGGTGAACGCACTCGGATCCTTAAAGGGCAGATGAAT 180
Qy 187 GGGAACTGGACCTGAGCAACCCCTGGCCATGACCAAGTTCCCATACGTGGCTGTCC 246
Db 181 GGGAACTGGACCTGAGCAACCCCTGGCCATGACCAAGTTCCCATACGTGGCTGTCC 240
Qy 247 AAGACATCAACAGTGGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTTACCTG 306
Db 241 AAGACATCAACAGTGGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTTACCTG 300
Qy 307 TGTGGGTCAGGGGCAACTACAGAACCATCGGTGTAAGTGACAGCCGCCGCTTACATCAG 366
Db 301 TGTGGGTCAGGGGCAACTACAGAACCATCGGTGTAAGTGACAGCCGCCGCTTACATCAG 360
Qy 367 TGCAACACGACACGTGGGAATGAGGTCAAGTCTGTGATCAACCGGGCCAAAGAACAGGG 426
Db 361 TGCAACACGACACGTGGGAATGAGGTCAAGTCTGTGATCAACCGGGCCAAAGAACAGGG 420
Qy 427 AAGCCGTGGAGTGTGACCAACCAAGGCTGACAGATGCTCCCAAGCGGGGCTTAC 486
Db 421 AAGCCGTGGAGTGTGACCAACCAAGGCTGACAGATGCTCCCAAGCGGGGCTTAC 480

QY 487 GCGCACACGGTGAACCGAACTGTACTGACGCGGACCTGCTGTGATGCACAGAAG 546
DB 481 GCGCACACGGTGAACCGAACTGTACTGACGCGGACCTGCTGTGATGCACAGAAG 540
QY 547 AATGCTGCCAGGACATCGCCGACAGCTGGTCTACACATGGATATTGACGTGATCCTG 606
DB 541 AATGCTGCCAGGACATCGCCGACAGCTGGTCTACACATGGATATTGACGTGATCCTG 600
QY 607 GGTGAGAGCCGAATGTACATGTTTCTGTGAGGGGACCCGACAGCCCTGAATACCCAGATGAT 666
DB 601 GGTGAGAGCCGAATGTACATGTTTCTGTGAGGGGACCCGACAGCCCTGAATACCCAGATGAT 660
QY 667 GCCAGTGTGAATGGAAGTCCGGAAGGACAGAACTGTGTGAGAAATGGCAGGCCAAG 726
DB 661 GCCAGTGTGAATGGAAGTCCGGAAGGACAGAACTGTGTGAGAAATGGCAGGCCAAG 720
QY 727 CACCAAGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCCTTCAGGCGCGGATGACTCC 786
DB 721 CACCAAGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCCTTCAGGCGCGGATGACTCC 780
QY 787 AGTGAACACACCTCATGCGGCTTTTGAACCGGACAGACATGAATATATGTTACAGAA 846
DB 781 AGTGAACACACCTCATGCGGCTTTTGAACCGGACAGACATGAATATATGTTACAGAA 840
QY 847 GACCAACACCAAGAACCCGACCCCTGGCGGAGATGACGGAGGCGGCGCTTCAAGTGTGAGC 906
DB 841 GACCAACACCAAGAACCCGACCCCTGGCGGAGATGACGGAGGCGGCGCTTCAAGTGTGAGC 900
QY 907 AGGAACCCCGGGGCTTCTACCTCTTGTGAGGGAGGCGCGCATTGACACGGTCACCAT 966
DB 901 AGGAACCCCGGGGCTTCTACCTCTTGTGAGGGAGGCGCGCATTGACACGGTCACCAT 960
QY 967 GACGCGAAGCTTATATGCACTGACGTGAGCGATCATGTTTGACAAATGCCATGCCAAG 1026
DB 961 GACGCGAAGCTTATATGCACTGACGTGAGCGATCATGTTTGACAAATGCCATGCCAAG 1020
QY 1027 GCTAACGAGCTCACTAGCGAAGTGAACGCTGATCCTTGTCACTGACAGACCACTCCAT 1086
DB 1021 GCTAACGAGCTCACTAGCGAAGTGAACGCTGATCCTTGTCACTGACAGACCACTCCAT 1080
QY 1087 GTCTTCTCTTTTGGTGCTACACATGCGGTGGGACCTCCATTTTCCGCTGTGCCCCCGGC 1146
DB 1081 GTCTTCTCTTTTGGTGCTACACATGCGGTGGGACCTCCATTTTCCGCTGTGCCCCCGGC 1140
QY 1147 AAGGCTTTAGACAGCAAGTCTTACACCTTCATCTCTATGSCAATGGCCAGGCTATGCG 1206
DB 1141 AAGGCTTTAGACAGCAAGTCTTACACCTTCATCTCTATGSCAATGGCCAGGCTATGCG 1200
QY 1207 CTTGGCGGGGCTCGAGGCGCGGATGTTAAATGGCAGACAAAGCGAAGAACCTCATACCGG 1266
DB 1201 CTTGGCGGGGCTCGAGGCGCGGATGTTAAATGGCAGACAAAGCGAAGAACCTCATACCGG 1260
QY 1267 CAGCAGCGGCGCTGCCCTGGCTAGCGAGACCCACGGGGGCGAAGACGTGGCGGTTC 1326
DB 1261 CAGCAGCGGCGCTGCCCTGGCTAGCGAGACCCACGGGGGCGAAGACGTGGCGGTTC 1320
QY 1327 GCGCGAGGCGCGGACAGCGGCACTGTGTGACGCGGCTGACAGGAGAGACCTTGTGGCGCAC 1386
DB 1321 GCGCGAGGCGCGGACAGCGGCACTGTGTGACGCGGCTGACAGGAGAGACCTTGTGGCGCAC 1380
QY 1387 ATCATGGCTTTTGGCGGCTGCGTGAGGCTTACACCGACTGCAATGTGCCAGCGCGGCC 1446
DB 1381 ATCATGGCTTTTGGCGGCTGCGTGAGGCTTACACCGACTGCAATGTGCCAGCGCGGCC 1440
QY 1447 ACCGCGACGACATCCCGACTAG 1470
DB 1441 ACCGCGACGACATCCCGACTAG 1464

RESULT 3
US-10-053-637-9
; Sequence 9, Application US/10053637
; Publication No. US20030158132A1

GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEAP/RGD fusion protein
; NAME/KEY: CDS
; LOCATION: (11)..(1585)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1538)..(1570)
; OTHER INFORMATION: RGD domain
; US-10-053-637-9

Query Match 67.9%; Score 1002.8; DB 15; Length 1597;
Best Local Similarity 80.1%; Pred. No. 1.7e-285;
Matches 1178; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGGAGGAAACCCCGCTTCTGGAACCGCGCAGCCAGGCCCT 65
DB 61 CATCATCCAGTTGAGGAGAGAACCCGGACTTCTGGAACCGCGCAGCCAGGCCCT 120
QY 66 TGATGATCCCAAGAGTTGACAGCCGATCCAGACAGCTGCGCAAGATGTATCTTCTT 125
DB 121 GGGTGCCCGCAAGAGCTGACGCTGCAACAGACAGCCGCGCAAGAACCTCATCTTCT 180
QY 126 GGGGATGGGATGGGGGTGCTTACGCTGACAGCCACTCGATCCTAAAGGGCAGATGAA 185
DB 181 GGGGATGGGATGGGGGTGCTTACGCTGACAGCTGCCAGATCCTAAAGGGCAGATGAA 240
QY 186 TGGCAACTGGGACCTGAGACACCCCTGGCCATGAGACCAAGTCCCATACGTGGCTGTG 245
DB 241 GGACAAACTGGGGCTGAGATACCCCTGGCCATGAGACCGCTTCCATATGTGGCTGTG 300
QY 246 CAAGACATACAAGCTGAGACAGAGTGCCAGACAGCGCAGGCACTGCTCACTACCT 305
DB 301 CAAGACATACAAGCTGAGACAAACATGTGCCAGACAGTGAGGCCACAGCCACGGCTTACCT 360
QY 306 GTGTGGGCTCAAGGGCAACTACAGAACCATCGGTGTAAGTGACGCGCGCTTACATCA 365
DB 361 GTGTGGGCTCAAGGGCAACTTCCAGACCATTTGGCTTGAAGTGACGCGCGCTTAACTCA 420
QY 366 GTGCAACAGACAGTGGGAATGAGTCACTGTGTGATCAACGGGCGCAAGAAAGCAGG 425
DB 421 GTGCAACAGACAGCGGCGCAAGGTCTATCTCCGTGATGTAATCGGGCGCAAGAAAGCAGG 480
QY 426 GAAGGCGTGGGAGTGTGACCAACCAAGGGTGACAGATGCTTCCCAAGCGGGGCTTA 485
DB 481 GAAGTCAGTGGGAGTGTGTAACCAACCAAGAGTGACAGCAAGCTTCCCAAGCGGGCACTTA 540
QY 486 CGCGCACAGGTGAACCGAACTGGTACTCAGACGCGGACCTGCTGTGATGCACAGAA 545
DB 541 CGCGCACAGGTGAACCGAACTGGTACTCAGACGCGGACCTGCTGTGATGCACAGAA 600
QY 546 GAATGCTGCCAGGACATGCGCGGACAGCTGTGTTCAACAATGATATTGACGTGATCCT 605
DB 601 GAGGGGTGCCAGGACATGCTAGCTAGCTCATCTCAACATGGAATGACGTGATCCT 660
QY 606 GGTGAGGCGCGAATGTATCATGTTTCTGAGGGGACCCGACAGCCCTGAATATCCAGATGA 665
DB 661 AGGTGAGGCGCGAAGTATCATGTTTCCCATGGGAACCCGACAGCCCTGAATATCCAGATGA 720
QY 666 TGCCAGTGTGAATGAGTCCGGAAGACAGACAGAACCTGTGTCAGGAATGGCAGGCCAA 725
DB 721 CTACAGCCAAAGGTGGAGCCAGGCTGACGGGAAGAAATCTGTGTGACGAATGGCTGGCGAA 780

[illegible]

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RESULT 4
US-10-053-637-11
; Sequence 11, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1675
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEAP/Decorasin fusion
; NAME/KEY: CDS
;

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; LOCATION: (11)..(1663)
; OTHER INFORMATION:
; NAME/KEY: misc.feature
; LOCATION: (1544)..(1663)
; OTHER INFORMATION: decorsin domain
US-10-053-637-11

```

| | | | | |
|----------------------------|--------|---------------------|-----------|--------------|
| Query Match | 67.9%; | Score 1002.8; | DB 15; | Length 1675; |
| Best Local Similarity | 80.1%; | Pred. No. 1.7e-285; | | |
| Matches 1178; Conservative | 0; | Mismatches 292; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|-------------|-----|
| QY | 6 | CCTCATCCCA | 65 |
| Db | 61 | CATCATCCCA | 120 |
| QY | 66 | TGATGTAGCC | 125 |
| Db | 121 | GGGTGCCGCC | 180 |
| QY | 126 | GGGGGATGGG | 185 |
| Db | 181 | GGGCGATGGG | 240 |
| QY | 186 | TGGCAACTGG | 245 |
| Db | 241 | GGACAACTGG | 300 |
| QY | 246 | CAAGACATCA | 305 |
| Db | 301 | CAAGACATCA | 360 |
| QY | 306 | GTGTGGGGT | 365 |
| Db | 361 | GTGCGGGGT | 420 |
| QY | 366 | GTGCACACGA | 425 |
| Db | 421 | GTGCACACGA | 480 |
| QY | 426 | GAAAGCGGTG | 485 |
| Db | 481 | GAAGTAGTGG | 540 |
| QY | 486 | CGCGCACACG | 545 |
| Db | 541 | CGCCACACCG | 600 |
| QY | 546 | GAATGGCTGC | 605 |
| Db | 601 | GGAGGGGTGC | 660 |
| QY | 606 | GGGTGAGGCC | 665 |
| Db | 661 | AGGTGAGGCC | 720 |
| QY | 666 | TGCCAGTGTGA | 725 |
| Db | 721 | CTACAGCCAA | 780 |
| QY | 726 | GCACCAAGGA | 785 |
| Db | 781 | GGCGCAAGGT | 840 |
| QY | 786 | CAGTGTAAACA | 845 |
| Db | 841 | GTCGTGAACCA | 900 |
| QY | 846 | AGACCAACCA | 905 |
| Db | 901 | AGACTCCACA | 960 |
| QY | 906 | CAGGAACCCC | 965 |

Db 961 CAGAACCCCGGCTTCTTCTTCTGAGGGGTGTCGATCGACCATGATCATCA 1020
Qy 966 TGACGGCAAAAGCTTATATGGCACTGAGCGCATCATGTTGACAAATGCCATCGCCAA 1025
Db 1021 TGAAGACAGGGCTTACCGGGCACTGACTGACATCATGTTGACGAGCCATTGAGAG 1080
Qy 1026 GGCTAACGAGCTCACTAGCGAAGTGAACAGCTGATCCTTGTCACTGCAAGCACTCCCA 1085
Db 1081 GGGGGCCAGCTCAACGAGAGAGACAGCTGAGCTCGTCACTGCCGACCACTCCA 1140
Qy 1086 TGTCTTCTCTTTGGTGGCTACACACTGCGTGGGAACTCCATTTTCGGTTCGGCCCCGG 1145
Db 1141 CGTCTTCTCTTCCGAGGCTACCCCTGCGAGGAGCTCCATCTTCGGGCTGGCCCCCTGG 1200
Qy 1146 CAAGGCTTAGACAGCAAGTCTACACCTTCATCTCTATGSCAATGGCCAGGCTATGC 1205
Db 1201 CAAGGCCCGGACAGGAAGGCTACACGGTCTCTATACGMAACGGTCCAGGCTATGT 1260
Qy 1206 GCTTGGCGGGGCTCGAGGCCGATGTTAAATGGCAGCACAAGCGAGAACCTTCATACCG 1265
Db 1261 GCTCAAGGACGGCGCCCGCGGATGTTACGAGAGAGAGCGGAGGCCGAGTATCG 1320
Qy 1266 GCAGCAGGGCGGCTGCCCCCTGGCTAGCGAAGCCACGGGGCGAAGAGTGGCGGT 1325
Db 1321 GCAGCAGTCAAGCAGTGCCTCGGACGAGAGACCCACGAGCGAGGACGTGGCGGT 1380
Qy 1326 CGCGCGAGGGCCGAGGCGGACCTGGTGCACGGCGCTGCAGAGAGAGACCTTCGTGGCGCA 1385
Db 1381 CGCGCGGGCGGACGAGGCGGACCTGGTTCAGGGCGGTGCAGAGAGAGACCTTCATAGCGCA 1440
Qy 1386 CATCATGGCTTTTGGGGCTGCGTGGAGCCCTACACCGAGTGCATCTGGCAGCCCGCGC 1445
Db 1441 CGTCATGGCTTTCGCGCTGCGCTGGAGCCCTACACCGCCTGCGACCTGGCGCCCCCGC 1500
Qy 1446 CACCGCCACGACATCCCGACTAGGTAC 1475
Db 1501 CGGCACCAACGACGCGCGCACCCGGGTTTC 1530

RESULT 5
US-10-053-637-19
; Sequence 19, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEAP/MK fusion
; NAME/KEY: CDS
; LOCATION: (11)..(1735)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1538)..(1732)
; OTHER INFORMATION: MK domain
US-10-053-637-19

Query Match 67.9%; Score 1002.8; DB 15; Length 1748;
Best Local Similarity 80.1%; Pred. No. 1.7e-285;
Matches 1178; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

Qy 6 CCTCATCCAGCTGAGAGGAAACCCCGCTTCTGGAACCGCCAGGCAAGCCAGGCCCT 65
Db 61 CATCATCCCAAGTTGAGAGAGAAACCCGACTTCTGGAACCGCCAGGCAAGCCAGGCCCT 120

Qy 66 TGATGTAGCCAAAGAGTTGACGCCGATCCAGACAGCTGCGCAAGAAATGTCATCTCTTCT 125
Db 121 GGGTGCCGCCAAGAAAGCTGACGCTTGACAGACAGACGCCCAAGAACTTCATCTTCT 180
Qy 126 GGGGATGGATGGGGGTGCTTACGGTGAACAGCCACTCGATCCTAAAGGGCAGATGAA 185
Db 181 GGGCGATGGATGGGGGTGTCTACGGTGAACAGCTGCCAGATCCTAAAGGGCAGAGAA 240
Qy 186 TGGCAACTGGCACTGAGACACCCCTGGCCATGAGACCAGTTCCCATATGCTGCTGTG 245
Db 241 GGACAAACTGGGGCTGAGATACCCCTGGCCATGAGACCAGTTCCCATATGCTGCTGTG 300
Qy 246 CAAGACATACAACTGTGACAGACAGTGGCCAGACAGCGCAGGCACTGCTTACCT 305
Db 301 CAAGACATACAACTGTGACAAACATGTGCCAGACAGTGGAGCCACAGCCAGCTTACCT 360
Qy 306 GTGTGGGTCAAGGGCAACTACAGAACATCGGTGTAAGTGACGCCGCCCTACATCA 365
Db 361 GTGCGGGTCAAGGGCAACTTCCAGACATTTGGCTTGAAGTGACGCCGCCCTTAAACA 420
Qy 366 GTGCAACAGCACAGTGGGAATGAGTCACTGTGTATCAACCGGSCCAAGAAAGCAGG 425
Db 421 GTGCAACAGCACAGCGGCAAGAGTCACTCGGTATGAATCGGGSCCAAGAAAGCAGG 480
Qy 426 GAAGCGCTGGGAAGTGTGACCAACCAAGGGTGCAGCATGCTCCCAAGCCGGGCTTA 485
Db 481 GAAGTCAGTGGGAAGTGTAAACCAACCAAGAGTGCAGACGCTTCGCCAGCCGGCACCTA 540
Qy 486 CGCGCACAGGTGAACCGAAACTGTACTAGACGCCGACCTGCTGTATGCACAGAA 545
Db 541 CGCCACACGGTGAACCGCAACTGTACTGGAGCGGACGCTGCTGCTGGCCCCGCCA 600
Qy 546 GAATGCTGCCAGAGACATCGCCGACAGCTGCTTCAACATGATATGACGTGATCCT 605
Db 601 GGAGGGTGCAGAGACATCGTACGAGCTCATCTCAACATGACATGACGTGATCCT 660
Qy 606 GGGTGAAGCCGAATGTATCATGTTCTTGAAGGGAGCCCAAGCCCTGAATAACAGATGA 665
Db 661 AGGTGAAGCCGAAGATACATGTTCCCATGGGAACCCAGACCTGAAGTACAGATGA 720
Qy 666 TGCCAGTGTGATGAGTCCGGAAGCAAGACAGAACCTGTTGACGAATGGCAGGCCAA 725
Db 721 CTACAGCCAAAGTTGGAGACGAGCTGGAACGGAAGAATCTGTTGACGAATGGCTGGCAA 780
Qy 726 GCACCAAGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCTTCAAGCGCGGCGATGACTC 785
Db 781 GCGCCAGGTGCCCGGTATGTGTGAACCGCACTGAGCTCATGACGAGCTTCCCTGGAACC 840
Qy 786 CAGTGTAAACACACTCATGGGCTTTTGAAGCCGGCAGACATGAATATATGTTACGCA 845
Db 841 GTCTGTGACCATCTCATGGGTCTTTTGAAGCCTGAGACATGAATAACAGATCCACCG 900
Qy 846 AGACCAACCAAGAGACCCGACCTGCGAGATGACGAGGCGGCCCTGCAAGTGTGAG 905
Db 901 AGACTCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGAG 960
Qy 906 CAGGAACCCCGGGGCTTACCTTTCGTGGAGGAGGCGCGCATTTGACCAAGTCAACCA 965
Db 961 CAGGAACCCCGGGGCTTCTTCTTCTTGTGAGGGGTGTCGATGACCATGTGATCA 1020
Qy 966 TGACGGCAAAAGCTTATATGGCACTGAGGCGGATCATGTTGACAAATGCCATCGCCAA 1025
Db 1021 TGAAGCAGGGCTTACCGGGCACTGAGACGATCATGTTGACGAGCCCATTTGAGAG 1080
Qy 1026 GGCTAACGAGCTCACTAGCGAAGTGAACAGCTGATCCTTGTCACTGCAAGCACTCCCA 1085
Db 1081 GGGGGCCAGCTCACAGCGAGAGACAGCTGAGCCTGTCATGCGGACCACTCCCA 1140
Qy 1086 TGTCTTCTTTTGGTGGCTACACTGCGTGGGACCTCCATTTTGGTTCGGCCCCCGG 1145
Db 1141 CGTCTTCTCTTCCGAGGCTACCCCTGCGAGGAGCTCCATCTTCGGGCTGGCCCCCTGG 1200
Qy 1146 CAAGGCTTAGACAGCAAGTCTTACACTCCATCTCTATGGCAATGGCCAGGCTATGC 1205

[illegible]

RESULT 7

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US-10-053-637-23
; Sequence 23, Application US/10053637
; Publication No. US20030158132A1
GENERAL INFORMATION:
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
FILE REFERENCE: 206211
CURRENT APPLICATION NUMBER: US/10/053,637
CURRENT FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 1915
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SEAP/VEGF121 fusion
NAME/KEY: CDS
LOCATION: (11)..(1903)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (1538)..(1900)
OTHER INFORMATION: VEGF121 domain
US-10-053-637-23

```

| | | | | |
|----------------------------|--------|---------------------|-----------|--------------|
| Query Match | 67.9% | Score 1002.8; | DB 15; | Length 1915; |
| Best Local Similarity | 80.1%; | Pred. No. 1.8e-285; | | |
| Matches 1178; Conservative | 0; | Mismatches 292; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| Qy | 6 | CCTCATCCCAAGCTGAGGAGGAAAACCCCCGCTTCTTGGAAACCGCCAGGACGCCAGGCGCTT | 65 |
| | | | |
| Db | 61 | CATCATCCCAAGTTGAGGAGGAGAAACCCGGACTTCTGGAAACCGGAGGCGAGCCGAGGCCCT | 120 |
| Qy | 66 | TGATGTAGCCAAAGAAGTTGCAGCCGATCAGACAGCTGCCAAGATGTATCTCTTCTT | 125 |
| | | | |
| Db | 121 | GGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCCTATCTTCTT | 180 |
| Qy | 126 | GGGGGATGGGATGGGGGTGCCTACGGTGAAGCCACTCGGATCCTAAAGGGGAGATGAA | 185 |
| | | | |
| Db | 181 | GGCGGATGGGATGGGGGTGTCTACGGTGAACAGCTGCCAGGATCTTAAAGGGCAGAGAA | 240 |
| Qy | 186 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGGAACCAAGTTCCTATACGTGGCTGTGC | 245 |
| | | | |
| Db | 241 | GGACAAACTGGGGCCTGAGATACCCCTGGCCATGGAACCGCTTCCATATGTGGCTGTGC | 300 |
| Qy | 246 | CAAGACATACAACGCTGACAGACAGAGTGCCAGACAGCGCAGGCACTGCCACTGGCTTACCT | 305 |
| | | | |
| Db | 301 | CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGAGCCACAGCCACGGGCTTACCT | 360 |
| Qy | 306 | GTGTGGGGTCAAGGGCAACTACAGAAACCATCGGTGAAGTGCAGCGCGCCGCTACATCA | 365 |
| | | | |
| Db | 361 | GTGCGGGGTCAAGGGCACTTCCAGACCAATTGGCTTGAAGTGCAGCGCGCCGCTTTAACCA | 420 |
| Qy | 366 | GTGCAACACGACACAGTGGGAATGAGGTCAAGTCTGTGATCAACCGGGGCCAAGAAAGCAGG | 425 |
| | | | |
| Db | 421 | GTGCAACACGACACGCGGCCAACGAGGTCACTCCGTGATGAATCGGGCCAAAGAAAGCAGG | 480 |
| Qy | 426 | GAAAGCCGTGGAGTGTGTGACCAACCAAGGCTGAGCATGCTCCCGAGCGGGGCTTA | 485 |
| | | | |
| Db | 481 | GAAGTCAGTGGAGTGTGAACCAACCAAGAGTGCAGCAGCCTTCGACAGCGGCACTTA | 540 |
| Qy | 486 | CGCGCACACGGTGAAACCGAAACTGTGTACTCAGACGCCGACCTGCTGTGATGCACAGAA | 545 |
| | | | |

| | | | |
|----|------|--|------|
| Db | 541 | CGCCCAACACGGGTGAACCGCACTGGTACTCGGACGCCGACGTCCTGCCTCGGCCGCCA | 600 |
| QY | 546 | GAATGGCTGCCAGACATCGCCGCACAGCTGCTCTACAATGGATATTGACGTGATCTT | 605 |
| Db | 601 | GGAGGGGTGCCAGACATCGCTACGCAAGCTCATCTCCAATGACATTGACGTGATCTT | 660 |
| QY | 606 | GGGTGGAGGCCGAATGTACATGTTCTCTGAGGGGACCCCAAGACCTTGATACCAGATGA | 665 |
| Db | 661 | AGGTGGAGGCCGAAGTACATGTTCTCCCATGGAAACCCCAAGACCTTGAGTACCAGATGA | 720 |
| QY | 666 | TGCCAGTGTGAATGAGTCCGGGAAGACACAGCAGAACTGCTGTGAGGATGGCAGGCCAA | 725 |
| Db | 721 | CTACAGCCCAAGGTGGGACCAGGCTGGACGGGAGAAGATCTGTGACAGGAATGGCTGGCGAA | 780 |
| QY | 726 | GCACCAAGGAGGCCAGTATGTGTGGAACCGCACTGCGCTCTTCAGGGCGCCGATGACTC | 785 |
| Db | 781 | GCGCCAGGGTGCCTCCGTTATGTGTGGAACCGCACTGAGCTCATGCAAGCTTCCCTGACCC | 840 |
| QY | 786 | CAGTGTACACACCTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTACGA | 845 |
| Db | 841 | GTTGTGACCCCATCTCATGGGTCTTTGAGCCTGGAGACATGAATACGAGATCCACCG | 900 |
| QY | 846 | AGACCACACCAAGAGACCCGACCTTGCGGAGATGACGAGCGGCCCTGCAAGTGTGAG | 905 |
| Db | 901 | AGACTCCACACTGGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTGAG | 960 |
| QY | 906 | CAGGAACCCCCCGGGCTCTAACCCTTCGTGAGGAGGCCGATTGACCACGCTACCA | 965 |
| Db | 961 | CAGGAACCCCCCGGGCTTCTCTCTCTCTGAGAGGTGATCGCATGACCATGCTATCA | 1020 |
| QY | 966 | TGACGGCAAGCTTATATGCACTGACTGAGGCGATATGTTGACAATGCCATCGCCAA | 1025 |
| Db | 1021 | TGAAGCAGAGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGACGCCATTGAGAG | 1080 |
| QY | 1026 | GGCTAACGAGCTCACTAAGCGAACTGACACCGCTGATCTTGTCACTGCAGACCACTGCCA | 1085 |
| Db | 1081 | GCGCGGCAGCTCACAGCAGAGAGGACACAGCTGAGCTGTCACTGCCACCACTGCCA | 1140 |
| QY | 1086 | TGCTTCTCTTTTGGTGGCTACACACTGCGTGGGACCTTCATTTTCGCTTGCCCCCGG | 1145 |
| Db | 1141 | CGTCTTCTCTTCGAGGCTACCCCTGCGAGGAGCTTCATCTTCGGGCTGGCCCCCTGG | 1200 |
| QY | 1146 | CAAGGCTTAGACACAGAACTTACACCTCCATCCTCTATGGCAATGGCCCAAGCTATGC | 1205 |
| Db | 1201 | CAAGGCCCCGGGACAGGAAGGCTTACACGGTCTCTCTATACGAAACGGTCCAGGCTATGT | 1260 |
| QY | 1206 | GCTTGGCGGGGCTCGAGGCCCGGATGTTAATGGCAGCACAAGCGAGGAACCTTCATACCG | 1265 |
| Db | 1261 | GCTCAAGAGACGGCGGCCCGGATGTTAACGAGCGAGAGCGGGAGGCCCGAGTATCG | 1320 |
| QY | 1266 | GCAGCAGGCGGCGGTGCTGCTGCTAGCGAGACCAAGGGGCGAAGACCTGGCGGTGTT | 1325 |
| Db | 1321 | GCAGCAGTCAAGCAGTCCCCCTGGACGAAGAGACCAAGCAGCGAGGACGTGGCGGT | 1380 |
| QY | 1326 | CGCGCAGAGCCCGCAGCGCACTGTGTACACGGCGCTGCAGAGAGAGACCTTCGTGGCGCA | 1385 |
| Db | 1381 | CGCGCGCGGCCCGCAGCGCACTGTGTTACGGCGCTGCAGAGACGACCTTCATAGCGCA | 1440 |
| QY | 1386 | CATCATGGCTTTGGCGGCTGCGTGAGAGCCTTACACCGACTGCAATCTGCAGGCCCCCGC | 1445 |
| Db | 1441 | CGTCATGGCTTCGCGCGCTGCTGAGAGCCTTACACCGCCTGCGACCTGGCGGCCCCCGC | 1500 |
| QY | 1446 | CACCGCCACCAAGCATCCCGACTAGGGTAC | 1475 |
| Db | 1501 | CGGCACCAACCGACGCGCGCACCCCGGGTTC | 1530 |

RESULT 8

US-10-053-6337-27
; Sequence 27, Application US/100536337
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE

```

; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1975
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEAP/W/VEGF121 fusion
; NAME/KEY: CDS
; LOCATION: (11)..(1963)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (1538)..(1591)
; OTHER INFORMATION: Spacer (W) encoded by the annealed nucleotides (SEQ ID NOS: 25 an
; OTHER INFORMATION: d 25)
; NAME/KEY: misc feature
; LOCATION: (1598)..(1960)
; OTHER INFORMATION: VEGF121 domain
; US-10-053-637-27
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Query Match 67.9%; Score 1002.8; DB 15; Length 1975;
Best Local Similarity 80.1%; Pred. No. 1.8e-285;
Matches 1178; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

```

QY 6 CCTCATCCAGCTGAGAGAGAAACCCGCTTCTGGAACCGCCAGCCAGCCCT 65
Db 61 CATCATCCAGCTGAGAGAGAACCCGCACTTCTGGAACCGCCAGCCAGCCCT 120
QY 66 TGATGTAGCCAAAGAGTTGCAAGCCGATCCAGACAGCTGCCAAGATGTCATCTTCTT 125
Db 121 GGGTGCCGCAAGAGAGCTGCAAGCTGCAAGACAGCCGCCAAGAACCTCATCTTCTT 180
QY 126 GGGGATGGGATGGGGGTGCTTACCGGTGACAGCCACTCGGATCTTAAAGGGCAGATGA 185
Db 181 GGGCGATGGGATGGGGGTGTCTACGGTGAACAGCTGCCAGGATCTTAAAGGGCAGAA 240
QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGACCAAGTCCCATACGTGGCTGTG 245
Db 241 GGACAAACTGGGGCTGAGATACCCCTGGCCATGACCCGCTTCCATATGTGGCTGTG 300
QY 246 CAAGACATACAACGTGACACAGAGTGCACAGACAGCGCAGGCACTGCCACTGCTACT 305
Db 301 CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGAAGCACAAGCAGCGCTACT 360
QY 306 GTGTGGGCTCAAGGGCACTACAGAACCATCGGTGTAAGTGACGCGCCGCTACAATCA 365
Db 361 GTGCGGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAGTGACGCGCCGCTTAAACA 420
QY 366 GTGCAACACGACAGTGGGAATGAGTCAAGTCTGTGATCAACGGGGCCAAGAAAGCAG 425
Db 421 GTGCAACACGACAGCGGGCAAGAGTCACTCCGTGATGAATCGGGCCAAGAAAGCAG 480
QY 426 GAAGGCCGTGGAGTGTGACCAACCAAGGGTGACAGCATGCTCCAGCGGGGCTTA 485
Db 481 GAAGTCAAGTGGAGTGTAAACCAACAGAGTGACAGCAGCTCGCCAGCGGCACTTA 540
QY 486 CGCGCACACGGTGAACCGAACTGCTACTAGACGCGCGCACTGCTGTGACACAGAA 545
Db 541 CGCCCAACAGGTGAACCGCACTGCTACTCGACGCGCGAGCTGCTCGGCCGCA 600
QY 546 GAATGGCTGCAGACATCGCCGCAAGCTGCTTACAAATGATATGACGTGATCTT 605
Db 601 GAGAGGGGTGCAGACATCGCTAAGCAGCTCATCTCAACATGACATGACGTGATCTT 660
QY 606 GGGTGAAGGCCGAATGTATCTTTCTGAGGGGAGCCCAAGACCTGAATACCAAGTGA 665
Db 661 AGGTGAAGGCCGAAGTATCTTTTCCATGGGAACCCCAAGACCTGAGTACCCAGATGA 720
QY 666 TGCCAGTGTGAATGAGTCCGGAAGACAAGCAAGAACCTGTGTGAGGAATGGCAGGCCAA 725
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Db 721 CTACAGCCCAAGGTGGAGCAGGCTGACGGGAAGATCTGCTCAGGAATGCTGGCAA 780
QY 726 GCACCAAGGAGCCCAAGTATGTGAAACCGCACTGCGCTCTTCAAGCGCGCGATGATC 785
Db 781 GCGCAGGGTGCCCGTATGTGAAACCGCACTGAGTCAAGGCTTCCCTGAGACC 840
QY 786 CAGTGTAAACACACTCATGGGCTCTTTGAGCCCGGACATGAAGTATATGTTACGA 845
Db 841 GTCTGTAGCCCATCTCATGGGTCTTTGAGCCTGAGACATGAATACAGATCCACCG 900
QY 846 AGACCAACCAAGAGACCCGACCTGGCGGAGATGACGAGCGGCCCTGCAAGTGTGAG 905
Db 901 AGACTCCACACTGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCTGTAG 960
QY 906 CAGAACCCCGCGGCTTCTACCTCTTCGTGAGGAGGCGCCATGACCAAGTCAACA 965
Db 961 CAGGAACCCCGCGGCTTCTTCTTCTTCTGAGGAGGTGTCGCATCGACCATGTATCA 1020
QY 966 TGACGCCAAAGCTTATATGSCACTGACTGAGGCGATATGTTGACAATGCCATGCCAA 1025
Db 1021 TGAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGACGCCATGAGAG 1080
QY 1026 GGCTAACGAGCTCACTAGCGAACTGACACGCTGATCTTGTCACTGCAGACCACTCCA 1085
Db 1081 GGGGGGCGAGCTCACCAAGAGAGAGACACGCTGAGCTTGTCACTGCCAGCACTTCCA 1140
QY 1086 TGCTTCTCTTTTGTGCTACACACTGCGTGGGACCTTCATTTTCGTGCGCCCGG 1145
Db 1141 GCTCTTCTCTTTCGAGGCTACCCCTGCGAGGAGCTTCATCTTGGGCTGGCCCTGG 1200
QY 1146 CAAGCCTTAGACAGCAAGTCTTACACCTCCATCTTATGCAATGCCCAGGCTATGC 1205
Db 1201 CAAGGCCCGGACAGAGAGGCTTACACGCTCTCTATACGGAACGCTCAGGCTATGT 1260
QY 1206 GCTTGGCGGGGCTCGAGCCCGATGTTAATGACACACAAGCGAAGACCTTCAATCCG 1265
Db 1261 GCTCAAGGACGGCGCCCGCGGATGTTACCGAGAGCGAAGCGGAGGCCCAATATCG 1320
QY 1266 GACAGAGGCGCGCTGCGCTGCTAGCGAGACCCAGGGGGCGAAGACGTGGCGGT 1325
Db 1321 GCAGCAGTACAGCAGTCCCTTGACGAAAGAGACCCAGCAGGACGTGGCGGT 1380
QY 1326 CGCGGAGGCGCGCAGGCGCACTGTGTCAAGCGGCTGACAGAGAGACCTTGTGCGCA 1385
Db 1381 CGCGCGCGCGCGCAGGCGCACTGTGTCAAGCGGCTGACAGAGACCTTATAGCGCA 1440
QY 1386 CATCATGGCTTTGCGGCTGCGTGTGAGCCCTTACACCGAATCTGCCAGCCCGCGC 1445
Db 1441 CGTATGGCTTTCGCGCTGCTGTGAGCCCTTACACCGCCTGCGACCTGGCGCCCGCGC 1500
QY 1446 CACCGCACCAAGATCCCGCACTAGGATAC 1475
Db 1501 GGGACACCAAGCAGCGCGGCAACCGCGGTT 1530
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RESULT 9
US-10-053-637-5
; Sequence 5, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1918
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (11)..(1531)
; OTHER INFORMATION:
US-10-053-637-5

Query Match 67.9%; Score 1002.4; DB 15; Length 1918;
Best Local Similarity 80.2%; Pred. No. 2.3e-285;
Matches 1177; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTGGAACCGCCAGGAGCCAGGCCCT 65
DB 61 CATCATCCAGTTGAGAGAGAAACCCGACTTCTGGAACCGCCAGGAGCCAGGCCCT 120

QY 66 TGATGTAGCCAGAAGTTGACGCCGATCCAGACGCTGCCAAGAATGTATCTTCTT 125
DB 121 GGGTCCGCCAGAGAGCTGCAGCCTGCACAGACAGCCGCCAAGAACTCATCTTCT 180

QY 126 GGGGATGGATGGGGGTGCTTACGCTGACAGCCACTCGATCTTAAGGGGAGATGAA 185
DB 181 GGGCGATGGATGGGGGTGCTTACGCTGACAGCTGCCAGATCTTAAGGGGAGATGAA 240

QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGGAACCATGTTCCCATAGCTGCT 245
DB 241 GGACAACTGGGGCTGAGATACCCCTGGCCATGGAACCGCTTCCCATATGTGGCTCT 300

QY 246 CAAGACATACACCTGGAACAGACAGAGTGGCCAGACGCGAGGACATGCTGCTTACCT 305
DB 301 CAAGACATACATGTAGACAAACATGTGCCAGACAGTGAGCCACAGCCACGGCTTACCT 360

QY 306 GTGTGGGCTCAAGGCACTACAGAACCATCGGTGTAGTGACAGCCGCCGCTACATCA 365
DB 361 GTGCGGGCTCAAGGCACTTCCAGACCATGTGCTTGTAGTGACAGCCGCCGCTTAACTCA 420

QY 366 GTGCAACAGACAGTGGGAATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 425
DB 421 GTGCAACAGACAGTGGGAATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 480

QY 426 GAAGCGCTGGAGTGTGACCAACCAAGGCTGACATGCTCCCAAGCCGGGCTT 485
DB 481 GAAGTCAAGTGGAGTGTGACCAACCAAGGCTGACATGCTCCCAAGCCGGGCTT 540

QY 486 CGCGCACACGCTGAACCGAACTGTACTAGACGCGGACCTGCTGATGACAGAA 545
DB 541 CGCGCACACGCTGAACCGCAACTGTACTAGACGCGGACCTGCTGATGACAGAA 600

QY 546 GAATGCTGCCAGACATGCGCCGACAGCTGTCTACAACATGATATGACGTGATCCT 605
DB 601 GAGGGGTGCCAGACATGCTGACGAGCTCATCTCAACATGACATGACGTGATCCT 660

QY 606 GGGTGAAGCCGATGTATCATGTTTCTGAGGGGAGCCCGAGACCCCTGAATACCCAGATGA 665
DB 661 AGGTGAGGCGCGAAGTACATGTTTCCCATGGAAACCCAGACCCCTGAGTACCCAGATGA 720

QY 666 TGCCAGTGTGAATGAGTCCGGAAGACAGAACTGTGTGAGGAATGGCAGGCCAA 725
DB 721 CTACAGCCCAAGTGGGAGCCAGGCTGAGCGGAAGAACTGTGTGAGGAATGGCTGGCGAA 780

QY 726 GCACCAAGGAGCCAGTATGTGTGAACCGCACTGCGCTCTTACAGCGCCGATGACTC 785
DB 781 GCGCAGGAGTGGCGGTATGTGTGAACCGCACTGAGCTCATGAGGCTTCCCTGAGCCC 840

QY 786 CAGTGTACACACTCATGGGCTCTTGTGAGCCGCGAGACATGAAGTAAATGTTACAGA 845
DB 841 GTCTGTAGCCATCTCATGGGTCTTGTGAGCCTGAGACATGAATGAATGATCCACCG 900

QY 846 AGACCAACCAAGAGACCCGACCTGGCGAGATGACGAGGCGGCGCTGCAAGTGTAG 905
DB 901 AGACTCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTAG 960

QY 906 CAGGAACCCCGGGGCTTCTACTCTTCTGTGAGGAGGAGCGCCATGACCAAGCTACCA 965
DB 961 CAGGAACCCCGGGGCTTCTCTCTTCTGTGAGGAGGAGGCTGCGCATGACCATGTGATCA 1020

QY 966 TGACGGCAAGCTTATATGCACTGATGAGGCGATCATGTTTGAATGCCATCGCCAA 1025
DB 1021 TGAAAGCAGGCTTACCGGGCACTGATGAGACGATCATGTTTGAACGCCATGTAGAG 1080

QY 1026 GGCTAACGACTCACTAGCGAACTGACACGCTGATCCTTGTACTGACAGCACTCCCA 1085
DB 1081 GGGGGGCACTCACAGCAGAGAGACAGCTGAGCCTGCTACTGCGGACCACTCCCA 1140

QY 1086 TGTCTTCTTTTGGTGTACACACTGCTGGGACCTCCATTTTGGTCTGGCCCCGG 1145
DB 1141 GGTCTTCTCTTGGAGGCTACCCCTGCGAGGAGCTCCATCTTGGGCTGGCCCCGG 1200

QY 1146 CAAGGCTTACAGCAAGTCTTACCTCCATCTCTATGGAATGSCCAAGCTATGC 1205
DB 1201 CAAGGCTTACAGCAAGGCTTACAGCTCTCTATACGGAACGCTCCAGGCTATGT 1260

QY 1206 GCTTGGCGGGGCTCGAGGCCCGATTTAATGGCAGCACAAGCGAACCCTCATACCG 1265
DB 1261 GCTCAAGACGCGCGCCCGGATGTTAACGAGAGCAGAGCGGAGCCCGAGTATCG 1320

QY 1266 GCAGAGCGGCGCTGCGCCCTGCTAGCAGAACCCAGCGGGCGAAGCTGGCGGT 1325
DB 1321 GCAGAGCTAGCAGTGCCTGAGCAAGAACCCAGCAGGCGGAGCTGGCGGT 1380

QY 1326 CGCGGAGCGCCGACAGGCGCACTGTGTCAAGGCTGACAGAGAGACCTTGTGCGCA 1385
DB 1381 CGCGGCGCGCCGACAGGCGCACTGTGTCAAGGCTGACAGAGAGACCTTGTATAGCGCA 1440

QY 1386 CATCATGCGCTTGTGCGGCTGCTGAGACCTTACACCGACTGCAATCTGCCAGCCCCGC 1445
DB 1441 GGTATGCGCTTGTGCGGCTGCTGAGACCTTACACCGCTGCGACTTGGCGCCCCGC 1500

QY 1446 CACCGCCACGACATCCCGACTAGGCT 1473
DB 1501 CGGACCAACGACGCGCGGACCCCGGT 1528

RESULT 10
US-09-908-943A-127
; Sequence 127, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasek, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heintz, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908, 943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219, 795
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 127
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleic acid
; OTHER INFORMATION: encoding recombinant fusion protein
US-09-908-943A-127

Query Match 67.9%; Score 1002.2; DB 10; Length 1728;
Best Local Similarity 80.1%; Pred. No. 2.6e-285;
Matches 1178; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTGGAACCGCCAGGAGCCAGGCCCT 65
DB 51 CATCATCCAGTTGAGGAGGAGAAACCCGACTTCTGGAACCGCCAGGAGGAGGCCCT 110

QY 66 TGATGTAGCCAAAGAGTTGCAGCCGATCCAGACAGCTGCCAAGATGTCTCTTCTT 125
Db 111 GGGTGCCGCAAGAAAGCTGCAGCCTTGACACAGACGCCGCAAGAACTCATCTTCTT 170
QY 126 GGGGGATGGATGGGGGTGCTTACGGTGACAGCCACTCGATCCTTAAAGGGCAGATGA 185
Db 171 GGGCGATGGATGGGGGTGTCTACGGTGACAGCTGCCAGATCCTTAAAGGGCAGAGAA 230
QY 186 TGGCAAACTGGGACCTTGAGACACCCCTGSCCATGGACCAGTTCCCATACGTGGCTGTG 245
Db 231 GGACAAACTGGGGCTTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGCTGTG 290
QY 246 CAAGACATACAGCTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCCACTCT 305
Db 291 CAAGACATACATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCCTACT 350
QY 306 GTGTGGGGTCAAGGGCACTACAGAACCATCGGTGTAACTGACGGCGCCGCTACAATCA 365
Db 351 GTGCGGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAGTGCAGCGCCGCTTTAACCA 410
QY 366 GTGCAACAGCACAGTGGGAATGAGTCAAGTGTGATCAACCGGGCCAAAGAACAGG 425
Db 411 GTGCAACAGCACAGCGCGCAACGAGTCAATCTCCGTGATGAATCGGGCCAAAGAACAGG 470
QY 426 GAAAGCCGTGGGAGTGTGACCAACCAAGGCTGACAGCATGCTCCCAAGCCGGGCTTA 485
Db 471 GAAGTCAGTGGAGTGTGAACCAACCAAGAGTGACAGCAGCCTCGCCAGCCGACCTTA 530
QY 486 CGCGCACAGGTGAACCGAACTGGTACTCAGACGCCGACCTGCTGTGATGCACAGAA 545
Db 531 CGCCCAACAGGTGAACCGCACTGGTACTCGGACGCCGACGTGCTGCTCGGCCGCCA 590
QY 546 GAATGGCTGCCAGGACATCGCCGACAGCTGCTTACAAACATGATATTGACGTGATCT 605
Db 591 GGAGGGGTGCCAGGACATCGCTACGACGCTCATCTCCAACATGACATTTGACGTGATCT 650
QY 606 GGGTGAAGCCCGAATGTACATGTTTCTGAGGGGACCCCAAGCCCTGAATACCAGATGA 665
Db 651 AGGTGAGAGGCCGAAAGTACATGTTTCCCATGGGAACCCCAAGCCTGAGTACCAGATGA 710
QY 666 TGCCAATGTGAATGAGTCCGGAAGACAAAGCAGAACCTGTGCAAGAAATGGCAGGCCAA 725
Db 711 CTACAGCCAAAGGTGGACCAAGCTGGAACGGAAGAAATCTGTGCAAGAAATGGCTGCGAA 770
QY 726 GCAACAGGAGCCCAAGTATGTGGAACCGCACTGCGCTCTTCAAGCCGGCCGATGACTC 785
Db 771 GCGCCAGGGGTGCCCGGATGTGTGGAACCGCACTGAGCTCATGCAAGGCTTCCCTGAGCCC 830
QY 786 CAGTGTAAACACACCTCATGGGCTCTTTGAGCCGCGACACATGAATATATGTTACGA 845
Db 831 GTCTGTGAACCATCTCATGGGTCTTTTGAGCCTGGAACATGAATAACGAGATCCACCG 890
QY 846 AGACCAACCAAGGACCCGACCTTGGCCGAGATGACGGAGCGGCCCTGCAAGTGCTGAG 905
Db 891 AGACTCCAACACTGGACCCCTCCCTGATGGAGATGACAGAGGCTGCCCTGCGCTGCTGAG 950
QY 906 CAGGAACCCCCGGGGCTTCTACTCTTCTGTTGAGGGGAGGCCGCAATTGACCACGGTCA 965
Db 951 CAGGAACCCCCGGGGCTTCTTCTCTTCTGTTGAGGGGTGTGCAATGCAATGTTCA 1010
QY 966 TGAACGCAAAAGCTTATATGGCACTGACTGAGGCGATCATGTTGACAATGCCATGCCAA 1025
Db 1011 TGAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGAGCCATTGAGAG 1070
QY 1026 GGGTAAAGAGCTCACTAGCGAACTGGAACAGCTGATCCTTGTCACTGCAGACCACTCCA 1085
Db 1071 GGGGGGGCCAGCTCACAGGAGAGGACACGCTGAGCCTGTCACTGCCGACCACTCCA 1130
QY 1086 TGTCTTCTCTTTTGGTGGCTACACACTGGCGTGGGACCTTCCATTTTCGGTCTGGCCCCGG 1145
Db 1131 CGTCTTCTCTTTCGAGGGCTTACCCCCCTGCGAGGAGGCTCCATCTTCGGGCTGGCCCCCTGG 1190
QY 1146 CAAGGCTTGAACAGCAAGTCTTAACCTCCTCATCTTATGGCAATGGCCAGGCTATGC 1205

Db 1191 CAAGCCCCGGGACAGAGAGGCTTACACGGTCTCTCTTATACGGAACGSTCCAGGCTATGT 1250
QY 1206 GCTTGGCGGGGCTCGAGGCCCATGTTATATGGCAGACAAAGCGAAGAACCTCTCATACCG 1265
Db 1251 GCTCAAGGACGGCGCCCGCCCGGATGTTATCCGAGAGCGAAGCGGGAGCCCGGAGTATCG 1310
QY 1266 GCAGCAGGCGGCGCTGCGCTGGCTAGCGAGACCCAGGGGGCGAAGACGTGGCGGT 1325
Db 1311 GCAGCAGTACAGATGCCCCCTGGAAGAGAGACCAAGAGGCGAGAGACGTGGCGGT 1370
QY 1326 CGCGCAGGCCCCGACAGCGCAGCTGTGACAGCGCGCTGCAAGAGAGACCTTCTGGCGCA 1385
Db 1371 CGCGCGCGGGCCGACAGGCGCACTGTTCACGCGCGTGCAGAGCAGACCTTCAATAGCGCA 1430
QY 1386 CATCATGGCCTTTGCGGGCTGCGTGGAGCCCTACACCGACTGCAATCTGCAAGCCCCCG 1445
Db 1431 CGTCATGGCCTTCGCGCGCTGCTGAGGCCCTACACCGCCTGCGACCTGGCGCCCCCG 1490
QY 1446 CACCGCCACCAAGCATCCCCGACTAGGGTACC 1476
Db 1491 CGGCACCAACGACGCGCGCGCAACCAAGGTAA 1521

RESULT 11
US-10-071-645-4
; Sequence 4, Application US/10071645
; Publication No. US20030148389A1
; GENERAL INFORMATION:
; APPLICANT: Bihaun, Bernard
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Schizophrenia Related Gene and Protein
; FILE REFERENCE: 92.US2.CIP
; CURRENT APPLICATION NUMBER: US/10/071,645
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/223,482
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01891
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO 4
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-071-645-4

Query Match 67.9%; Score 1002; DB 15; Length 1779;
Best Local Similarity 80.2%; Pred. No. 3e-285;
Matches 1176; Conservative 0; Mismatches 290; Indels 0; Gaps 0;
QY 8 TCATCCAGCTGAGAGGAAAAACCCGCTTCTGGAACCGCCAGGCGAGCCGACGCCCTTG 67
Db 215 TCATCCAGTTGAGAGGAGAAACCCGACTTCTGGAACCGCGAGGCGAGGCCCTTG 274
QY 68 ATGTAGCCAAAGATTGACAGCCGATCCAGACAGCTGCCAAGATGTATCTTCTTGG 127
Db 275 GTGCCGCCAAGAGCTGACGCTGCACAGACAGCCGCCAAGAACCTCATCATCTTCTTG 334
QY 128 GGGATGGATGGGGGTGCTTACGCTGACAGACCACTCGATCCTTAAAGGGCAGATGA 187
Db 335 GCGATGGATGGGGGTGTCTACGCTGACAGCTGCCAGATCCTTAAAGGGCAGAAAGG 394
QY 188 GCAAACTGGGACCTGAGACACCCCTGGCCATGGACCAAGTTCCCATACGTGGCTGTCCA 247
Db 395 ACAAACTGGGGCTGAGATTAACCCCTGGCCATGACCCGCTTCCCATATGTGCTGTCCA 454
QY 248 AGACATACAACGTGACAGACAGAGTGGCAGACAGCGCAGGCACTGGCCTACCTGT 307
Db 455 AGACATACAATGTAGCAAAACATGTGCCAGACAGTGAAGCCACAGCCACGGCCTACCTGT 514
QY 308 GTGGGTCAAGGGCACTACAGAACCATCGGTGTAAAGTGACAGCCGCGCCTACAAATCAGT 367

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Db      515 GCGGGGTCAAGGCACTTCCAGACCATTGGCTTGAGTGCAGCCGCGCCCTTTAAACAGT 574
Qy      368 GCAACACGACACGTGGGAATGAGTCACTGTGTGATCAACCGGGCCAGAAAGCAGGGA 427
Db      575 GCAACACGACACCGCGCAACGAGGTCACTCTCGGTGATGAATCGGGCCAGAAAGCAGGGA 634
Qy      428 AGCGCGTGGAGTGTGATCCACCACGAGGGTGCAGCATGCTCCCGCAGCGGGGCTTACG 487
Db      635 AGTCAGTGGAGTGTGATCCACCACGAGTGCAGCAGCTCTCGCAGCGGCACTTACG 694
Qy      488 CGCACACGCGTGAACCGAACTGTACTCAGACGCGGACCTGCTGTGATGACAGAGA 547
Db      695 CCCACACGCGTGAACCGCACTGTACTCGAGCGCGACGTGCTGCTCGGCGCCGACAG 754
Qy      548 ATGCTGCCAGACATCGCCGACAGCTGGTCTACAACATGATATGACGTGATCCTGG 607
Db      755 AGGGGTGCCAGACATCGCTACGACGCTCATCTCCAACATGACATTGACGTGATCCTAG 814
Qy      608 GTGAGCGCCGAATGATCATGTCTTCTGAGGGGACCCGAGACCCTGAATGCCAGATGATG 667
Db      815 GTGAGGCGCGAAGTACATGTCTTCCCATGGGAACCCGAGACCCTGAGTACCCAGATGACT 874
Qy      668 CCAGTGTGAATGAGACTCCGGAAGACAGACGAACCTGTGCAGGAATGGAAGGCCAAGC 727
Db      875 ACAGCCAAAGGTGGACCAAGCTGACGCGGAAGATCTGTGCAGGAATGGCTGGCGAAGC 934
Qy      728 ACCAGGAGCCCAATATGTGTGAAACCGCACCTGCTCTTCAAGCGCGCGCATGACTCCA 787
Db      935 GCCAGGGTCCCGTATGTGTGAAACCGCACCTGATGACAGGCTTCCCTGGAACCCGT 994
Qy      788 GTGTAACACACTCATGGGCTCTTTGAGCCGCGACAGCATGAATATAATGTTAGCAAG 847
Db      995 CTGTGACCCATCTCATGGGTCTCTTTGAGCCGCGAGACATGAATACAGATCCACCGAG 1054
Qy      848 ACCACACCAAGACCCGACCCCTGCGGAGATGACGAGCGCGCCCTGCAAGTGTGAGCA 907
Db      1055 ACTCCACACTGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTGAGCA 1114
Qy      908 GGAACCCCGGGGCTTCTAACCCTCTGTGAGGAGGAGCGCCGATGACCAAGTCAACCATG 967
Db      1115 GGAACCCCGGGGCTTCTTCTCTTGTGAGGAGGTGTCGATCGACCATGTGTCATCATG 1174
Qy      968 ACGGCAAAAGCTTATATGCACTGACCTGAGGCGATCATGTTGACAATGCCATGCCAAGG 1027
Db      1175 AAAGCAGGCTTACCGGGCACTGACTGAGCATGATGTTGACGACGCCATTTGAGAGGG 1234
Qy      1028 CTAACGAGCTCACTAGCGAACTGACACGCTGATCCTTGTCACTGACAGCACTCCCATG 1087
Db      1235 CGGCGCACTCACGAGAGGAGACACGCTGACCTCGTCACTGCCAGCACTCCACG 1294
Qy      1088 TCTTCTCTTTGGTGGCTACACACTGCGTGGGACCTCCATTTCGGTCTGCGCCCGGCA 1147
Db      1295 TCTTCTCTTCCGAGGCTACCCCTGCGAGGAGCTCCATCTTCGGGCTGCGCCCTGGCA 1354
Qy      1148 AGGCTTAGACAGCAAGTCTTACACCTCCATCCTATGGAATGAGCCAGGCTATGCGC 1207
Db      1355 AGGCGCGGACAGGAAGGCTTACACGCTCTCTATACGAAAAGGTCCAGGCTATGTGC 1414
Qy      1208 TTGGCGGGGCTCGAGGCGCGATGTTAATGGACACAAGCGAGGAACCTCTATACCGGC 1267
Db      1415 TCAAGGACGCGCGCGCGCGGATGTTACCGAGAGCGAGCGGAGCCCGAGTATCGGC 1474
Qy      1268 AGCAGGCGCGCGCTGCGCTGCGTAGCGAGACCAAGCGGGCGAAGACGTGCGTGTTCG 1327
Db      1475 AGCAGTACAGCATGCGCGCTGAGCAAGAGACCAAGCGAGCGAGACGTGCGGTGTTGC 1534
Qy      1328 CGCAGGCGCGCGACGCGCACCTGTGACGCGGTGCAGAGAGAGACCTTCGTGGCGACA 1387
Db      1535 CGGCGCGCGCGCAGCGCACCTGTGTCACGCGGTGCAGAGAGACCTTCATAGCGCACG 1594
Qy      1388 TCATGGCTTTGCGGGCTGCGTGAAGCCCTACACCGAATGCAATCTGCCAGCCCCGCCA 1447
Db      1115 TCATGGCTTTGCGGGCTGCGTGAAGCCCTACACCGAATGCAATCTGCCAGCCCCGCCA 1447
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Db      1595 TCATGGCTTCCGCGCGCTGCGCTGAGCCCTACACCGCGCTGCGACTGGCGCCCCCGCG 1654
Qy      1448 CCGCCACACGATCCCGACTAGGCT 1473
Db      1655 GCACCACCGACGCGCGCACCCGGGT 1680

RESULT 12
US-10-182-094-7
; Sequence 7, Application US/10182094
; Publication No. US20040019193A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; TITLE OF INVENTION: MOB-5/HMOB-5 AS A CANCER DIAGNOSTIC MARKER
; FILE REFERENCE: 22000.0091U3
; CURRENT APPLICATION NUMBER: US/10/182,094
; PRIOR FILING DATE: 2002-07-25
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20040019193A1e =
US-10-182-094-7

Query Match      67.9%; Score 1002; DB 16; Length 2051;
Best Local Similarity 80.2%; Pred. No. 3.1e-285;
Matches 1176; Conservative 0; Mismatches 290; Indels 0; Gaps 0;

Qy      8 TCATCCCACTGAGGAGGAGGAAAAACCCCGCTTGTGAACCGCCAGGAGCCCGCCCTTG 67
Db      583 TCATCCCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 642
Qy      68 ATGTAGCAAGAAAGTTGACAGCCGATCCAGACAGCTGCGCAAGATGATCCTCTTCTGG 127
Db      643 GTGCGCGCAAGAAAGTTGACAGCCGATCCAGACAGCTGCGCAAGATGATCCTCTTCTGG 702
Qy      128 GGGATGGATGGGGGTGCTTACGGTGAAGCACTCGGATCCTAAAGGGCAGATGATG 187
Db      703 GCGATGGATGGGGGTGCTTACGGTGAAGCACTCGGATCCTAAAGGGCAGATGATG 762
Qy      188 GCAAACTGGGACCTGAGACACCCCTGGCCATGGAACAGTTCCCATACGTGGCTGTGCA 247
Db      763 ACAAACTGGGGCTGAGATACCCCTGGCCATGGAACAGTTCCCATACGTGGCTGTGCA 822
Qy      248 AGACATACAACTGACAGACAGAGGTGCGACAGCGGACAGGACCTGCACTGCTACCTGT 307
Db      823 AGACATACAACTGACAGCAAAACATGTGCGACAGAGTGAAGCCACAGCGGCTACCTGT 882
Qy      308 GTGGGTCAAGGGCAACTACAGAAACCATGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 367
Db      883 GCGGGTCAAGGGCAACTTCCAGACCAATGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 942
Qy      368 GCAACACGACAGCTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAAGAAAGCAGGGA 427
Db      943 GCAACACGACAGCGGCGCAACGAGGTCACTCCGTGATGAATCGGCGCAAGAAAGCAGGGA 1002
Qy      428 AGGCGGTGGAGTGTGACCAACCAAGGTCAGCATGCTCCCGACCGGGGCTTACG 487
Db      1003 AGTCAGTGGAGTGTGTAACCAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1062
Qy      488 CGCACACGCGTGAACCGAACTGTACTCAGACGCGGACCTGCTGTGATGACAGAGA 547
Db      1063 CCCACACGCGTGAACCGCAACTGTACTCAGACGCGGACGCTGCTGTGCGCGCGCACG 1122
Qy      548 ATGCTGCCAGGACATGCGCGCACAGCTGCTTACAACATGATATGACGTGATCCTGG 607
Db      1123 AGGGGTGCAGGACATGCTACGCAAGCTCATCTCCAACATGAGACTGACGTGATCCTAG 1182
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QY      608 GTGAGGCCGAATGTACATGTTTCTGAGGGGAGCCCCAGACCCTGAATACCAGATGATG 667
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Db      1183 GTGAGGCCGAAGTACATGTTTCCCATGGGAACCCAGACCCTGAGTACCAGATGACT 1242
QY      668 CCAGTGTGAATGAGAGTCCCGAAGGACAGACGAACCTGCTGAGGAATGGCAGGCCAAGC 727
      |||||
Db      1243 ACAGCCAAAGGTGGGACCAGGCTGGACGGGAAGAATCTGCTGAGGAATGGCTGGCGAAGC 1302
QY      728 ACCAGGAGCCCAAGTATGTGGAACCGCACTGCGCTCCTTCAAGCGCGCCGATGACTCCA 787
      |||||||
Db      1303 GCCAGGCTGCCGCTATGTGTGAACCGCACTGAGCTCATGCAAGGCTTCCCTGAGCCCGT 1362
QY      788 GTGTAACACACTCATGGGCTCTTGGACCGCGCAGACATGAAGTAAATGTTTCAAGCAAG 847
      |||||||
Db      1363 CTGTGACCACTCATGGGTCTTTGAGCCTGGAACATGAATAAGATCCACCGAG 1422
QY      848 ACCACACCAAGACCCGACCCCTGCGGAGATGACGGAGCGGCCCTGCAAGTGTGAGCA 907
      |||||
Db      1423 ACTCCACACTGACCCCTCCTGATGAGATGACAGAGCTGCCCTGCGCTGTGAGCA 1482
QY      908 GGAACCCCCGGGCTTCTACCTCTTGTGAGGAGGAGCGCCGATGACCAAGTCAACCATG 967
      |||||||
Db      1483 GGAACCCCCGGGCTTCTTCTCTTGTGAGGAGGTGTCGATCAACCATGTCATCATG 1542
QY      968 ACGGCAAAAGCTTATATGGCACTGACTGAGGCGCATCATGTTTGAACAATGCCATCGCCAAG 1027
      |||||
Db      1543 AAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGACGCCCATTTGAGAGGG 1602
QY      1028 CTAAAGAGCTCACTAGCGAACTGACACGCTGATCTTGTCACTGACAGCAACTCCCATG 1087
      |||||
Db      1603 CGGGCCAGCTCACAGAGGAGAGGACACGCTGAGCCTGTCACCTGCCGACCACTCCCAAG 1662
QY      1088 TCTTCTCTTTTGTGGCTACACACTGCGTGGGACCTCCATTTTGGGTGCCCCCGGCA 1147
      |||||||
Db      1663 TCTTCTCTTGGAGGCTACCCCTGCGAGGAGCTTCATCTTGGGCTGGCCCCCTGCA 1722
QY      1148 AGGCTTAGACAGCAAGTCTTACACCTCCATCTCTATGGAATGCGCAAGGCTATGCGC 1207
      |||||||
Db      1723 AGGCCCGGAGACAGAAAGGCTTACACGCTCTCTTATACGAAACGCTCAAGGCTATGTGC 1782
QY      1208 TTGCGGGGCTGAGGCCCGATGTTAATGGGACCAAGCGAGAAACCTTCATACCGGC 1267
      |||||
Db      1783 TCAAGGACGGCGCGCGCGCGGATGTATACCGAGAGGAGCGGAGCCCGAGTATCGGC 1842
QY      1268 AGCAGCGCGCTGCCCTGGCTAGCGAGACCAAGGCGGAGGAGAGCTGCGGTTCG 1327
      |||||||
Db      1843 AGCAGTACGAGTGCCTCGACGAGAGACCCACGAGGCGAGAGCTGCGGTTCG 1902
QY      1328 CGCGAGGCGCGGAGGCGCACTGTGCAAGGCGCTGAGGAGAGGAGACCTTGTGGCGACA 1387
      |||||||
Db      1903 CGCGCGGCGCGGAGGCGCACTGTTCACGCGCTGAGGAGAGACCTTCATAGCGCAGC 1962
QY      1388 TCATGGCTTTGCGGGCTGCGTGGAGAGCCCTACACCGACTGCAATCTGCCAGCCCCCGCA 1447
      |||||||
Db      1963 TCATGGCTTTGCGCGCTGCTGAGAGCCCTACACCGCTGCGACCTGCGCGCCCCCGCG 2022
QY      1448 CCGCCACCAAGCATCCCGACTAGGGT 1473
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Db      2023 GCACCAACGACGCGCGACCCGGGT 2048
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RESULT 13

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US-10-182-094-9
; Sequence 9, Application US/10182094
; Publication No. US20040019193A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; TITLE OF INVENTION: MOB-5/HMOB-5 AS A CANCER DIAGNOSTIC MARKER
; FILE REFERENCE: 22000.0091U3
; CURRENT APPLICATION NUMBER: US/10/182,094
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: US 60/178,185
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; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2121
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20040019193A1e =
US-10-182-094-9
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Query Match      67.9%; Score 1002; DB 16; Length 2121;
Best Local Similarity 80.2%; Pred. No. 3.1e-285;
Matches 1176; Conservative 0; Mismatches 290; Indels 0; Gaps 0;
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QY      8 TCATCCAGCTGAGAGGAAAAACCCGCTTCTGAAACCGCCAGAGCCCAAGCCCTTG 67
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Db      653 TCATCCAGTTGAGAGGAGAAACCCGACTTCTGAAACCGCAGGCAAGCCCTTG 712
QY      68 ATGTAGCCAAGATTGACGCCGATCCAGACAGCTGCCAAGAAATGTCATCTTCTTG 127
      |||||||
Db      713 GTGCCGCCAAGAGCTGACAGCTGCACAGACAGCCGCAAGAACTCATCTTCTTG 772
QY      128 GGGATGGATGGGGTGCCCTACGCTGACAGCACTCGGATCCTAAAGGCGCAGATGATG 187
      |||||||
Db      773 GCGATGGATGGGGGTCTCTACGCTGACAGCTGCAGATCCTAAAGGCGCAGAAAGG 832
QY      188 GCAAACTGGGACCTTGAGACACCCCTGGCCATGACCAAGTCCCATACGTGCTGTCCA 247
      |||||||
Db      833 ACAAACTGGGGCTTGAGATACCCCTGGCCATGACCGCTTCCCATATGTGGCTGTCCA 892
QY      248 AGACATCAACGCTGACAGACAGAGTGCCAGACAGCGCAGGCACTGCCACTGCTACTGT 307
      |||||||
Db      893 AGACATCAATGTAGACAAACATGTGCCAGACAGTGAAGCCACAGCCAGGCTACTGT 952
QY      308 GTGGGCTCAAGGGCAACTACAGAAACCATCGGTGTAAGTGACAGCCGCCGCTACAAATCAGT 367
      |||||||
Db      953 GCGGGGTCAAGGGCAACTTCCAGAACCATTTGGCTTGAGTGACAGCCGCCCTTTAAACAGT 1012
QY      368 GCAACACGACAGTGGGATGAGGTACGCTGTGATCAACCGGGCCAAAGACAGGGA 427
      |||||||
Db      1013 GCAACACGACAGCGGCAAGAGGTATCTCCGTGATGAATCGGGCCAAAGACAGGGA 1072
QY      428 AGCGCTGGAGTGTGACCAACAGGCTGACAGATGCTCCAGCCGCGGCTTACG 487
      |||||||
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QY      488 CGCACACGCTGAACCGAACTGTACTCAGACGCGCAGCTGCTGTATGACAGAAAG 547
      |||||||
Db      1133 CCCACACGCTGAACCGCACTGTGTACTCGAGCGCGAGCTGCTCGCGCCGACAGG 1192
QY      548 ATGCTGCCAGGACATCGCCGCAAGCTGTCTACACATGGAATATTGACGTGATCTTG 607
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Db      1193 AGGGGTGCCAGGACATCGCTACGCAAGCTCATCTCCAAATGGAATGACGTGATCTTAG 1252
QY      608 GTGAGGCCGAATGTACATGTTTCTGAGGGGACCCCGACCCCTGAATACCAAGATGATG 667
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Db      1253 GTGAGGCCGAAGTACATGTTTCCCATGGGAACCCCGACCCCTGAGTACCAAGATGACT 1312
QY      668 CCAAGTGAATGAGTCCGGAAGACAAAGCAAGAACTGTGTCAAGGAATGGCAGGCCAAGC 727
      |||||
Db      1313 ACAGCCAAGGTGGACCAAGGCTGACGGGAAGAAATCTGTGCAAGGAATGGCTGCGCAAGC 1372
QY      728 ACCAGGAGCCCAAGTATGTGGAACCGCACTGCGCTCTTCAGGCGCGGATGACTCCA 787
      |||||||
Db      1373 GCCAGGCTGCCGCTATGTGTGAACCGCACTGAGCTCATGAGGCTTCCCTGAGCCCGT 1432
QY      788 GTGTAACACACTCATGGGCTCTTGGACCGGACAGACATGAAGTAAATGTTTCAAGCAAG 847
      |||||||
Db      1433 CTGTGACCACTCATGGGTCTTTTGAAGCTGAGACATGAATAACGATCCACCGAG 1492
QY      848 ACCACACCAAGAACCCGACCCCTGGGGAAGATGACGAGGCGGCCCTGCAAGTGTGAGCA 907
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Db      1493  ACTCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGCTGAGCA 1552
Qy      908  GGAACCCCGGGGCTTCTACCTCTTCTGAGGAGGCCGCTATGACCAAGTCAACCATG 967
Db      1553  GGAACCCCGGGGCTTCTTCTCTTCTGAGGAGGTCGTCATGACCAATGTCATCATG 1612
Qy      968  ACGGCAAGCTTATATGCACTGACTGAGGCGCATATGTTGACAATGCCATCGCCAAAG 1027
Db      1613  AAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTCGACGACCAATTGAGAGGG 1672
Qy      1028  CTAACGAGCTCACTAGCGAACTGACACGCTGATCTTGTCACTGACAGCACTCCCATG 1087
Db      1673  CGGCGCAGCTCACCAAGAGAGAGACACGCTGAGCTCTGCTACTGCGGCACTCCACG 1732
Qy      1088  TCTTCTCTTTTGTGGCTACACACTGCGTGGGACTTCCATTTTGGTCTGCGCCCGGCA 1147
Db      1733  TCTTCTCTTCTGAGGCTACCCCTGCGAGGAGCTCCATCTTCCGGGCTGCGCCCTGGCA 1792
Qy      1148  AGGCTTAGACAGCAAGTCTACACCTCCATCTCTATGGAATGCGCCAGGCTATGCGC 1207
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Qy      1268  AGCAGCGCGCGCGCGCGCGCTGCTGCTAGCAGACCAAGCGGCGAAGACGCGGCTTGC 1327
Db      1913  AGCAGTACAGAGTGCCTTGGACGAAAGACCCACGACGCGAGCGAGCGGCTGTTGC 1972
Qy      1328  CGCGAGCGCGCGCGCGCGCACTGTGTCACGCGCTGCAAGAGAGACCTTGTGCGGACA 1387
Db      1973  CGCGCGCGCGCGCGCGCGCACTGTGTCACGCGCTGCAAGAGAGACCTTATAGCGCAGC 2032
Qy      1388  TCATGGCTTTTGGCGGCTGCGTGAGGCGCTTACACCGAAGTCAATCTGCCAGCGCCGCA 1447
Db      2033  TCATGGCTTTTGGCGGCTGCGTGAGGCGCTTACACCGGCTGCGAGCGCGCGCGCGCG 2092
Qy      1448  CCGCCACGAGCATCCCGCACTAGGGT 1473
Db      2093  GCACACCGAGCGCGCGCGCGCGGGT 2118

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RESULT 14 US-09-006-298-22

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; Sequence 22, Application US/09006298
; Patent No. US2002008224A1
; GENERAL INFORMATION:
;   APPLICANT: Jolly, Douglas J.
;   APPLICANT: Moore, Margaret D.
;   APPLICANT: Chada, Sunil
;   TITLE OF INVENTION: NON-IMMUNOGENIC PRODRUGS AND SELECTABLE
;   TITLE OF INVENTION: MARKERS FOR USE IN GENE THERAPY
;   NUMBER OF SEQUENCES: 32
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SEED and BERRY LLP
;   STREET: 6300 Columbia Center, 701 Fifth Avenue
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/006,298
;   FILING DATE: 13-JAN-1998
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Mcmasters, David D.

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; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.459
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1634 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 13..1617
;     US-09-006-298-22
;
Query Match      67.8%; Score 1001.4; DB 9; Length 1634;
Best Local Similarity 80.2%; Pred. No. 4.4e-285;
Matches 1176; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

Qy      6  CCTCATCCCACTGAGGAGGAAAAACCCGCTTCTGGAACCGCGCAGCAGCCAGGCCCT 65
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Qy      66  TGATGTAGCCAGAAGTTGCAGCCGATCCAGACAGCTGCCAAGAAATGTCATCTTCTT 125
Db      138  GGGTGCAGGCAAGAGCTGCAGCCTGACAGACAGACAGCCGCAAGAACTCATCTTCTT 197
Qy      126  GGGGATGGATGGGGGGTGCCTTACGCTGACAGCCACTCGGATCTTAAAGGGCAGATGA 185
Db      198  GGGCGATGGATGGGGGGTGTCTACGCTGACAGCTGCCAGGATCTTAAAGGGCAGATGA 257
Qy      186  TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGACCAAGTTCCATACGTGCTGTG 245
Db      258  GGACAACTGGGGGCTGAGATACCCCTGGCCATGAGACCGCTTCCATATGTGGCTGTG 317
Qy      246  CAAGACATCAACGTGAGACAGACAGTGGCCAGACAGCGCAGGCACTGCACTGCTACT 305
Db      318  CAAGACATCAATGTAGACAAACATGTGCCAGACAGTGAAGCCAGCCAGCGCTACT 377
Qy      306  GTGTGGGTCAAGGGCACTACAGAACCATCGGTGTAGTGCAGCCGCGGCTTACAATCA 365
Db      378  GTGCGGGGTCAAGGGCACTTCCAGACATTTGGCTTGAAGTGCAGCCGCGGCTTAAACA 437
Qy      366  GTGCAACACGACACGTGGGAATGAGTCACTGTGTGATCAACCGGCGCAAGAAAGCAG 425
Db      438  GTCAACACGACACCGCGGCAAGAGTCACTTCCGTGATGATGGGCGCAAGAAAGCAG 497
Qy      426  GAAGCGCTGGAGTGTGACCAACCAAGGCTGACAGCATGCTTCCAGCGGGGCTTA 485
Db      498  GAAGTCAAGTGGAGTGTAAACCAACAGAGTGAAGCAGCAGCTTCCAGCGGCACTTA 557
Qy      486  CGGCAACGCTGAACCGAAACTGTACTCAGACGCGGCACTGCTGCTGATGACAGAA 545
Db      558  CGCCACACGCTGAACCGCACTGTACTGAGACGCGGCACTGCTGCTGCGCGGCA 617
Qy      546  GAATGCTGCAAGACATGCGCGGCAAGCTGCTTCAACATGATATTTGACGTGATCT 605
Db      618  GAAGGGGTGCAAGACATGCTACGCACTCATCTTCAACATGACATTTGACGTGATCT 677
Qy      606  GGGTGAAGCGCAATGTACATGTTTCTGAGGGGAGCCCGAGACCTGGAATACCCAGATGA 665
Db      678  AGGTGAGGCGCAAGTACATGTTTCCATGGGAACCCAGACCTGAGTACCCAGATGA 737
Qy      666  TGCCAGTGTGATGAGTCCGGAAGACAAGCAGAACTGTGTGAGGAATGGCAGGCCAA 725
Db      738  CTACAGCCAGGTGGAGACGAGGCTGACGGAAGAAATGTGTGAGGAATGGCTGGCAA 797
Qy      726  GCACAGGAGCCAGTATGTGTGAACCGCACTGCGCTCTTCAAGCGCGGCGGATGACTC 785
Db      798  GCGCCAGGGTGCCTGATGTGTGAACCGCACTGAGCTCATGAGGCTTCCCTGAGCCC 857
Qy      786  CAGTGTACACACCTCATGGGCTTTTGAAGCCGCGAGACATGAATATATGTTACGA 845

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Db 858 GTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGAAATACGAGATCCACCG 917
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Db 918 AGACTCCACACTGGACCCCTCCCTGATGAGATGACAGAGGCTGCTGCGCCTGTGAG 977
Qy 906 CAGGAACCCCCGGGCTTCTACCTCTTCGTGAGGAGGAGGCCGCAITGACCACGGTACCA 965
Db 978 CAGGAACCCCGCGGCTTCTCTCTTCGTGAGGAGGTGTCGCAITGACCATGTGATCA 1037
Qy 966 TGACGGCAAGCTTATATGACACTGAGGCGATCATGTTTGAACAATGCCATGCCAA 1025
Db 1038 TGAAGCAGGGCTTAACGGGCACTGACGATCATGTTCGACGACGCCATTGAGAG 1097
Qy 1026 GGCTAACGAGCTCACTAGCGAAGTGAACGCTGATCCTTGTCACTGACAGCACTCCA 1085
Db 1098 GCGGGGCCAGCTCACCAAGGAGGACACGCTGAGCCTCGTCACTGCCGACCACTCCA 1157
Qy 1086 TGTCTTCTCTTTTGGTGTGCTACACACTGCGTGGGACCTCCATTTTCGCTGCCCCGG 1145
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Qy 1146 CAAGGCTTGAACAGCAAGTCTTACACTTCATCTCTATGGAATGGCCAGGCTATGC 1205
Db 1218 CAAGGCCCGGGAACAGGAAGGCTTACACGGTCTCTCTATACGAAACGGTCCAGGCTATGT 1277
Qy 1206 GCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCAACAAGGAAACCTCATATACG 1265
Db 1278 GCTCAAGACGCGCGCCCGCGATGTTAACGAGAGCAGAGCGGGAAGCCCGAGTATCG 1337
Qy 1266 GCAGCAGGCGCGCTGCCCCCTGGCTAGCGAGACCCACGAGGGCGAAGAGCTGGCGTGT 1325
Db 1338 GCAGCAGTCAAGAGTGGCCCTTGACGAGAGAGACCCACGACGAGGAGAGCGTGGGTGT 1397
Qy 1326 CGCGCAGGCGCGCAGGCGCACTGTGTGACGCGGCTGACAGAGAGACCTTCTGGCGCA 1385
Db 1398 CGCGCGCGCGCGCAGGCGCACCTGTGTTACGCGGCTGACAGAGACCTTACATAGCGCA 1457
Qy 1386 CATCATGGCTTTTGGGGCTGCGTGGAGCCCTACACCGACTGCAATCTGCCAGCCCCGC 1445
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Qy 1446 CACCGCAACGACATCCCCGACTAGGG 1472
Db 1518 CGGCACCAACGACGCGCGCACCCGGG 1544

RESULT 15
US-10-332-733-26
; Sequence 26, Application US/10332733
; Publication No. US20040106565A1
; GENERAL INFORMATION:
; APPLICANT: Margarette Odenthal and Diana Jung
; TITLE OF INVENTION: Gene Expression, Genome Alteration And Reporter Expression
; FILE REFERENCE: 1472/68806
; CURRENT APPLICATION NUMBER: US/10/332,733
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 26
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: SEAP
US-10-332-733-26

Query Match 67.8%; Score 1000.8; DB 17; Length 1558;
Best Local Similarity 80.1%; Pred. No. 6.6e-285;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

Qy 6 CCTCATCCAGCTGAGAGGAAAAACCCCGCTTCTGGAACCGCCAGGACGCCAGGCCCT 65
Db 51 CATCATCCAGTTGAGGAGGAGAACCCCGACTTCTGGAACCGCGAGGACGCCAGGCCCT 110
Qy 66 TGATGTAGCCAAGATTGACCGCATCCAGACAGCTGCCAAGATGTATCTTCTT 125
Db 111 GGGTCCCGCAAGAGAGCTGACGCTTGACACAGACGCCCAAGAACCTCATCTTCT 170
Qy 126 GGGGATGGGATGGGGTGCCTACGCTGACAGCCACTCGGATCCTAAAGGGGAGATGAA 185
Db 171 GGGCATGGGATGGGGGTGTCTACGGTGACAGCTGCGCAGGATCCTAAAGGGGAGAGAA 230
Qy 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGGACCAAGTTCCATACGTGGCTGT 245
Db 231 GGACAAACTGGGCTGAGATACCCCTGGCCATGGAACCGCTTCCATATGTGGCTGTCT 290
Qy 246 CAAGACATTAACGTGACAGACAGGTGCGACAGACGCGAGGACACTGCGACTGCTACT 305
Db 291 CAAGACATTAACATGTAGCAAAACATGTGCCAGACAGTGAAGCCACAGCCAGGCTTACT 350
Qy 306 GTGTGGGTCAAGGGCACTACAGAACCATCGGTGTAAGTGACAGCCCGCGCTTCAATCA 365
Db 351 GTGGGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAAGTGACAGCCCGCTTAAACA 410
Qy 366 GTGCAACACGACACGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCAAGAACAGG 425
Db 411 GTGCAACACGACACGCGGCAACGAGTCAATCTCGGTGATGAATCGGCAAGAACAGG 470
Qy 426 GAAAGCCGTGGAGTGTGACCAACCAAGGCTGCAACATGCTCCCAAGCCGGGCTTA 485
Db 471 GAAGTCAAGTGGAGTGTGTAACCAACCAACGAGTGAACAGCCCTCGCCAGCGGCACTTA 530
Qy 486 CGCGCACACGGTGAACCGGAACTGGTACTCAGACGCGGCACTGCTGCTGATGACAGAA 545
Db 531 CGCCACACGGTGAACCGCAACTGGTACTCGACGCGCAAGTGCCTCGGCGCGCA 590
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Db 591 GGAAGGGTGCCAGACATCGCTTACGACCTCATCTCCAACATGACATGACGTGATCT 650
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Db 651 AGGTGAAGCGCAAGTATGTTTTCGATGGGAACCCAGACCTGAGTACCAGATGA 710
Qy 666 TGCAGTGTGATGATGCCGAAGAGACAAAGCAAGACTGTGAGAAATGGAGGCCAA 725
Db 711 CTACAGCCAAAGGTGGACACAGGCTGACCGGAAATCTGCTGACAGAAATGGCTGGCAA 770
Qy 726 GCACCAAGGAGCCCAATATGTGGAACCGCACTGCGCTCTCAGCGGCGCAATGACTC 785
Db 771 GCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGACCTCATGCAAGCTTCCCTGGAACC 830
Qy 786 CAGTGTACACACCTCATGGGCTCTTTGAGCCGCGACATGAAGTATATGTTCAGCA 845
Db 831 GTCTGTACCATCTCATGGGTCTTTGAGCCTGAGACATGAATATACGATCCACCG 890
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Qy 906 CAGGAACCCCGGGCTTCTACCTTCTGAGGAGGAGCGCATTTGACCAAGCTGACCA 965
Db 951 CAGGAACCCCGCGGCTTCTCTCTTCTGAGGAGGTGTCGATGACCAATGTGATCA 1010
Qy 966 TGACGGCAAGCTTATATGCACTGACTGAGGCGATCATGTTTGAACAATGCCATGCCAA 1025
Db 1011 TGAAGCAGAGGCTTACCGGCACTGACTGAGACGATCATGTTGACGACGCCATTGAGAG 1070
Qy 1026 GGCTAACGAGCTCACTAGCGAACTGACACGCTGATCTTGTCACTGACAGCACTCCA 1085
Db 1071 GCGGGGCCAGCTCACCAAGGAGGAGACACGCTGAGCTTGTCACTGCCGACCACTCCA 1130
Qy 1086 TGTCTTCTCTTTTGGTGTGCTACACACTGCGTGGGACCTTCATTTTGGGTGCGCCCCGG 1145

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QY      1146 CAAGGCTTAGACAGCAAGTCTACACCTCCATCCTCTATGGCAATGGCCAGGCTATGC 1205
Db      1191 CAAGGCCCGGACAGGAAGGCTTACACGGTCTCTCTATACGGAACGGTCCAGGCTATGT 1250
QY      1206 GCTTGGCGGGGCTGAGAGCCCGATGTATATGCGAGACAAAGCGAGGAACCTCATACCG 1265
Db      1251 GCTCAAGGACGGCGCGCGCGCGGATGTATACCGAGAGCGAGAGCGGAGCCCGAGTATCG 1310
QY      1266 GCAGCAGGCGGCGCGTGGCCCTGCTAGCGAGACCAAGGGGCGAAGACGTGGCGGTGTT 1325
Db      1311 GCAGCAGTACAGTGTGCCCCCTGACGAAGAGACCAAGCAGGCGAGACGTGGCGGTGTT 1370
QY      1326 CGCGCAGGCGCGCGCAGCGCACCTGTGTGACAGCGCGTGCAGAGAGAGACCTTCGTGGCGCA 1385
Db      1371 CGCGCGCGCGCGCGCAGCGCACCTGTGTGACAGCGCGTGCAGAGAGAGACCTTCATAGCGCA 1430
QY      1386 CATCATGGCCCTTTGCGGGCTGCGTGAAGCCCTACACCGACTGCATCTGCCAGCCCCCGC 1445
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QY      1446 CACCGCCACAGCATCCCCGACTAGGGT 1473
Db      1491 CGGCACCACCGACGCGCGCACCCGGGT 1518
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 1476
Sequence: 1 gaatccctcatccacagctga.....gcattcccgactaggggtacc 1476

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Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_hcc:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 635.4 | 43.0 | 733 | 7 CK956273 | CK956273 4096346 B |
| 2 | 603.4 | 40.9 | 1027 | 5 BX439339 | BX439339 BX439339 |
| 3 | 588.2 | 39.9 | 991 | 5 BX379970 | BX379970 BX379970 |
| 4 | 582.6 | 39.5 | 950 | 5 BX458398 | BX458398 BX458398 |
| 5 | 574.8 | 38.9 | 984 | 1 AL552555 | AL552555 AL552555 |
| 6 | 561 | 38.0 | 1593 | 9 AY404253 | AY404253 Homo sapi |
| 7 | 557.6 | 37.8 | 772 | 7 CK453205 | CK453205 908900 MA |
| 8 | 537.6 | 36.4 | 1587 | 9 AY404255 | AY404255 Mus muscu |
| 9 | 526.2 | 35.7 | 1125 | 5 BX343739 | BX343739 BX343739 |
| 10 | 522 | 35.4 | 2459 | 3 AK076459 | AK076459 Mus muscu |
| 11 | 517.4 | 35.1 | 902 | 1 AL553521 | AL553521 AL553521 |
| 12 | 516.6 | 35.0 | 936 | 5 BX417625 | BX417625 BX417625 |
| 13 | 511.2 | 34.6 | 681 | 7 CK834465 | CK834465 4058791 B |
| 14 | 492.8 | 33.4 | 905 | 1 AL540746 | AL540746 AL540746 |
| 15 | 476.6 | 32.3 | 929 | 1 AL551653 | AL551653 AL551653 |
| 16 | 476.2 | 32.3 | 636 | 7 CN792609 | CN792609 4127499 B |
| 17 | 476 | 32.2 | 992 | 1 AL548705 | AL548705 AL548705 |
| 18 | 475.4 | 32.2 | 1083 | 1 AL545591 | AL545591 AL545591 |
| 19 | 470.2 | 31.9 | 928 | 1 AL549703 | AL549703 AL549703 |
| 20 | 469 | 31.8 | 1593 | 9 AY404254 | AY404254 Pan trogl |
| 21 | 457.6 | 31.0 | 625 | 9 AY416259 | AY416259 Homo sapi |
| 22 | 439 | 29.7 | 616 | 6 CF176922 | CF176922 805350 MA |
| 23 | 438.6 | 29.7 | 724 | 6 BY732148 | BY732148 BY732148 |
| 24 | 437.6 | 29.6 | 890 | 4 B1161220 | B1161220 602865678 |

| | | | | | |
|----|-------|------|------|------------|--------------------|
| 25 | 425.2 | 28.8 | 550 | 9 AY416260 | AY416260 Pan trogl |
| 26 | 421.6 | 28.6 | 625 | 9 AY416261 | AY416261 Mus muscu |
| 27 | 421.2 | 28.5 | 782 | 6 CB989365 | CB989365 AGENCOURT |
| 28 | 421 | 28.5 | 653 | 7 CN788362 | CN788362 4122694 B |
| 29 | 418.8 | 28.4 | 935 | 4 BG832086 | BG832086 602765105 |
| 30 | 400.8 | 27.2 | 2084 | 3 CR681888 | CR681888 Tetraodon |
| 31 | 398.6 | 27.0 | 855 | 6 CB998271 | CB998271 AGENCOURT |
| 32 | 397.4 | 26.9 | 1422 | 3 AK008000 | AK008000 Mus muscu |
| 33 | 397.2 | 26.9 | 799 | 4 BG480361 | BG480361 602529434 |
| 34 | 397 | 26.9 | 740 | 6 CB959579 | CB959579 AGENCOURT |
| 35 | 384.8 | 26.1 | 722 | 6 BY732151 | BY732151 BY732151 |
| 36 | 375.6 | 25.4 | 535 | 2 AW450908 | AW450908 UI-H-B13- |
| 37 | 365.4 | 24.8 | 700 | 7 CN793186 | CN793186 4128172 B |
| 38 | 364.2 | 24.7 | 596 | 4 BM742455 | BM742455 K-EST0015 |
| 39 | 362 | 24.5 | 821 | 6 CB996560 | CB996560 AGENCOURT |
| 40 | 361.4 | 24.5 | 809 | 6 CB995228 | CB995228 AGENCOURT |
| 41 | 360.4 | 24.4 | 799 | 6 CB994156 | CB994156 AGENCOURT |
| 42 | 359.8 | 24.4 | 590 | 4 BM742176 | BM742176 K-EST0014 |
| 43 | 358.8 | 24.3 | 650 | 7 CN723202 | CN723202 E0856C01- |
| 44 | 354.2 | 24.0 | 607 | 7 CN721228 | CN721228 E0818D06- |
| 45 | 350.4 | 23.7 | 685 | 6 BY736065 | BY736065 BY736065 |

ALIGNMENTS

RESULT 1
CK956273
LOCUS
DEFINITION CK956273 733 bp mRNA linear EST 15-MAR-2004
4096346 BARC 10BOV Bos taurus cDNA clone 10BOV35_H01 5', mRNA
sequence.
ACCESSION CK956273 GI:45470653
VERSION CK956273.1
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 733)
Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically
activated bovine gut
Unpublished (2004)
JOURNAL Contact: Tad S. Sonstegard
COMMENT Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt "-trim fasta. Vector identified
by cross match using options -mismatch 12 -minscore 18
Plate: 35 row: H column: 01
Seq primer: CCCAGTCACGACGTTGTAACG
High quality sequence stop: 733.
FEATURES
location/Qualifiers
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/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="10BOV35_H01"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small Intestine; Vector: pagen-1; Site 1:
ECORV; Site 2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunums of 18 and 21 wk old steers, and

distal ileums of 14 day old calves. proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"

ORIGIN

Query Match 43.0%; Score 635.4; DB 7; Length 733;
Best Local Similarity 96.2%; Pred. No. 3.4e-144;
Matches 651; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 791 TAACACACCTCATGGGCTCTTTGAGCCGCGACACATGAAGTATATGTTACGAAGACC 850
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Db 12 TAACACACCTCATGGGCTCTTTGAGCCGCGACACATGAAGTATATGTTACGAAGACC 71

QY 851 ACACCAAGACCCGACCCTGGCGAGATGACGAGGCGGCCCTGCAAGTGTGAGCAGGA 910
|||
Db 72 ACACCAAGACCCGACCCTGCAAGAAATGACAGAGGTGCCCTGCGAGTGCTAAGCAGGA 131

QY 911 ACCCCGGGGCTTCTACCTCTTCGTGAGGAGGAGGCCGCAATTGACCACGGTCACCATGACG 970
|||
Db 132 ACCCCGAGGGCTTCTACCTCTTGTGTGAGGAGGAGGCCGCAATTGACCACGGTCACCATGATG 191

QY 971 GCAAGCTTATATGGCACTGACTGAGGCGATCATGTTTGACATGCGCATCGCCAAAGGCTA 1030
|||
Db 192 ACAAGCTTATATGGCACTGACTGACCGAGGCGGTCAITGTTGACAAATGCCATCGCCAAAGGCTA 251

QY 1031 ACCAGCTCACTAGCGAACTGGACACGCTGATCCTTGTCACTGCAAGCACTCCCATGTCT 1090
|||
Db 252 ATGAGCTCACTAGCGAACTGGACACGCTGATCCTTGTCACTGCAAGCACTCTCATGTCT 311

QY 1091 TCTCTTTTGGTGCTACACACTGCGTGGGACCTCCATTTTCGTCGTGCCCCGGCAAGG 1150
|||
Db 312 TCTCTTTTGGTGCTATACACTGCGTGGGACCTCCATTTTGTGTCGTGCCCCGGCAAGG 371

QY 1151 CCTTGAACAGCAAGTCTCTACACCTCCATCCTCTATGTGCAATGGCCAGGCTATGCGCTTG 1210
|||
Db 372 CCTTGAACAGCAAGTCTCTACACCTCCATCCTCTATGTGCAATGGCCAGGCTATGCGCTTG 431

QY 1211 GCGGGGCTCGAGGCGCCGATGTTAATGGCAGACACAAGCGAGAACTTCATACCGGCAAGC 1270
|||
Db 432 GCGGGGCTCGAGGCGCCGATGTTAATGACACAGCAACAAGCGAGAACTTCATACCGCAAGC 491

QY 1271 AGGCGGCGCTGCCCTTGCTAGCGAGACCCACGGGGGCGAAGACGTGGCGGTGTTCCGCGC 1330
|||
Db 492 AGGCGGCGCTGCCCTTGCTAGCGAGACCCACGGGGGCGAAGACGTGGCGGTGTTCCGCGC 551

QY 1331 GAGGCCCGCAGGCGCACCTGTGTGACGCGCGGTGACGAGGAGACCTTCTGTGGCGACATCA 1390
|||
Db 552 GCGGCCCGCAGGCGCACCTGTGTGACGCGCGGTGACGAGGAGACCTTCTGTGGCGACATCA 611

QY 1391 TGGCCTTTGGGGGCTGCGTGAGCCCTACACCGACTGCAATCTGCCAGCCCCCGCACCG 1450
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Db 612 TGGCCTTTGGGGGCTGCGTGAGCCCTACACCGACTGCAATCTGCCAGCCCCCGCACCG 671

QY 1451 CCACCAACATCCCCGAC 1467
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Db 672 CCACCAACATCCCCGAC 688

RESULT 2
BX439339 1027 bp mRNA linear EST 05-MAY-2004
LOCUS BX439339 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YD10
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX439339
VERSION BX439339.2 GI:47036618
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1027)
AUTHORS Li,W.B., Gruber,C., Jesssee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization

JOURNAL
COMMENT

Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30789748.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0DE009YD10&c=1699.f.

FEATURES

source

1. 1027
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE009YD10"
/issue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites of the
pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 40.9%; Score 603.4; DB 5; Length 1027;
Best Local Similarity 79.9%; Pred. No. 2.4e-136;
Matches 739; Conservative 6; Mismatches 177; Indels 3; Gaps 3;

QY 6 CCTCATCCACGCTGAGGAGGAAACCCCGCTTCTGGAACCGCCAGCAGCCAGGCCCT 65
|||
Db 104 CATCATCCAGTTGAGGAGGAAACCCGACTTCTGGAACCGCCAGCAGGCCCT 163

QY 66 TGATGTAGCCAAAGAGTTGACGCCGATCCAGACAGCTGCCAAGATGTCTCTTCTT 125
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Db 164 GGGTGCCGCCAAGAGAGCTGACGCTTGACACAGACGCCGCCAAGAACTCATCTTCT 223

QY 126 GGGGAGTGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCTTAAAGGGCAGATGAA 185
|||
Db 224 GGGGAGTGGATGGGGGTGCTTACGGTGACAGCTGCGAGATCTTAAAGGGCAGAGAA 283

QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGGAACAATTCCATACGTGCTGTG 245
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Db 284 GGACAAACTGGGCGCTGAGTTAACCCCTGGCCATGGAACGCTTCCATATGTGCTGTG 343

QY 246 CAAGACATACAACGTGACAGACAGGTGCCAGACAGCGCAGCACTGCCACTGCCCTACCT 305
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Db 344 CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGAAGCCACAGCCAGGCTTACCT 403

QY 306 GTGTGGGGTCAAGGGCACTACAGAACCATCGGTGTAAGTGCAAGCCGCCGCTACATCA 365
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Db 404 GTGCGGGGTCAAGGGCACTTCCAGAACCATTTGGCTTGAAGTGCAAGCCGCCGCTTAAACA 463

QY 366 GTGCAACACGACAGCTGGGGAATGAGGTCACGTTCTGTGATCAACCGGGCCAAAGCAGG 425
|||
Db 464 GTGCAACACGACAGCGGGCAACGAGGTCACTCTCGTGATGAATCGGGCCAAAGAACAGG 523

QY 426 GAAAGCCGTGGAGTGTGACCAACCAAGGCTGACGATGCTCCCGCAGCGGGGCTTA 485
|||
Db 524 GAAGTCAGTGGAGTGTGTAACCAACACAGAGTGCAGCAGCCTCGCCAGCGGGCACTTA 583

QY 486 CGGCACACGGTGAACCGAAACTGTACTCAGAGCGCGAAGCTGCTGTGATGACAGAA 545
|||
Db 584 CGCCACACGGTGAACCGCAACTGTACTCGAGCGCGAAGCTGCTGTGATGACAGAA 643

QY 546 GAATGGCTGCCAGACATGCCCGCACAGCTGTCTTACAACATGATATTTGACGTTCTCT 605
|||
Db 644 GGAAGGGTGCCAGACATCGCTTACGACGCTCATCTTCCAACATGACATTGACGTTCTCT 703

QY 606 GGGTGGAGGCCGAATGTACTGTTCCTCTGAGGGGACCCCGACAGACCTTGAATACCCAGATGA 665
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 Db 704 AGGTGGAGGCCGAAGTACTGTTT-CGCATGGGAACCGACCTGAGTACCCAGATGA 762
 QY 666 TGCCAGTGTGAATGAGTCCGGAAGGACAGCAGAACTGTGTGAGGAATGGCAGGCCAA 725
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 Db 763 CTACAGCCAAAGTGG-GACAGGCTGGACGGGAAGATCTGTGTGAGGAATGGCTGGCGAM 821
 QY 726 GCACCAGGAGCCCACTATGTGTGAAACCGCACTGCGCTCTCAGGCGGCCGATGACTC 785
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 Db 822 GCCCAGGGGTGCCCGGTACGTGTGGAACCGCACTGAGCTCATGCAAGCTTCCCTGAGCCC 881
 QY 786 CAGTGTAAACACACTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATAATGTTCA-GC 844
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 Db 882 GTCTGTGACCCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGAAMAMGAGATCCACCC 941
 QY 845 AAGACCAACCAAGGACCCGACCTCTGGCGGAGATGACGAGGGCGCCCTGCAAGTGCTGA 904
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 Db 942 GAGACTCCMCACCTGGRCCCTCCYTGATGGAAGTGAACAAGGCTGCCCTCGCCTGCTGA 1001
 QY 905 GCAGGAACCCCGGGGCTTCACT 929
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 Db 1002 GCAGGAACCCCGGGCTTTTCTCT 1026

| | |
|------------|--|
| RESULT 3 | |
| BX379970 | |
| LOCUS | 991 bp |
| DEFINITION | mrna linear EST 26-APR-2004 |
| | BX379970 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA |
| | clone CS0D1042YG09 5-PRIME, mRNA sequence. |

| | |
|-----------|-------------|
| ACCESSION | BX379970 |
| VERSION | BX379970.2 |
| | GI:46573405 |

| | |
|----------|----------------------|
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |

REFERENCE
1 (bases 1 to 991)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessbe, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30448840.

Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: segreff@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?S=CS0DJ042AD05QPl&c=1699.f>.

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .991 |

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/db_xref="taxon:9606"
/clone="CSODI042YG09"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

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| Query Match | 39.9% | Score 588.2; | DB 5; | Length 991; |
| Best Local Similarity | 80.2% | Pred. No. 1.2e-132; | | |
| Matches 711; Conservative | 3; | Mismatches 171; | Indels 2; | Gaps 2; |

6 CCTCATCCGAGCTGAGGAGGAACCCCGCCTTCTGGAACCGCCAGGCAGCCAGGCCCT 65

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| Db | 106 | CATCATCCCAAGTGTGAGAGAGAAACCCGGA | CTTCTGGAAACCGGAGGCGAGCCGACCT | 165 |
| QY | 66 | TGATGTAGCCAAAGATTGCAGCCGATCCAGACAGCTGCCAAGAAATGTCACTCTTCTT | | 125 |
| Db | 166 | GGGTGCCGCCAAGAAAGCTGCAGCCTTCACACAGACAGCCGCCAAGAACTCATCTTCTCCT | | 225 |
| QY | 126 | GGGGGATGGGATGGGGGTGCTTACGGGTGACAGCCACTCGGATCCTTAAAGGGCAGATGAA | | 185 |
| Db | 226 | GGGCGATGGGATGGGGGTGTCTTACGGGTGACAGCTGCCAGATCCTTAAAGGGCAGAA | | 285 |
| QY | 186 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGGACACAGTTCCTATAGTGGCTGTGC | | 245 |
| Db | 286 | GGACAAACTGGGGCCTGAGTTAACCCCTGGCCATGGACCGCTTCCATATGTGGCTGTGC | | 345 |
| QY | 246 | CAAGACATACACGCTGACACAGCAGGTGCCAGACAGCGCAGGCACTGCCACTGCCTACCT | | 305 |
| Db | 346 | CAAGACATACATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCCTACCT | | 405 |
| QY | 306 | GTGTGGGGTCAAGGGCACTTACAGAAACCATTCGGTGTAAAGTCACAGCCCGGCTACAATCA | | 365 |
| Db | 406 | GTGCGGGGTCAAGGGCACTTCCAGACCAATTGGCTTGAATGCAGCCCGGCTTTAACCA | | 465 |
| QY | 366 | GTGCAACACGACACGCTGGGAATGAGGTCACGTCTGTATCAACCGGGCAAGAAAGCAGG | | 425 |
| Db | 466 | GTGCAACACGACACGCGGGCAAGAGTCACTCCGTATGAATCGGGCCAGAAAGCAGG | | 525 |
| QY | 426 | GAAGGCCGTGGAGTGTGACCAACACAGGGTGCAGCATGCTCCCGAGCCGGGCTTA | | 485 |
| Db | 526 | GAAGTCAGTGGAGTGTGTAAACCAACACAGAGTGCAGCACGCTCGCCAGCCGGCACCTA | | 585 |
| QY | 486 | CGCGCACACGGGTGAACCGAAACTGTGTACTCAGACGCGGACCTGCTGCTGATGCAC-AGA | | 544 |
| Db | 586 | CGCCCAACAGGTGAACCGCACTGTGTACTCGAGCGCGGACGCTGCTCGGGCCGCCA | | 645 |
| QY | 545 | AGAAATGGCTGCAGGACATCGCCGACAGCTGGTCTTCAACATGTGATAATGACGTATCC | | 604 |
| Db | 646 | GGAGGGGGTGCAGGACATCGGTACGACGCTCATCTCCAACATGACATGACGTGATCC | | 705 |
| QY | 605 | TGGGTGGAGGCCGAATGTACATGTTTCTTGAGGGGACCCAGACCTGTAATACCCAGATG | | 664 |
| Db | 706 | TAGGTGAGGCCGAAGTACATGTTTCCGATGGGAACCCAGACCTGATGATACCCAGATG | | 765 |
| QY | 665 | ATGCCAGTGTGAATGAGTCCCGAAGAGACAAGCAAGAACCTGGTGCAGGAATGGCAGGCCA | | 724 |
| Db | 766 | ACTACAGCCAAAGTGGGACCAAGGCTGGACGGGAAGAACTGGTGCAGGAATGGCTGGCGA | | 825 |
| QY | 725 | AGCACCCAGGAGCCCAGTATGTGTGAAACCGCACTGCGCTCTTACGGCGGCCGATGACT | | 784 |
| Db | 826 | CGC-CAAGGGTGCCCGTACGTGTGAAACCGCACTGAGCTCATGCAAGCTTCCCTGGAAC | | 884 |
| QY | 785 | CCAAGTAAACACACCTCATAGGCTCTTTGAGCCGCGACATGAATATATATGTTACGC | | 844 |
| Db | 885 | CGTCTGTGACCCATCTCATAGGCTCTTTGAGCCTGGAGAMATGAATAAGAGATCCACC | | 944 |
| QY | 845 | AAGACCAACACCAAGGACCCGACCCCTGGCGGAGATGACGAGGCGGCC | 891 | |
| Db | 945 | GAGACTCCACACTGAMCCCTCCTTGATGAGATGACARAGCTGCC | 991 | |

| | |
|------------|--|
| RESULT 4 | |
| BX458398 | |
| LOCUS | 950 bp mRNA linear EST 05-MAY-2004 |
| DEFINITION | BX458398 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE002YN211 |
| 5-PRIME, | mRNA sequence. |

| | |
|-----------|-------------|
| ACCESSION | BX458398 |
| VERSION | BX458398.2 |
| | GI:47053565 |

| KEYWORDS | EST. |
|----------|----------------------|
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |

REFERENCE
1 (bases 1 to 950)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31023009.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DE002CG11QP1&c=1699.f.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE002YN21"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 39.5%; Score 582.6; DB 5; Length 950;
Best Local Similarity 80.8%; Pred. No. 2.8e-131;
Matches 678; Conservative 1; Mismatches 160; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGGAAAAACCCGCTTCTGAAACCGCAGGAGCCAGGCCCT 65
DB 112 CATCATCCAGTTGAGAGAGAGAACCCGACTTCTGAAACCGCAGGAGGCCCT 171
QY 66 TGATGTAGCCAGAAGTTGACGCCGATCCAGACAGCTGCCAAGATGTCTCTTCT 125
DB 172 GGGTGCGGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCTTCT 231
QY 126 GGGGATGGGATGGGGTGCCTACGGTGACAGCCACTCGGATCTTAAAGGGGAGATGA 185
DB 232 GGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCTTAAAGGGGAGAA 291
QY 186 TGGCAAACTGGGACCTGAGACACCCCCCTGGCCATGAGCCAGTTCCTATCGTGGCTGTC 245
DB 292 GGACAAACTGGGGCCTGAGTTACCCCTGGCCATGAGCCGCTTCCTATGTGGCTGTC 351
QY 246 CAAGACATACAACGTTGACAGACAGGTGCGACAGCAGCGCAGGCACTGCCACTGCTTACT 305
DB 352 CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGAGGCCACAGCCAGGCTTACT 411
QY 306 GTGTGGGGTCAAGGGCACTACGAACCATCGTGTAGTGACAGCCGCCGCTTACAATCA 365
DB 412 GTGCGGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAAGTGACAGCCGCCGCTTAAACA 471
QY 366 GTGCAACACGACAGCTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAGAAAGCAGG 425
DB 472 GTGCAACACGACAGCGCGGCAAGAGTCTATCTCCGTATGAATCGGGCCAGAAAGCAGG 531
QY 426 GAAGCCGTGGAGTGTGACCAACCAAGGGTGACAGCATGCTCCCAAGCCGGGGCTTA 485
DB 532 GAAGTCAAGTGGAGTGTGAACCAACCAAGAGTGACAGCAGCCTCGCCAGCCGGCACTTA 591
QY 486 CGCGCACACGGGTGAACCGAACTGGTACTCAGACGCCGAGCTGCTGTATGACACAGAA 545
DB 592 CGCCACACAGGTGAACCGCACTGGTACTCGAGCGCCGAGCTGCTCGGCCCGCA 651
QY 546 GAATGGCTGCAGGACATCGCCGACAGCTGTGTCTACAACATGGAATATTGACGTGATCCT 605

DB 652 GGAGGGGTGCCAGACATCGCTACGACGCTCATCTCCACATGAGACATTGACGTGATCCT 711
QY 606 GGGTGAGGCGCCGAATGTACATGTTTCTTGAGGGAGGAGCCAGACCTGATATACCAAGATGA 665
DB 712 AGGTGAGAGCCGAAAGTACATGTTTGCATGGAACCCAGACCTGAGTACCCAGATGA 771
QY 666 TGCCAGTGTGAATGAGTCCGGAAGACAGACAGAACTGTGACAGAAATGGAGCCCAA 725
DB 772 CTACAGCCAAGGTGGACACAGGCTGACCGGAAGAAATCTGTGACAGAAATGGCTGGCGAM 831
QY 726 GCACCAAGGAGGCCAGTATGTGTGAACCGCAGCACTGCGCTCTTCAAGCGGCGGATGACTC 785
DB 832 GGGCAGGGGTGCCCGGTACGTGTGGAACCGCACTGAGCTCATGACAGGCTTCCCTGAGACC 891
QY 786 CAGTGTAAACACACCTCATGGGCTCTTGAGCCGGCAGACATGAATATATGTTACG 844
DB 892 GTCTGTGARCACATCTCATGGGTCTCTTGAGCCTGAGACATGAATACGAGATCCACC 950

RESULT 5
AL552555 984 bp mRNA linear EST 30-MAR-2004
LOCUS AL552555
DEFINITION AL552555 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI067YC24 5-PRIME, mRNA sequence.
ACCESSION AL552555
VERSION AL552555.3 GI:45857340
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31274370.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DI067B12QP1&c=1699.f.

FEATURES
source
1..984
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI067YC24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoRV
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 38.9%; Score 574.8; DB 1; Length 984;
Best Local Similarity 80.5%; Pred. No. 2.3e-129;
Matches 708; Conservative 1; Mismatches 168; Indels 3; Gaps 3;

QY 6 CCTCATCCAGCTGAGAGGAAAAACCCGCTTCTGAAACCGCAGGAGCCAGGCCCT 65
DB 106 CATCATCCAGTTGAGAGAGAGAACCCGACTTCTGGAACCGCAGGAGCCGAGGCCCT 165
QY 66 TGATGTAGCCAGAAGTTGACGCCGATCCAGACAGCTGCCAAGAATGTATCTTCTT 125
DB 166 GGGTGCGGCCAAGAAGCTGACGCTGCACAGACAGCCGCCAAGAACCTCATCTTCTT 225

| | | | |
|----|-----|---|-----|
| QY | 126 | GGGGGATGGGATGGGGGTGCTTACGGGTGACAGCCACTCGGATCTTAAAGGGGCAGATGAA | 185 |
| Db | 226 | GGGCGATGGGATGGGGGTGTCTACGGTGA CAGCTGCGAGATCTTAAAGGGCAGAA | 285 |
| QY | 186 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCCAGTTC CATACGTGGCTGTGC | 245 |
| Db | 286 | GGA CA AACTGGGGCCTGAGTTA C C C T G G C C A T G A C C G C T T C C A T A T G T G C T G T C | 345 |
| QY | 246 | CAAGACATACAACGTGAGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTTACT | 305 |
| Db | 346 | CAAGACATACAATGTAGACAACATGTGCCAGACAGTGGAGCCACAGCCACGGCTTACT | 405 |
| QY | 306 | GTGTGGGGTCAAGGGGCACTACAGAACCATCGGTGTAAGTGCAGCCGCCCTACAATCA | 365 |
| Db | 406 | GTGCGGGGTCAAGGGGCACTTCCAGACCATTGGCTTGA GTGCAGCCGCCCTTTAACCA | 465 |
| QY | 366 | GTGCAACACGACACGTGGGAA TGAGGTCACGCTGTGTATCA CCGGGCCAAGAAAGCAGG | 425 |
| Db | 466 | GTGCAACACGACACGGCGCA CAGGTCATCTCGTGATGAATCGGGCCAAGAAAGCAGG | 525 |
| QY | 426 | GAAGGCCGTGGAGTGTGTGACCA CCA CAGGGGTGCAGCATGCTTCC CAGCCGGGCTTA | 485 |
| Db | 526 | GAA GT CAGTGGAGTGTGTAA CCA CCA CAGAGTGCAGCAGCTTGC CAGCCGGCACTTA | 585 |
| QY | 486 | CGCGCACACGGTGAAACCGAAACTGGTACTCAGACGCGCGACTGCTGTATGAC-AGA | 544 |
| Db | 586 | CGCCACACCGGTGAACCGCACTGTACTCGGACGCGCAGCTGCTGCTCGGCCCA | 645 |
| QY | 545 | AGAATGGCTGCCAGGACATCGCCGACACAGCTGGTCTTACAATGGATATTGACGTGATCC | 604 |
| Db | 646 | GGAGGGGGTGCCAGGACATCGCTACGCA GCTCATCTCCAATGGA CATTGACGTGATCS | 705 |
| QY | 605 | TGGGTGGAGGCCCGAATGTACATGTTTCTTGAGGGGACCCCGACACCTGGAATACCCAGATG | 664 |
| Db | 706 | TAGGTGAGGCCGAAAGTACATGTTTCGATGGGAACCCAGACCCTGAGTACCAGATG | 765 |
| QY | 665 | ATGCCAGTGTGAATGAGTCCGGAAGGACAAGACAGAACTGTGTCAAGGAATGGCAGGCCA | 724 |
| Db | 766 | ACTACAGCCAAAGTGGGACCA G G C T G G A C G G A A G A A T T G G T G C A G G A A T G C T G G C G A | 825 |
| QY | 725 | AGCACCAAGGAGCCCAATGTGTGTGAAACCGCACTGCGCTCTTCAAGCGGCCGATGACT | 784 |
| Db | 826 | CGC-CAGGGGTGCCCGGTACGTGTGAAACCGCACTGAGTCA TGCA G G C T T C C T G A C C | 884 |
| QY | 785 | CCA GTGT-AA C A C A C C T C A T G G G C C T T T G A G C C G G C A G A C A T G A A G T A T A T G T T C A G | 843 |
| Db | 885 | CGTCTGTGAACCCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGAATAACGAGATCCAC | 944 |
| QY | 844 | CAAGACCA C A C C A A G G A C C C G A C C T G G C G G A G A T G A C G G | 883 |
| Db | 945 | CGAGACTCCACACTGGACCCCTCTCTGTATGGAGATGACAG | 984 |

RESULT 6
AY404253
LOCUS
DEFINITION
AY404253 1593 bp DNA linear GSS 15-DEC-2003
Homo sapiens ALPLP2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY404253
VERSION
AY404253.1 GI:39760230
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1593)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Fierlera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

| | |
|-----------|---|
| JOURNAL | Science 302 (5652), 1960-1963 (2003) |
| PUBMED | 14671302 |
| REFERENCE | 2 (bases 1 to 1593) |
| AUTHORS | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA |
| COMMENT | This sequence was made by sequencing genomic exons and ordering them based on alignment. |
| FEATURES | Location/Qualifiers |
| source | 1. .1593 |
| | /organism="Homo sapiens" |
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| | <1. .>1593 |
| gene | /gene="ALPPL2" |
| | /locus_tag="HCM1829" |
| ORIGIN | |

| Query Match | 38.0%; | Score 561; | DB 9; | Length 1593; |
|-----------------------|--|-------------------|-----------|--------------|
| Best Local Similarity | 45.3%; | Pred. No. 6e-126; | | |
| Matches 664; | Conservative 0; | Mismatches 797; | Indels 6; | Gaps 1; |
| QY 6 | CCTCATCCAGCTGAGAGAGAAAACCCGCTTCTTGAAACCGCAGGACCCAGGCCCT | 65 | | |
| Db 57 | CATCATCCCACTGTAGAGAGAGAACCCGCACTTCTGAAACCGCAGGACCCAGGCCCT | 116 | | |
| QY 66 | TGATGTAGCCAAGAGATTGCAGCCGATCCAGACAGCTGCCAAGATGTCACTCTTCTT | 125 | | |
| Db 117 | GGGTGCCGCCAAGAGACTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCTTCTT | 176 | | |
| QY 126 | GGGGGATGGATGGGGGTGCTTACGGTGAACGCCACTCGATCCTAAAGGGGACATGAA | 185 | | |
| Db 177 | GGG-----GATGGGGGTGTCTACGGTGAACAGCTGCCAAGATCCTAAAGGGGACAGAA | 230 | | |
| QY 186 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGSAACAGTTCCCATACGTGCTGTCTC | 245 | | |
| Db 231 | GGACAAACTGGGGCTTGAGACCTTCTTGCCATGSAACGCTTCCCGTACGTGCTGTCTC | 290 | | |
| QY 246 | CAAGACATACAACGTGAGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTTACT | 305 | | |
| Db 291 | CAAGACATACAGTGTAGACAAGCATGTGCCAGACAGTGAAGCCACAGCCACGCGCTTACT | 350 | | |
| QY 306 | GTGTGGGTCAAGGGCACTACAGAACCATCGGTGTAAGTGCAGCGCGCGCTAACATCA | 365 | | |
| Db 351 | GTGCGGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAAGTGCAGCGCGCGCTTAACCA | 410 | | |
| QY 366 | GTGCAACACGACACCTGTGGGAATGAGGTCACGTCTGTGATCAACCGGGCCAGAAGCAGG | 425 | | |
| Db 411 | GTGCAACACGACACCGGGCAACGAGGTCACTCCGTGATGAATCGGGCCAGAAGCAGG | 470 | | |
| QY 426 | GAAAGCCGTGGAGTGTGTGACCAACACAGGTTGACATGCTCCCCAGCGGGGCTTA | 485 | | |
| Db 471 | AAAGTCAGTGGAGTGTGTAAACCAACACAGGTTGACATGCTCGCCAGCGGGGCTTA | 530 | | |
| QY 486 | CGCGCACACGTTGAACCGAAACTGTACTCAGACCGGACCTGCTGTATGCAGAA | 545 | | |
| Db 531 | CGCCACACAGTGAACCGCAACTGTACTCGATGCGGACGTCCTCGGCCGCA | 590 | | |
| QY 546 | GAATGCTGCGCAGACATCGCCGACAGCTGTTCAACATGATATTGACGTGATCTT | 605 | | |
| Db 591 | GGAGGGGTGCCAGACATCGCCACGCACTCATCTCAACATGACATTTATNNNNNNN | 650 | | |
| QY 606 | GGGTGAGGCGCAATTATCATGTTTCTGAGGGGACCCAGACCTGAATACCAAGATGA | 665 | | |
| Db 651 | NN | 710 | | |
| QY 666 | TGCCAGTGTGAATGAGTCCGGAAGACAAGCAACCTGCTGACGAATGGCAGGCCAA | 725 | | |
| Db 711 | NN | 770 | | |

QY 726 GCACGAGGAGCCAGTATGTGTGAACCGCACTGCGCTCCTTCAGCGCGCGATGACTC 785

Db 771 NNN 830

QY 786 CAGTGTAAACACACCTCATGGGCTCTTTGAGCCGGCAGACATGATAATGTTACGA 845

Db 831 NNN 890

QY 846 AGACCACACCAAGACCCGACCTTGCGGAGATGACGAGGCGGCTGCAAGTGTAG 905

Db 891 NNN 950

QY 906 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGCGGCAATTGACACGTCACCA 965

Db 951 NNN 1010

QY 966 TGACGCGAAGCTTATATGCACTGAGCGGATCATGTTGACATGCCATCGCCA 1025

Db 1011 NNN 1070

QY 1026 GGCTAACGAGCTCACTAGCGAAGTGAACGCTGATCCTTGTCACTGACAGCACTCCCA 1085

Db 1071 NNN 1130

QY 1086 TGTCTTCTCTTTTGGTGTGCTACACTGCGTGGGACCTCCATTTCGGTCTGCCCCGG 1145

Db 1131 NNN 1190

QY 1146 CAAGGCTTAGACAGCAAGTCTTACACTCCATCCTCTATGGAATGGCCAGGCTATGC 1205

Db 1191 NNN 1250

QY 1206 GCTTGGCGGGGCTCGAGGCCGATGTTAATGCGACACAAAGCAAGCAACCTCATACCG 1265

Db 1251 NNN 1310

QY 1266 GCAGCAGGCGGCGCTGCCCCCTGCTAGCGAGACCCAGGGGCGAAGACGTGGCGTGT 1325

Db 1311 GCAGCAGTCAAGAGTGCCCCCTGACGAGAGAGACCCAGCGAGAGACGTGGCGTGT 1370

QY 1326 CGCGCGAGGCGCGCAGCGCACTGTGCAAGCGGCTGCAAGAGAGACCTTGTGGCGCA 1385

Db 1371 CGCGCGCGGCGCGCAGCGCACTGTGTTCAAGCGGCTGCAAGAGAGACCTTATAGCGCA 1430

QY 1386 CATCATGGCCTTTCGGGCTGCGTGGAGCCCTACACCGGACTGCAATCTGCCAGCCCCGC 1445

Db 1431 CGTCTAGGCTTCGCGCGCTGCTGAGGCCCTACACCGGCTGCACTGCGCGCCCCGC 1490

QY 1446 CACGCGCACGAGCATCCCCGACTAGGG 1472

Db 1491 CGGCACCAACGAGCGCGCGCACCGGG 1517

RESULT 7
CK453205
LOCUS 772 bp mRNA linear EST 12-JAN-2004
DEFINITION 908900 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CK453205
VERSION CK453205.1 GI:40800419
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 772)
AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonheman,D.J., Wray,J.E. and Keele,J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_al option. Vector identified with
cross_match v0.990329.
Plate: TMW8024 row: H column: 10
Seq primer: GTAATACGACTCATATAGG.
Location/Qualifiers
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/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4PIG"
/note="Vector: pcdNA3.1; Site_1: EcoRI; Site_2: NotI;
library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN
Query Match 37.8%; Score 557.6; DB 7; Length 772;
Best Local Similarity 82.6%; Pred. No. 3.5e-125;
Matches 638; Conservative 0; Mismatches 134; Indels 0; Gaps 0;
QY 627 GTTCTCTGAGGGAGCCCGAGACCTGATATACCAGATGATCCAGTGTGAATGAGTCCG 686
Db 1 GTTCTCTGAGGAGACTCCGAGCCTGATATACCAGATATCCAGATGAGTGTGCG 60
QY 687 GAAGACAAGCAGAACTGTGTGCAAGAAATGGCAGGCCCAAGCAACGAGGAGCCAGTATGT 746
Db 61 GAAGACAAGCAGAACTGTGTGTAAGAGAGTGGCAGGCCCAAGCAACGAGGAGCCGATGT 120
QY 747 GTGGAACCGCACTGCGCTCTTCAAGCGGCGGATGACTCCAGTGTAAACACACCTCATGGG 806
Db 121 GTGGAACCGCACTGCGCTCTTCAAGCGGCGGATGACTCCAGGAGCCCAAGCTCATATGGG 180
QY 807 CCTCTTGAGCGGCGAGCATGAATATATGTTTCAAGCAAGACCAACCAAGAGCCGAGC 866
Db 181 CCTTTTGAGCGGCGAGCATGAATATGAAAAGGAAGAGACCTCAGCAGGAGCCCTC 240
QY 867 CTTGCGGAGATGACGAGGCGGCGCTGCAAGTGTGAGCAGGAACCCCGGGCTTCTA 926
Db 241 CTTGTTGAGATGACGAGGAGTGGCCCTGCGCTGTGAGCAGGAACCCCGGTGCTTCT 300
QY 927 CCTCTTCTGAGGAGGCGCGCATTTGACCAACGCTGACCATGACGGAAGCTTATATGGC 986
Db 301 CCTCTTCTGAGGAGGCGCGCATTTGACCAACGCTGACCATGAGAACATCGCTTATAGGC 360
QY 987 ACTGACTGAGGCGATCATGTTTGAACAATGCCATGCCAAGGCTAAGAGCTCATAGCGA 1046
Db 361 GCTGATCGAGGCGCTCATGTTTGAACACCGCCATCGACAAAGGCTGGCCAGCTCATAGCGA 420
QY 1047 ACTGACACGCTGATCCTTGTCACTGACAGACCACTGCCATGCTTCTTTGGTGGCTA 1106
Db 421 AGAGACACACTGACCTGTGTCAAGCGCGACCACTCATGTCTTCACTATGTGGCTA 480
QY 1107 CACACTGCGTGGAGCTTCATTTTTCGGTCTGCGCCCGGCAAGGCTTAGACAGCAAGTC 1166
Db 481 CCCGCTGCGTGAAGCTCCGTTTTCGGCTGCTGATGGCAAGGCTTTGATGGCAAGC 540
QY 1167 CTACACCTCCATCCTTATGGAATGAGCCAGGCTATGCGCTTGGCGGGGCTCGAGGCC 1226
Db 541 CTACACCTCCATCCTTATGGAATGAGCCAGGCTATGAGCTCAGCGAAGGCGCAAGGCC 600
QY 1227 CGATGTTATGCGACGACAAGCGAGAACCTTCATACCGGCGAGAGCGGCGCTGCCCT 1286
Db 601 TGATGTTGATGAACCAAGACGAGGAGCCCGCATACGTGACAGCAGGCGGCGCTGCCCT 660
QY 1287 GGCTAAGGAGACCCAGGCGGCGGAAGAGCTGGCGGTTCGCGGAGGCGCGCGAGCGCA 1346
Db 661 GGTGCGGAGACCCAGGCGGCGAGAGAGCTGGCGGTTCGCGGCGGCGCGCGCGCA 720

Qy 1347 CCTGTGCACGGCGCTGCAGAGAGACCTTCGTGGCCGACATCATGGCCTTT 1398
Db 721 CCTGTGCACGGCGCTGCAGAGAGACGAGCTTCTGTGGCCGACGTAATGGCCTT 772

RESULT 8
LOCUS AY404255 1587 bp DNA linear GSS 15-DEC-2003
DEFINITION Mus musculus ALPPL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY404255
VERSION AY404255.1 GI:39760232
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1587)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1.1587
Location/Qualifiers
gene /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/gene="ALPPL2"
/locus_tag="HCM1829"

ORIGIN
Query Match 36.4%; Score 537.6; DB 9; Length 1587;
Best Local Similarity 44.3%; Prid. No. 3.1e-120;
Matches 643; Conservative 0; Mismatches 801; Indels 6; Gaps 1;

Qy 8 TCATCCCACTGAGAGAGAAAACCCCGCTTCTGGAACCGCCAGCGCCAGCCCTTG 67
Db 59 TCATTCACAGTGGAGAGAGAACCCCGCTTCTGGAACAGAGGCGAGGCCCTGG 118
Qy 68 ATGTAGCCAGAGATTGCAGCCGATCCAGACAGCTGCCAAGAATGTCTCTTGG 127
Db 119 ATGCTGCCAAGAGCTGCAGCCCATTCAGATCACTAAGAACTCATCTTCTGG 178
Qy 128 GGGATGGATGGGGGTGCTACGCTGACAGCACTCGATCCTAAGGGGAGATGATG 187
Db 179 G-----GATGGGGGTACCCACAGTACAGCAACAGATCCTAAGGGGAGTTGGAAG 232
Qy 188 GCAAACTGGAGCTGAGACACCCCTGGCATGAGACCAAGTCCCATAGTGGCTGTCCA 247
Db 233 GCCATCTAGACCGGAGACACCCCTAGCATGACCTCTTCCCATATGCTGTCCA 292
Qy 248 AGACATACAAGTGGACAGACAGAGTGGCAGACGCGAGGACTGGCTTACTCTGT 307
Db 293 AGACATACAAGTGGACAGACAGAGTGGCAGACGCGGCGGCGCTTACTCTGT 352
Qy 308 GTGGGCTCAAGGCAACTACAGAACCATCGGTGTAAAGTGCAGCGCGCGCTACAATCAGT 367

Db 353 GTGGGTCAGAACCAACTACAGAACCATCGCGCTGAGCGGAGCCGCGAGATTGACCACT 412
Qy 368 GCAACACGACACGTGGGAATGAGTCACTGTGTATCAACCGGCGCAAGAAAGCAGGGA 427
Db 413 GCAACACGACATTTGGCAATGAGGCTTCTCAGTATGATACCGTCCAAAGAACGAGGA 472
Qy 428 AGGCGGTGGAGTGTGACCAACACGAGGTGACAGATGCTCCCGAGCGGGGCTACG 487
Db 473 AGTCTGTGGAGTGTGACCAACGAGGTTGACAGATGCTCTCCAGCGGACCTACG 532
Qy 488 CGCACACGGTGAACCGAACTGGTACTCAGACGCGGACCTGCTGTGATGCACAGAGA 547
Db 533 CACACACGGTGAACCGTAATTGGTACTCAGATGACAGATGCTGCTGCACTGCAGG 592
Qy 548 ATGCTGCGAGACATCGCCGACAGCTGCTTACACATGATATTGACGTATCCTGG 607
Db 593 ACGGCTGACAGACATCGCCACTCACTCATCTCCAACATGACATGATTGATNNNNNNNN 652
Qy 608 GTGAGCGCGAATGTACATGTTCTTGAGGGGACCCAGACCTGGAATACCCAGATGATG 667
Db 653 NNN 712
Qy 668 CCAAGTGAATGAGTCCGGAAGACAGACAACTGTGTGACAGAAATGGCAGGCCAAGC 727
Db 713 NNN 772
Qy 728 ACCAGGAGCCAGTATGTGTGAACCGCACTGCGCTCCTTACGCGGCGGATGACTCA 787
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Qy 788 GTGTAACACACTCATGCGCTCTTTGAGCCGCGACACATGAAGTAAATGTTCAAGAA 847
Db 833 NNN 892
Qy 848 ACCACACCAAGACCCGACCTGGCGAGATGACGAGGCGGCGCTGCAAGTCTGAGCA 907
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Qy 908 GGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGAGCGCATGACCAAGTCAACATG 967
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Qy 1028 CTAACGAGCTCACTAGCGAAGTGCAGACGCTGATCCTGTCTACCTGCAGACCACTCCATG 1087
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Qy 1088 TCTTCTTTTGTGTGCTACACACTGCGTGGACCTCATTTTGGTCTGCGCCCGGCA 1147
Db 1133 NNN 1192
Qy 1148 AGGCTTAGACAGCAAGTCTTACACTCTCTATGCAATGGCCAGGCTATGCGC 1207
Db 1193 NNN 1252
Qy 1208 TTGGCGGGGCTCGAGGCGCATGTTAATGGCAGCACAAGCGAGAACCTCATACCGGC 1267
Db 1253 NNN 1312
Qy 1268 AGCAGGCGGCGTCCCTGCTAGCGAGACCCAGGGGCGAAGAGTGGCGGTGTCG 1327
Db 1313 AGCAGGCTGTGTACCCCTGTCTGACAGACCCACAGCGGGAGAGCTGGCAATATTGG 1372
Qy 1328 CGCAGGCGCGCAGCGCACTGTGTGACGCGGTGACAGGAGAGACTTGTGCGGACACA 1387
Db 1373 CGGCTGCGCCACAGCGCACCTGTGTGACGAGTTCAAGAGCAGAACTACATCGGCACG 1432
Qy 1388 TCATGCGCTTTCGCGGCTGCTGAGCCCTTACACGAGCTGCAATCTGACAGCCCGGCA 1447
Db 1433 TCATGCGCTTTCGACGCTGCTGAGCCCTTACACTGACTGCGGCTTGGCATCCCTGCTG 1492

QY 1448 CCGCCACCAG 1457
Db 1493 GCCAGAGCAG 1502

RESULT 9
BX343739

LOCUS 1125 bp mRNA linear EST 07-APR-2004
DEFINITION BX343739 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI017YB14 5-PRIME, mRNA sequence.

ACCESSION BX343739
VERSION BX343739.2 GI:46270510
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1125)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30336211.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS1A1005ZB08QP1&c=1699.f.

FEATURES

source

location/Qualifiers
1..1125
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI017YB14"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 35.7%; Score 526.2; DB 5; Length 1125;

Best local Similarity 80.6%; Pred. No. 1.8e-117;

Matches 662; Conservative 1; Mismatches 154; Indels 4; Gaps 4;

QY 6 CCTCATCCCACTGAGAGAGAAAACCCGCTTCTGAAACCGCCAGGAGCCGACCTT 65
Db 211 CATCATCCCACTGAGAGAGAAACCCGACTTCTGAAACCGGAGGACGCCGAGCCCT 270
QY 66 TGAATGAGCCAAGAAGTTGCAGCCGATCCAGACAGCTGCCAAGAAATGTCATCCTTCTT 125
Db 271 GGGTGCCTCCCAAGAAGCTGCAGCTGCACAGACAGCCGCCAAGAACTCATCATCTTCTT 330
QY 126 GGGGATGGGATGGGGGTGCTTACCGGTGACAGCCCACTCGGATCTTAAAGGGGAGATGAA 185
Db 331 GGGCGATGGGATGGGGGTGTCTTACGGTGAACAGCTGCCAGGATCTTAAAGGGGAGAGAA 390
QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGGACCAAGTTCCATACGTGGCTTGTGTC 245
Db 391 GGACAAACTGGGGCTGAGTTACCCCTGGCCATGAGCCGCTTCCATATGTGGCTTGTGTC 450
QY 246 CAAGACATACAACGTGAGACAGACAGGTGCAGACAGCGCAGCACTGCCACTGCTTACTT 305
Db 451 CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGAAGCCACAGCCAGCCTTACTT 510

QY 306 GTGTGGGGTCAAGGGCAACTACAGAAACCATCGGTGTAAGTGCAGCCGCCGCTTACAATCA 365
Db 511 GTCCGGGGTCAAGGGCAACTTCCAGACCATTTGCTTGAGTGCAGCCGCCGCTTAAACCA 570
QY 366 GTGCACACGACACGTTGGGAATGAGTGCAGCTGTGTGATCAACCGGGCCAGAAAGCAGG 425
Db 571 GTGCACACGACACGCGGCACGAGTGCATCTCCGTGATGAATCGGGCCAAAGAAAGCAGG 630
QY 426 GAAAGCCGTGGAGTGTGATCCACACAGGAGTGACAGTGCCTCCCGACCGGGGCTTA 485
Db 631 GAAGTCAGTGGAGTGTGATCCACACAGAGTGCAGCAGCGCTCGCCAGCGGCACCTA 690
QY 486 CGCGACACCGGTGAACCGAACTGCTACTCAGACCGCCGACCTGCTGTGATGCAC-AGA 544
Db 691 CGCCACACCGGTGAACCGCACTGCTACTCGGACGCCGACGTGCTGCTGCGCCGCCA 750
QY 545 AGAATGGCTGCCAGACATCGCCGCACAGCTGCTGTCTTACAACATGATATTGACGTGATCC 604
Db 751 GGAGGGGGTGCAGGACATCGCTACGACGCTCATCTTCCAACATGACATGACGTGATCC 810
QY 605 TGGGTGAGGGCCGAATGTACATGTTTCTGTAGAGGAGCCCGACCCCTGAATACCCAGATG 664
Db 811 TAGGTGAGAGCCGAAAGTACATGTTT-CGCATGGGAACCCAGACCCCTGAGTACCCAGATG 869
QY 665 ATGCCAGTGTGAATGAGTCCGGAAGACAAAGACAGAACTGTGTGAGGAATGGAGGC-C 723
Db 870 ACTACAGCCCAAGTGTGGACCAAGCTGCAGCGGAAGAATCTGTGTGACGAATGGCTGGCGG 929
QY 724 AAGCACCAGGAGAGCCCAATGATGTGTGGAACCCGACCTGCTTACAGCGGCGCGATGAC 783
Db 930 ACGCCAAGGGGTGCCCGGTACGTGTGGRACCGCACTGAGCTCATGACAGGCTTCCCTGGAC 989
QY 784 TCCAGTGTACACACCTCATGGCCCTCTTTGAGCCGCGACA 824
Db 990 CCGTCTGTGAC-CATCTCATAGGTCTCTTTGAGCTTGGA 1029

RESULT 10
AK076459

LOCUS AK076459 2459 bp mRNA linear HTC 03-APR-2004

DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
library, clone:4833407E05 product:alkaline phosphatase 2, liver,
full insert sequence.

ACCESSION AK076459
VERSION AK076459.1 GI:26096820
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

JOURNAL MEDLINE 99279253
PUBMED 10349636

REFERENCE
AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL MEDLINE 20499374
PUBMED 11042159

REFERENCE
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format

[illegible]

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|----|------|---|------|
| QY | 71 | TAGCCAAGAGTTGACCCGATCCAGAC--AGCTGCCAAGATGTCATCTCTTCTTGG | 127 |
| Db | 294 | ATGCCCTGAAACTCCAAAAGCTCAACACCAATGTAGCCAAAGATGTCATCATGTTCTGG | 353 |
| QY | 128 | GGGATGGGATGGGGTGCCTACGGTGACAGCCACTCGGATCTTAAAGGGCAGATGAATG | 187 |
| Db | 354 | GAGATGGTATGGGCGTCTCCACAGTAACCGCTGCCCGAATCTTAAAGGCCAGCTACACC | 413 |
| QY | 188 | GCAAACTGGGACCTGAGACACCCCTGGCCATGGACCACTTCCCATACGTGGCTGTGCCA | 247 |
| Db | 414 | ACAACACGGGCGAGGAGACCCGGCTGGAGATGGACAAATTCCTTGTGTGGCCCTGCCA | 473 |
| QY | 248 | AGACATTAACAACGTGACAGACAGGTGCCAGACAGCGCACTGCCACTGCCCTTACCTGT | 307 |
| Db | 474 | AGACATATAACCAACCGCTCAGGTCCCTGACAGCGCGGCACTGCCACTGCCCTACTTGT | 533 |
| QY | 308 | GTGGGGTCAAGGCAACTACAAACCATCGGTGTAAGTGCAGCCGCCGCTACAATCAGT | 367 |
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| QY | 368 | GCAACACGACACGTGGGAATGAGGTCACGTCGTGTATCAACCGGGCCAAAGAACGAGGA | 427 |
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| QY | 548 | ATGGCTGCCAGACATCCCGCACAGCTGGTCTACA--CATGATATTGACGTGATCC | 604 |
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| Db | 894 | ATGAGAAGGCCAGGGGTACAGGCTAGATGGCCTGATCTCATCAGTATTGGAAGAGCT | 953 |
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| Db | 954 | TTAAACCCAGACACAAAGCATTCCTCACTATGTCTGAAACCGCACTGAACTGCT--GGCCC | 1010 |
| QY | 776 | CCGATGACTCCAGTGTAAACACACTCATGCGCTCTTTGAGCCGGCAGACATGAAGTATA | 835 |
| Db | 1011 | TTGACCCCTCCAGGGTGAATACTCTTAGTCTCTTTGAGCCCGGGACATGACATATG | 1070 |
| QY | 836 | ATGTTACGAAGACCAACCAAGAACCCGACCTGGCGGAGATGACGGAGCGGCCCTGC | 895 |
| Db | 1071 | AATTGAATCGGAACAACCTGACTGACCTTCGCTCTCCGAGATGCTGAGAGTGCGCCCTCC | 1130 |
| QY | 896 | AAGTGTGAGCAGGAACCCCCGGGGCTTCACTCTTTCGTGAGGAGGAGGCCGCAATTGACC | 955 |
| Db | 1131 | GGATCTTGACCAAAAACCTCAAAAGCTTCTTTCGTGTGGAAGGAGGACAGATTGACC | 1190 |
| QY | 956 | ACGTCACCATGACGGCAAAAGCTTATATGGCACTGAGGCGATCATGTTTGAATG | 1015 |
| Db | 1191 | ACGACATCATGAGGGTAAGGCCAAGCAGGCTCTGATGAAGCAGTGAGATGAGCAGG | 1250 |
| QY | 1016 | CCATCGCCAAGGCTAACGAGCTCACTAGCGAACTGACACGCTGATCTTGTCACTGCAG | 1075 |
| Db | 1251 | CCATTGGCAAGGCAAGCGCCCATGACATCCAGAAAGACACTTGACTGTGTTACTGCTG | 1310 |
| QY | 1076 | ACCACTCCCATGTCTTCTTTTGGTGCTAACACTGCGTGGGACCTCCATTTTCGGTC | 1135 |
| Db | 1311 | ATCATTTCCACGTTTTCACATTGGTGATACACCCCCGGGGCAACTCCATCTTTTGGTC | 1370 |
| QY | 1136 | TGGCCCCC--GGCAAGGCTTACAGACGAACTGCTACACTTCATCTCTATGGCAATG | 1192 |

Db 1371 TGGCTCCCATGCTGAGCGACACGACAGAACCCCTTCACGGCCATCTATATGTAACG 1430
Qy 1193 GCCCAGGCTATGCCCTTGCGGGGCTCGAGCCCGATGTTAATGCGACACAAGCAGG 1252
Db 1431 GGCCTGGCTACAAGGTGTGTGACCGGTGAACGGGAAATGTCTCCATGTAGATTACGCTC 1490
Qy 1253 AACCTCATACCGCGCAGCAGCGCGCTGCCCCCTGGCTAGCGAGACCCAGCGGGCGAAG 1312
Db 1491 ACAACAACCTACAGGCGCCAGTCCGCTGTTCCCTCGCCCATGAGACCCACGGTGAGAAG 1550
Qy 1313 ACGTGGCGGTGTTGCGCGCAGGCGCCGCGCAGCCACTG-GTGCACGGCGTGCAGGAGAG 1371
Db 1551 ACGTGGCGGTCTTCGCCAAGGGCCCGATGGACAACCTGCTTCACGGCGTCCATGAGCAG 1610
Qy 1372 ACCTTGTCGGCGCACATCATGGCCTTTGCGGGCTGCGTGAGAGCCCTACACCGAC 1425
Db 1611 AACTACATCCCATGTGATGGCGTATGCTCTGCATGGGGCCAACTTGAC 1664

RESULT 11
AL553521 902 bp mRNA linear EST 30-MAR-2004
LOCUS AL553521 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1076YD24 5-PRIME, mRNA sequence.
ACCESSION AL553521 GI:45858290
VERSION AL553521.3
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31275335.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1076D812QP1&c=1699.f.

FEATURES
Source 1. 902
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/db_xref="taxon:9606"
/clone="CS0D1076YD24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 35.1%; Score 517.4; DB 1; Length 902;
Best Local Similarity 81.0%; Pred. No. 2.4e-115;
Matches 626; Conservative 9; Mismatches 135; Indels 3; Gaps 3;

Qy 6 CCTCATCCAGCTGAGAGAGAAAACCCGCTTCTGAAACCGCAGCAGCCAGGCGCT 65
Db 106 CATCATCCAGTGTGAGAGAGAACCCGACTTCTGAAACCGCAGGCGAGCGCCT 165
Qy 66 TGATGTAGCCAAGAAGTTGCAGCGCATCCAGACAGCTGCCAAGAATGTATCTTCTT 125

Db 166 GGGTCCGCCCAAGAGCTGCAGCCTGCACAGACAGACCCGCCAAGAACTCATCATCTTCT 225
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Db 226 GGGCATGGGATGGGGGTGTCTTACGGTGACAGCTGCAGGATCTTAAAGGGCAGAGAA 285
Qy 186 TGGCAACTGGGACCTGAGACACCCCTGGCCATGAGACCAATTCCATACGTGCTGTGTC 245
Db 286 GGACAAACTGGGCTGAGATACCCCTGGCCATGAGACCGCTTCCATATGTGCTGTGTC 345
Qy 246 CAAGACATACAACGTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTTACT 305
Db 346 CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGAGCCACAGCCAGGCTTACT 405
Qy 306 GTGTGGGGTCAAGGGCACTACAGAACCATCGGTGTAACTGCAGCCGCCGCTTACAATCA 365
Db 406 GTGCGGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAAGTGCAAGCCGCCGCTTAA 465
Qy 366 GTGCACACGACACCGTGGGAATGAGGTACGTCCTGTGATCAACCGGGCCAAGAACGAG 425
Db 466 GTGCACACGACACCGCGCAAGGTGATCTCGTGATGAATCGGGCCAAGAACGAGG 525
Qy 426 GAAAGCCGTGGGAGTGTGACCAACACGAGGTGCAGCATGCTCCCGAGCGGGCTTA 485
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Db 586 CGCCACACAGGTGAACCGCAACTGTACTCGACGCGCAGCGTGCCTCCGCCGCCA 645
Qy 545 AGAATGGCTGCCAGACATGCCCGCACAGCTGTGTACAAATGATATTTGACGTATCC 604
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Qy 605 TGGGTGAGAGGCCGAATGTACATGTTTCTGAGGGGAGCCCCAGACCTGTAATACCCAGATG 664
Db 706 TAGGTGAGAGCCGGAAGTACATGTTTCCGATGGGAAMCCCARACCCTGAGTACCCARATG 765
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RESULT 12
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LOCUS BX417625 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YC17
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX417625 GI:46955936
VERSION BX417625.2
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30767760.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

Db 121 CTGGACACGCTGATCCTTGTCACCTGCAGACCACCTCTCATGTCTTCTTTGGTGGCTAT 180
QY 1108 ACACGTGGTGGGACCTCCATTTTCGGTCTGGCCCCCGGCAAGGCTTGAACAGCAAGTCC 1167
Db 181 ACATCGGTGGGACCTCCATTTTGTGTGGCCCCCAGCAAGGCTTGAACAGCAAGTCC 240
QY 1168 TACACCTCCATCCTCTATGGAATGGCCCCAGGCTATGCGCTTGGGGGGGCTCGAGGCC 1227
Db 241 TACACCTCCATCCTCTATGGAATGGCCCCAGGCTATGCGCTTGGGGGGGCTCGAGGCC 300
QY 1228 GATGTTAATGGCAGACACAAGCGAGAACCTCTATACCGGACAGAGCGGCGCTGCCCTG 1287
Db 301 GATGTTAATGACAGACACAAGCGAGAACCTCTGTACACAGACAGAGCGGCGCTGCCCTG 360
QY 1288 GCTAGCGAGACCCACGCGGGCGGAAGACTGGCGGTGTTCGCGCGAAGCCCCGACGGCGAC 1347
Db 361 GCTAGCGAGACCCACGCGGGCGGAGACGTGGCGGTGTTCGCGCGCGGCGCGACGGCGAC 420
QY 1348 CTGGTGCACGGCGGTGCAGGAGAGACTTTCGTGGCGCACATCATGGCCTTTGGGGGCTGC 1407
Db 421 CTGGTGCACGGCGGTGCAGGAGAGACTTTCGTGGCGCACATCATGGCCTTTGGGGGCTGC 480
QY 1408 GTGAGCCCTACACCGACTGCAATCTGCCAGCCCCCGCACCGGCCACAGCATCCCCGAC 1467
Db 481 GTGAGCCCTACACCGACTGCAATCTGCCAGCCCCCGCACCGGCCACAGCATCCCCGAC 540

RESULT 14
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DEFINITION AL540746 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE004YB05
5-PRIME, mRNA sequence.
ACCESSION AL540746
VERSION AL540746 GI:45716343
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 905)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:30544248.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE004CA03QP1&c=1699.f.
location/Qualifiers
1.905
/organism="Homo sapiens"
/mol_type="mRNA"
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

FEATURES
source
1.905
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE004YB05"
/issue_type="PLACENTA"
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 33.4%; Score 492.8; DB 1; Length 905;
Best Local Similarity 82.1%; Pred. No. 2.5e-109;

Matches 614; Conservative 1; Mismatches 128; Indels 5; Gaps 4;
QY 6 CCTCATCCAGCTGAGGAGGAAAACCCCGCTTCTGGAACCGCCAGGACCCAGGCCCT 65
Db 142 CATCATCCAGTTGAGGAGGAGAAACCCGACTTCTGGAACCGCGAGGACCCAGGCCCT 201
QY 66 TGATGTAGCCCAAGAGTTGAGAGCCCGATCCAGACAGCTGCGCAAGATGTATCTTCTT 125
Db 202 GGGTCCGCCAAGAGCTGCAGCTTCACACAGACAGCCGCCAAGAACCTCATCTTCTTCT 261
QY 126 GGGGATGGGATGGGGTGCTCTACGGTGACAGCCACTCGATCCTAAAGGGGAGATGAA 185
Db 262 GGGGATGGGATGGGGTGCTCTACGGTGACAGCTGCGAGATCCTAAAGGGGAGATGAA 321
QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGGACCACTTCCCATACGTGGCTGTG 245
Db 322 GGACAAACTGGGGCTGAGTTAACCCCTGGCCATGGACCGCTTCCCATATGTGGCTGTG 381
QY 246 CAAGACATACAACTGGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTTACT 305
Db 382 CAAGACATACAACTGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCAGCGCTTACT 441
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QY 366 GTGCAACACGACACGTGGGAATGAGTCAAGTCAAGTCAACCGGGCAAGAAAGCAGG 425
Db 502 GTGCAACACGACACCGGGCAACGAGTCACTCCGTGATGAATCGGGCAAGAAAGCAGG 561
QY 426 GAAGGCCGTGGAGTGTGTACCAACACAGGCTGACAGATGCTCCCAAGCGGGGCTTA 485
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Db 682 GAGGGGTGCCAGACATCGCTTACCGAGCTCATCTCCAAATGACATTGACGTGATCT 741
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QY 666 TGCAGTGTGAATGATCGGAAAGACAAAGCAAACTGTGACAGAAATGGAGGCCCAA 725
Db 800 CTMAAGCCAAGTGG-GACAGGCTGAGCGGAAGAACTGTGTGACAGAAATGGCTGGCA- 857
QY 726 GCACCAAGGAGGCCCAATGTGTGAAC 753
Db 858 -CGCCAGGGTGCCCGGTACGTGTGAAC 884

RESULT 15
LOCUS AL551653 929 bp mRNA linear EST 30-MAR-2004
DEFINITION AL551653 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI063YM05 5-PRIME, mRNA sequence.
ACCESSION AL551653
VERSION AL551653 GI:45856454
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 929)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31273469.
Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CSODI063AG03QP1&c=1699.f.
Location/Qualifiers

FEATURES
source

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ORIGIN

Query Match 32.3%; Score 476.6; DB 1; Length 929;
Best Local Similarity 81.9%; Pred. No. 2.2e-105;
Matches 584; Conservative 1; Mismatches 125; Indels 3; Gaps 3;

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OY 126 GGGGATGGATGGGGGTGCTTACGGTGACAG-CCACTCGATCCTAAAGGGCAGATGA 184
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OY 425 GGAAGGCCGTGGAGTGTGACCAACCAAGGTCAGCATGCTCCCAAGCGGGGCT 484
DB 560 GGAAGTCAAGTGGAGTGTGTAACCAACAGAGTCACTCTGATGAATCGGGCCAGAAAGCAG 619
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DB 800 GACTACAGCYAAGSTGGACCAAGGCTGAC-GGAARATCTGTGTCAGGAATG 851
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: October 19, 2004, 07:43:22 ; Search time 6521 Seconds
(without alignments)
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Sequence: 1 gaattcttgattccagctga.....gtattccagattaaggtacc 1476

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1476 | 100.0 | 1476 | 6 | AX356649 |
| 3 | 1476 | 100.0 | 1476 | 6 | AX840886 |
| 4 | 1474.4 | 99.9 | 1476 | 6 | AX840891 |
| 5 | 1472.8 | 99.8 | 1476 | 6 | AX840892 |
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| 10 | 834.8 | 56.6 | 1464 | 6 | AX840884 |
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| 24 | 613.8 | 41.6 | 1813 | 9 | HUMALP11 | M31008 Human intes |
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| 27 | 611.2 | 41.4 | 1587 | 9 | HUMALPHB | M15694 Human adult |
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| LOCUS | BD175594 | | | | |
| DEFINITION | Expression of alkaline phosphatase in yeast. | | | | |
| ACCESSION | BD175594 | | | | |
| VERSION | BD175594.1 | GI:29121292 | | | |
| KEYWORDS | JP 2002253269-A/4. | | | | |
| SOURCE | JP 2002253269-A/4. | | | | |
| ORGANISM | synthetic construct | | | | |
| REFERENCE | artificial sequences. | | | | |
| AUTHORS | 1 (bases 1 to 1476) | | | | |
| TITLE | Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W., Glaser,S., | | | | |
| JOURNAL | Eckstein,H., Kirschbaum,T. and Riebel,B.B.N. | | | | |
| COMMENT | Expression of alkaline phosphatase in yeast | | | | |
| | F HOFFMANN LA ROCHE AG | | | | |
| | OS Artificial Sequence | | | | |
| | PN JP 2002253269-A/4 | | | | |
| | PD 10-SEP-2002 | | | | |
| | PF 23-JUL-2001 JP 2001222153 | | | | |
| | PR 25-JUL-2000 DE 10036491.8 | | | | |
| | PI RAINER MUELLER,JOHANN PETER THALHOFER,FRANK GEIPEL,WERNER PI | | | | |
| | HOELKE, | | | | |
| | PI STEPHAN GLASER,HELMUT ECKSTEIN,THOMAS KIRSCHBAUM, PI | | | | |
| | BETTINA BOMMARIUS NEE RIEBEL | | | | |
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| | PC C12R1:78), | | | | |
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| Best Local Similarity | 100.0%; | Pred. No. 1.3e-266; | | | |
| Matches 1476; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; | |

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RESULT 2
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LOCUS AX356649
DEFINITION Sequence 5 from Patent EP1176205.
ACCESSION AX356649
VERSION AX356649.1 GI:18673989
KEYWORDS
SOURCE
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ORIGIN
Query Match 100.0%; Score 1476; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTGATTCACGCTGAAGAGAAATCCAGCTTTTGGATAGACAAGCTGCTCAA 60
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RESULT 3
AX840886 1476 bp DNA linear PAT 16-DEC-2003
LOCUS AX840886 Sequence 3 from Patent EP1348760.
DEFINITION AX840886
ACCESSION AX840886
VERSION AX840886.1 GI:39979033
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W., Hoelke,W. and Kirschbaum,T.
TITLE Production of inactive mutants or mutants with a low activity of an
JOURNAL alkaline phosphatase and their expression in yeast
Patent: EP 1348760-A 3 01-OCT-2003;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
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ORIGIN

Query Match 100.0%; Score 1476; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 1.3e-266;
Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTCCTGATTCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
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| Qy | 661 | GATGATGCTTCTGTTAATGTTAGAAAGAT | TAAGCAAAATTGGTTCAAGAATGGCAA | 720 |
| Db | 661 | GATGATGCTTCTGTTAATGTTAGAAAGAT | TAAGCAAAATTGGTTCAAGAATGGCAA | 720 |
| Qy | 721 | GCTAAGCATCAAGGTGCTCAATATGTTGG | AATAGAACTGCTTTGTTGCAAGCTGCTGAT | 780 |
| Db | 721 | GCTAAGCATCAAGGTGCTCAATATGTTGG | AATAGAACTGCTTTGTTGCAAGCTGCTGAT | 780 |
| Qy | 781 | GATTCATGTTTACTCATTGATGGGTTTGT | TGAACCAAGCTGATATGAATATATGTT | 840 |
| Db | 781 | GATTCATGTTTACTCATTGATGGGTTTGT | TGAACCAAGCTGATATGAATATATGTT | 840 |
| Qy | 841 | CAACAAGATCATACTAAGATCCAACTTT | GGCTGAATGACTGAAGCTGCTTTGCCAGTT | 900 |
| Db | 841 | CAACAAGATCATACTAAGATCCAACTTT | GGCTGAATGACTGAAGCTGCTTTGCCAGTT | 900 |
| Qy | 901 | TTGTCTAGAAATCCAAAGAGTTTCTACT | GTGTTGTTGTGAAGGTGTAGAAATGATCATGCT | 960 |
| Db | 901 | TTGTCTAGAAATCCAAAGAGTTTCTACT | GTGTTGTTGTGAAGGTGTAGAAATGATCATGCT | 960 |
| Qy | 961 | CATCATGATGGTAAAGCTTATATGGCTTT | GACTGAAGCTATATGTTGATAATGCTATTT | 1020 |
| Db | 961 | CATCATGATGGTAAAGCTTATATGGCTTT | GACTGAAGCTATATGTTGATAATGCTATTT | 1020 |
| Qy | 1021 | GCTAAGCTAATGAATGACTTCTGAATGG | ATTAATTGTTTACTGCTGATCAT | 1080 |
| Db | 1021 | GCTAAGCTAATGAATGACTTCTGAATGG | ATTAATTGTTTACTGCTGATCAT | 1080 |
| Qy | 1081 | AGTCATGTTTTTCTTTGGTGGTTACACT | TTTGAGAGGTAATTTTGGTTGGCT | 1140 |
| Db | 1081 | AGTCATGTTTTTCTTTGGTGGTTACACT | TTTGAGAGGTAATTTTGGTTGGCT | 1140 |
| Qy | 1141 | CCAGGTAAGGCTTTGATAGTAAGTCTT | CACTTCTATTTGTATGTAATGTCAGGT | 1200 |
| Db | 1141 | CCAGGTAAGGCTTTGATAGTAAGTCTT | CACTTCTATTTGTATGTAATGTCAGGT | 1200 |
| Qy | 1201 | TATGCTTTGGGTGGTGTCTTACACCA | GATGTTAATGTTAGTAAGTGAAGAACCATCT | 1260 |
| Db | 1201 | TATGCTTTGGGTGGTGTCTTACACCA | GATGTTAATGTTAGTAAGTGAAGAACCATCT | 1260 |
| Qy | 1261 | TACAGACAACAAGCTGCTGTTCCATT | GGCTAGTGAACCTCATGCTGGAAGATGTTGCT | 1320 |
| Db | 1261 | TACAGACAACAAGCTGCTGTTCCATT | GGCTAGTGAACCTCATGCTGGAAGATGTTGCT | 1320 |
| Qy | 1321 | GTTTTGCTAGAGGTCACCAAGCTCAT | TTGGTTCATGTTCAAGAAAGAACTTTTGT | 1380 |
| Db | 1321 | GTTTTGCTAGAGGTCACCAAGCTCAT | TTGGTTCATGTTCAAGAAAGAACTTTTGT | 1380 |
| Qy | 1381 | GCTCATATTAATGCTTTTGTGTTGTT | GAACCATACACTGATGTAATTTGCCAGCT | 1440 |
| Db | 1381 | GCTCATATTAATGCTTTTGTGTTGTT | GAACCATACACTGATGTAATTTGCCAGCT | 1440 |
| Qy | 1441 | CCAGCTACTGCTACTAGTATTCAGAT | TTAAGGTACC 1476 | |
| Db | 1441 | CCAGCTACTGCTACTAGTATTCAGAT | TTAAGGTACC 1476 | |

RESULT 4
LOCUS AX840891 1476 bp DNA linear PAT 16-DEC-2003
DEFINITION Sequence 8 from Patent EP1348760.
ACCESSION AX840891

| | | |
|----------------------------|--|--|
| VERSION | AX840891.1 | GI:39979034 |
| KEYWORDS | . | |
| SOURCE | synthetic construct | |
| ORGANISM | artificial sequences. | |
| REFERENCE | 1 | |
| AUTHORS | Mueller,R., Thalhoffer,J.P., Geipel,F., Hoelke,W. and Kirschbaum,T. | |
| TITLE | Production of inactive mutants or mutants with a low activity of an alkaline phosphatase and their expression in yeast | |
| JOURNAL | Patent: EP 1348760-A 8 01-OCT-2003; | |
| FEATURES | Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH) | |
| source | 1. 1476 | |
| | /organism="synthetic construct" | |
| | /mol_type="unassigned DNA" | |
| | /db_xref="taxon:32630" | |
| | /note="Nucleic acid" | |
| ORIGIN | | |
| Query Match | 99.9%; | Score 1474.4; DB 6; Length 1476; |
| Best Local Similarity | 99.9%; | Pred. No. 2.6e-266; |
| Matches 1475; Conservative | 0; | Mismatches 1; Indels 0; Gaps 0; |
| Qy | 1 | GAATTCCTGATTCCAGCTGTAAGAAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60 |
| Db | 1 | GAATTCCTGATTCCAGCTGTAAGAAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60 |
| Qy | 61 | GCTTTGGATGTTGCTAAGAGTGTCAACCAATTCAAACTGCTGCTAAGAAATGTAATTTTG 120 |
| Db | 61 | GCTTTGGATGTTGCTAAGAGTGTCAACCAATTCAAACTGCTGCTAAGAAATGTAATTTTG 120 |
| Qy | 121 | TTTTGGGTGATGTAAGGTGTTCCAACTGTACTGCTACTAGAAATTTTGAAGGCTCAA 180 |
| Db | 121 | TTTTGGGTGATGTAAGGTGTTCCAACTGTACTGCTACTAGAAATTTTGAAGGCTCAA 180 |
| Qy | 181 | ATGAATGTAAGTTGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCT 240 |
| Db | 181 | ATGAATGTAAGTTGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCT 240 |
| Qy | 241 | TTGTCTAAGACTTACAAATGTTGATAGACAAGTTCAGATTTGCTGTAAGTCTGCT 300 |
| Db | 241 | TTGTCTAAGACTTACAAATGTTGATAGACAAGTTCAGATTTGCTGTAAGTCTGCT 300 |
| Qy | 301 | TACTTGTGTGTTAAGGTAATTACAGAACTAATTTGTTCTGCTGCTGCTAGATAC 360 |
| Db | 301 | TACTTGTGTGTTAAGGTAATTACAGAACTAATTTGTTCTGCTGCTGCTAGATAC 360 |
| Qy | 361 | AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGAGTAAGAAG 420 |
| Db | 361 | AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGAGTAAGAAG 420 |
| Qy | 421 | GCTGTAAGGCTGTTGCTGTTTACTACTACTAGAGTTCAACATGCTTCCAGCTGCT 480 |
| Db | 421 | GCTGTAAGGCTGTTGCTGTTTACTACTACTAGAGTTCAACATGCTTCCAGCTGCT 480 |
| Qy | 481 | GCTTACGCTCATACCTGTTAATAGAAATTTGCTACTCTGATGCTGATTTGCCAGCTGATGCT 540 |
| Db | 481 | GCTTACGCTCATACCTGTTAATAGAAATTTGCTACTCTGATGCTGATTTGCCAGCTGATGCT 540 |
| Qy | 541 | CAAAAGAATGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGGAATATTGATGTT 600 |
| Db | 541 | CAAAAGAATGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGGAATATTGATGTT 600 |
| Qy | 601 | ATTTTGGGTGGTGTAGAAATGTACATGTTTCCAGAAAGGTACTCCAGATCCAGAAATACCA 660 |
| Db | 601 | ATTTTGGGTGGTGTAGAAATGTACATGTTTCCAGAAAGGTACTCCAGATCCAGAAATACCA 660 |
| Qy | 661 | GATGATGCTTCTGTTAATGTTAGAAAGGTAAGCAAAATTTGGTTCAAGAAATGGCAA 720 |
| Db | 661 | GATGATGCTTCTGTTAATGTTAGAAAGGTAAGCAAAATTTGGTTCAAGAAATGGCAA 720 |
| Qy | 721 | GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780 |
| Db | 721 | GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780 |

Db 721 GCTAAGCATCAAGGTGCTCAATATGTTTGGAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780

QY 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGGAACCAAGCTGATATGAAGTAAATGTT 840

Db 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGGAACCAAGCTGATATGAAGTAAATGTT 840

QY 841 CAACAAGATCATACTAAGAGTCCAACTTTGGCTGAATAAGACTGAAGCTGCTTTGCCAAGTT 900

Db 841 CAACAAGATCATACTAAGAGTCCAACTTTGGCTGAATAAGACTGAAGCTGCTTTGCCAAGTT 900

QY 901 TTGCTAGAAATCCAAGAGGTTTCTACTGTTGTGGAAGGTGGTAGAATTGATCATGCT 960

Db 901 TTGCTAGAAATCCAAGAGGTTTCTACTGTTGTGGAAGGTGGTAGAATTGATCATGCT 960

QY 961 CATCATGATGGTAAGGCTTATATGCTTTGACTGAAGCTATTATGTTGATAATGCTATT 1020

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QY 1021 GCTAAGGCTAATGAATTGACTTCTGAATTGGAATCTTGATTTTGGTTACTGCTGATCAT 1080

Db 1021 GCTAAGGCTAATGAATTGACTTCTGAATTGGAATCTTGATTTTGGTTACTGCTGATCAT 1080

QY 1081 AGTCATGTTTTTCTTTTGGTGTTACACTTTGAGAGTACTTCTATTTTTGGTTGGCT 1140

Db 1081 AGTCATGTTTTTCTTTTGGTGTTACACTTTGAGAGTACTTCTATTTTTGGTTGGCT 1140

QY 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGGTAAATGCTCCAGGT 1200

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Db 1201 TATGCTTTGGTGTTGGTCTTAGACACCAGATGTTAATGTTAGTACTAGTAGAAGAACCATCT 1260

QY 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACACTCATGCTGCTGAAGATGTTGCT 1320

Db 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACACTCATGCTGCTGAAGATGTTGCT 1320

QY 1321 GTTTTGTAGAGTCCACAAGCTCATTTGGTTCATGCTGTTCAAGAAGAACTTTTGT 1380

Db 1321 GTTTTGTAGAGTCCACAAGCTCATTTGGTTCATGCTGTTCAAGAAGAACTTTTGT 1380

QY 1381 GCTCATATTATGGCTTTTGTGCTGTTGTGTTGAACCATACACTGATTTGTAATTTGCCAGCT 1440

Db 1381 GCTCATATTATGGCTTTTGTGCTGTTGTGTTGAACCATACACTGATTTGTAATTTGCCAGCT 1440

QY 1441 CCAGCTACTGCTACTAGTATTTCCAGATTAAGGTACC 1476

Db 1441 CCAGCTACTGCTACTAGTATTTCCAGATTAAGGTACC 1476

RESULT 5
AX840892 1476 bp DNA linear PAT 16-DEC-2003

LOCUS AX840892 Sequence 9 from Patent EP1348760.

DEFINITION AX840892

ACCESSION AX840892

VERSION AX840892.1 GI:39979035

KEYWORDS

SOURCE

ORGANISM

synthetic construct

synthetic construct

artificial sequences.

REFERENCE

1 Mueller,R., Thalhofe,J.P., Geipel,F., Hoelke,W. and Kirschbaum,T.
Production of inactive mutants or mutants with a low activity of an
alkaline phosphatase and their expression in yeast
Patent: EP 1348760-A 9 01-OCT-2003;
Roche Diagnostics GmbH (DE) ; F.HOFEMANN-LA ROCHE AG (CH)

JOURNAL

Location/Qualifiers

1. 1476

FEATURES

source

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Nucleic acid"

ORIGIN

Query Match 99.8%; Score 1472.8; DB 6; Length 1476;
Best Local Similarity 99.9%; Pred. No. 5.3e-266;
Matches 1474; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAATTCCTGATTCACAGCTGAAGAGAAATCCAGCTTTTGGAAATAGCAAGCTGCTCAA 60

Db 1 GAATTCCTGATTCACAGCTGAAGAGAAATCCAGCTTTTGGAAATAGCAAGCTGCTCAA 60

QY 61 GCTTTGGATGTTGCTTAAGAAAGTTGCACCAATTCAAACTGCTGCTAAGAAATGTTATT 120

Db 61 GCTTTGGATGTTGCTTAAGAAAGTTGCACCAATTCAAACTGCTGCTAAGAAATGTTATT 120

QY 121 TTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180

Db 121 TTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180

QY 181 ATGAATGGTAAGTTGGGTCCAGAACTCCATGGCTATGGATCAATTTCCATACGTTGCT 240

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QY 421 GCTGTAAGGCTGTTGTTGTTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGT 480

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QY 481 GCTTACGCTCACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540

Db 481 GCTTACGCTCACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540

QY 541 CAAAAGAAATGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGATATTGATGTT 600

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Db 661 GATGATGCTTCTGTTAATGTTGTTAGAAAGATAAGCAAAATTTGGTTCAAGAATGGCAA 720

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Db 721 GCTAAGCATCAAGGTGCTCAATATGTTTGAATAAGAACTGCTTTGTGCAAGCTGCTGAT 780

QY 781 GATTCTAGTGTACTCATTTGATGGGTTGTTGAACCAAGCTGATATGAATGTAATGTT 840

Db 781 GATTCTAGTGTACTCATTTGATGGGTTGTTGAACCAAGCTGATATGAATGTAATGTT 840

QY 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCCAAGTT 900

Db 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCCAAGTT 900

QY 901 TTGCTAGAAATCCAAGAGGTTTCTACTGTTGTGGAAGGTGGTAGAATTGATCATGCT 960

Db 901 TTGCTAGAAATCCAAGAGGTTTCTACTGTTGTGGAAGGTGGTAGAATTGATCATGCT 960

QY 961 CATCATGATGGTAAGGCTTATATGCTTTGACTGAAGCTATTATGTTGATAATGCTATT 1020

Db 961 CATCATGATGGTAAGGCTTATATGCTTTGACTGAAGCTATTATGTTGATAATGCTATT 1020

QY 1021 GCTAAGGCTAATGATTGACTTCTGAATTGGATACTTTGATTGGTTACTGCTGATCAT 1080
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Db 1081 AGTCATGTTTTTTCTTTTGGTGCTTACACTTTTGAGAGGTACTTCTATTTTTGGTTGGCT 1140

QY 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGGTAATGCTCCAGGT 1200
|
Db 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGGTAATGCTCCAGGT 1200

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|
Db 1201 TATGCTTTGGGTGGTGCTTCTAGACCAAGATGTTAATGTAAGTACTAGTGAAGAACCATCT 1260

QY 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGCTGAAGATGTTGCT 1320
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Db 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGCTGAAGATGTTGCT 1320

QY 1321 GTTTTGCTAGAGGTCACACAAGCTCATTTGGTTCATGCTGCTCAAGAGAACAATTGTT 1380
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Db 1321 GTTTTGCTAGAGGTCACACAAGCTCATTTGGTTCATGCTGCTCAAGAGAACAATTGTT 1380

QY 1381 GCTCATATTATGGCTTTGCTGGTGTGTGAACCATACACTGATTTGTAATTTGCCAGCT 1440
|
Db 1381 GCTCATATTATGGCTTTGCTGGTGTGTGAACCATACACTGATTTGTAATTTGCCAGCT 1440

QY 1441 CCAGCTACTGCTACTAGTATTCCAGATTAAAGGTACC 1476
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Db 1441 CCAGCTACTGCTACTAGTATTCCAGATTAAAGGTACC 1476

RESULT 6
AX840893 1476 bp DNA linear PAT 16-DEC-2003
LOCUS AX840893 Sequence 10 from Patent EP1348760.
DEFINITION AX840893
ACCESSION AX840893
VERSION AX840893.1 GI:39979036
KEYWORDS
SOURCE .
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W. and Kirschbaum,T.
TITLE Production of inactive mutants or mutants with a low activity of an
alkaline phosphatase and their expression in yeast
JOURNAL Patent: EP 1348760-A 10 01-OCT-2003;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
FEATURES
source 1..1476
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/mol_type="unassigned DNA"
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/note="Nucleic acid"
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Query Match 99.7%; Score 1471.2; DB 6; Length 1476;
Best Local Similarity 99.8%; Pred. No. 1e-265;
Matches 1473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATCTTGATTCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
|
Db 1 GAATCTTGATTCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60

QY 61 GCTTTGGATGTTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGATGTTATTTG 120
|
Db 61 GCTTTGGATGTTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGATGTTATTTG 120

QY 121 TTTTGGGTGATGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGGTCAA 180
|
Db 121 TTTTGGGTGATGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGGTCAA 180

QY 181 ATGATGTAAGTTGGGTCCAGAAACTCCATTGGCTATGGAATCAATTTCCATACGTTGCT 240
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QY 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGAGCTAAGAG 420
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Db 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGAGCTAAGAG 420

QY 421 GCTGTAAGGCTGTTGGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
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QY 481 GCTTACGCTCATACTGTTAATAGAAATTGGTACTCTGATGCTGATTGGCCAGCTGATGCT 540
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QY 541 CAAAAGAAATGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGGAATATGATGTT 600
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QY 601 ATTTGGGTGGGTAGAAATGTACATGTTTCCAGAAAGTACTCCAGATCCAGATACCA 660
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Db 601 ATTTGGGTGGGTAGAAATGTACATGTTTCCAGAAAGTACTCCAGATCCAGATACCA 660

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|
Db 661 GATGATGCTTCTGTTAATGGTGTAGAAAGGATTAAGCAAAATTTGGTTCAAGATGGCAA 720

QY 721 GCTAAGCATCAAGGTGCTCAATATGTTTGGAAATAGAACTGCTTGTGCAAGCTGCTGAT 780
|
Db 721 GCTAAGCATCAAGGTGCTCAATATGTTTGGAAATAGAACTGCTTGTGCAAGCTGCTGAT 780

QY 781 GATTCTAGTGTACTCATTTGATGGGTGTTTGAACCAAGCTGATATGAAGTATATGTT 840
|
Db 781 GATTCTAGTGTACTCATTTGATGGGTGTTTGAACCAAGCTGATATGAAGTATATGTT 840

QY 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTT 900
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Db 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTT 900

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Db 961 CATCATGATGTAAGGCTTATATGGCTTTGACTGAAGCTATATGTTGATATGCTATT 1020

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QY 1141 CCAGTAAGGCTTTGGAATAGTAAGTCTTACACTTCTATTGTTATGTTAATGTTCCAGGT 1200
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Db 1201 TATGCTTTGGGTGGTGTCTAGACCAAGATGTTAATGTAAGTACTAGTGAAGAACCATCT 1260

QY 1261 TACAGACAACAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTGTGAGATGTGCT 1320
DB 1261 TACAGACAACAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTGTGAGATGTGCT 1320
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DB 1321 GTTTTGTAGAGTCCACAAGCTCATTTGGTTCATGTGTTCAAGAAGAACTTTGTT 1380
QY 1381 GCTCATATTATGGCTTTTGTGCTGTGTGTTGAACCATACACTGATTGTAAATTGCCAGCT 1440
DB 1381 GCTCATATTATGGCTTTTGTGCTGTGTGTTGAACCATACACTGATTGTAAATTGCCAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTATTCCAGATTAAAGGTACC 1476
DB 1441 CCAGCTACTGCTACTAGTATTCCAGATTAAAGGTACC 1476

RESULT 7
AX840894 1476 bp DNA linear PAT 16-DEC-2003
LOCUS AX840894
DEFINITION Sequence 11 from Patent EP1348760.
ACCESSION AX840894
VERSION AX840894.1 GI:39979037
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mueller, R., Thalhofer, J.P., Geipel, F., Hoelke, W. and Kirschbaum, T.
TITLE Production of inactive mutants or mutants with a low activity of an alkaline phosphatase and their expression in yeast
JOURNAL Patent: EP 1348760-A 11 01-OCT-2003;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
FEATURES
source 1. 1476
/organism="synthetic construct"
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/note="Nucleic acid"

ORIGIN
Query Match 99.6%; Score 1469.6; DB 6; Length 1476;
Best Local Similarity 99.7%; Pred. No. 2,1e-265;
Matches 1472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAATCTTGATTCAGCTGAGAAGAAATCCAGCTTTTGAATAGACAAGCTGCTCAA 60
DB 1 GAATCTTGATTCAGCTGAGAAGAAATCCAGCTTTTGAATAGACAAGCTGCTCAA 60
QY 61 GCTTGGATGTGCTAAGAAGTGCACCAATTCAAACCTGCTGAAGAATGTTATTTTG 120
DB 61 GCTTGGATGTGCTAAGAAGTGCACCAATTCAAACCTGCTGAAGAATGTTATTTTG 120
QY 121 TTTTGGGTGATGGTATGGGTGTTCCAACCTGTTACTGCTACTAGAAATTTGAAGGGTCAA 180
DB 121 TTTTGGGTGATGGTATGGGTGTTCCAACCTGTTACTGCTACTAGAAATTTGAAGGGTCAA 180
QY 181 ATGAATGTAAGTGGGTCCAGAACTCCATGGCTATGATCAATTTCCATACGTTGCT 240
DB 181 ATGAATGTAAGTGGGTCCAGAACTCCATGGCTATGATCAATTTCCATACGTTGCT 240
QY 241 TTGCTAAGACTTACAATGTGATAGACAAGTTCAGATTCGCTGCTACTGCTACTGCT 300
DB 241 TTGCTAAGACTTACAATGTGATAGACAAGTTCAGATTCGCTGCTACTGCTACTGCT 300
QY 301 TACTGTGTGTTAAGGGTAATTACAGAACTATGTTGTTCTGCTGCTAGATAC 360
DB 301 TACTGTGTGTTAAGGGTAATTACAGAACTATGTTGTTCTGCTGCTAGATAC 360
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DB 361 AATCAATGTAATACTAGAGGTATGAAGTTACTTCTGTATTATAGAGCTAAGAAG 420

QY 421 GCTGTAAGGCTGTGCTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
DB 421 GCTGTAAGGCTGTGCTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
QY 481 GCTTACGCTCACTACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540
DB 481 GCTTACGCTCACTACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540
QY 541 CAAAGAATGGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGATATGATGTT 600
DB 541 CAAAGAATGGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGATATGATGTT 600
QY 601 ATTTGGGTGGTGTAGAAATGATGATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCCA 660
DB 601 ATTTGGGTGGTGTAGAAATGATGATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCCA 660
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QY 721 GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTTCAAGCTGCTGAT 780
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DB 1021 GCTAAGGCTAATGAATTGACTTCTGAATGATATCTTTGATTTGGTACTGCTGATCAT 1080
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DEFINITION
ACCESSION   BD175591
VERSION     BD175591.1  GI:29121289
KEYWORDS    JP 2002253269-A/1.
SOURCE      Bos sp.
ORGANISM    Bos sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1 (bases 1 to 1476)
AUTHORS    Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W., Glaser,S.,
            Eckstein,H., Kirschbaum,T. and Riebel,B.B.N.
TITLE       Expression of alkaline phosphatase in yeast
JOURNAL     Patent: JP 2002253269-A 1 10-SEP-2002;
            F HOFMANN LA ROCHE AG
COMMENT     OS   Bos sp. (bovine)
            PN   JP 2002253269-A/1
            PD   10-SEP-2002
            PF   23-JUL-2001  JP 2001222153
            PR   25-JUL-2000  DE 10036491.8
            PI   RAINER MUELLER, JOHANN PETER THALHOFER, FRANK GEIPEL, WERNER PI
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            PI   STEPHAN GLASER, HELMUT ECKSTEIN, THOMAS KIRSCHBAUM, PI
            BETTINA BOMMARINUS NEE RIEBEL
            PC   C12N15/09, C12N1/19, C12N9/16// (C12N1/19, C12R1:645), (C12N1/19,
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Best Local Similarity 73.3%; Pred. No. 1.7e-148;
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DB      121 TTCTGGGGGATGGATGGGGGTGCTTACGCTGACAGCCACTCGGATCCTAAAGGGGCAG 180
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DB      301 TACTGTGTGGGTCAGAGGGCACTAACAAGAACCATCGGTGTAGTGCAAGCCGCCGCTAC 360
QY      361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTAATTAAGAGCTAAGAG 420
DB      361 AATCAGTGCAACACGACAGACGTTGGGAATGAGTCAAGTCTGTGATCAACCGGCCAAGAAA 420
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DB      421 GCAGGGAAGGCCGTGGAGTGTGACCAACACCAAGGTGACAGATGCTCCCGAGCGCG 480
QY      481 GCTTACGCTCATACTGTTAATAGAAATGGTACTGTGATGCTGATTTGCCAGCTGATGCT 540
DB      481 GCCTACGCGCACACGGTGAACCGAAACTGTACTCAAGCGCCGACCTGCTGTGATGCA 540
QY      541 CAAAAGATGTTGTCAAGATATGCTGCTCAATTGGTTTACAATATGATATGATATGTT 600
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DB      661 GATGATGCCAGTGTGAATGAGTCCGGAAGGACAAAGCAAACTGTTGACGAATGGCAG 720
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DB      721 GCCAAGCACCAAGGAGCCCATGTATGTGTGAACCGCACTGCGCTCTTACAGCGCGCAT 780
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DB      841 CAGCAAGACCAACCAAGGACCCGACCTGCGGAGATGACGAGGCGGCTGCAAGTG 900
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DB      901 CTGAGCAAGAACCCCGGGGCTTCTACCTCTTGTTGAGGGAGGCGGCATTGACCAAGCT 960
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DB      1381 GCGCAATCATGGCTTTGCGGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCCAGCC 1440
QY      1441 CCAGCTACTGCTACTAGTATTTCCAGATTAAAGTACC 1476
DB      1441 CCCGCCACCGCCACCAAGCATCCCGCACTAAGGTACC 1476
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RESULT 9
AX356645      1476 bp      DNA      linear      PAT 13-FEB-2002
LOCUS      AX356645
DEFINITION      Sequence 1 from Patent EP1176205.
ACCESSION      AX356645
VERSION      AX356645.1  GI:18673986
KEYWORDS
SOURCE      Bos taurus (cow)
ORGANISM      Bos taurus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
              Bovinae; Bos.
REFERENCE      1
AUTHORS      Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W., Glaser,S.,
              Eckstein,H., Kirschbaum,T. and Bommaritus,B.
TITLE      Expression of alkaline phosphatase in yeast
JOURNAL      Patent: EP 1176205-A 1 30-JAN-2002;
              Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
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Query Match      57.3%; Score 845.6; DB 6; Length 1476;
Best Local Similarity 73.3%; Pred. NO. 1.7e-148;
Matches 1082; Conservative 0; Mismatches 394; Indels 0; Gaps 0;
QY      1 GAATCTTGATTCAGCTGAAGAGAAAATCCAGCTTTTGAATAGACAGCTGCTCAA 60
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DB      1 GAATCTTCATCCAGCTGAGAGAAAACCCGCTTCTGAACCGCCAGGCCAG 60
QY      61 GCTTGGATGTGCTAAGAGAGTTGCAACCAATCAAACTGCTGTAAGATGTTATTTG 120
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DB      61 GCCCTGATGTAGCCAGAGAGTTGCAAGCCGATCCAGACAGCTGCCAAGATGTCATCTC 120
QY      121 TTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAATTTGAAGGGTCAA 180
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QY      181 ATGAATGTAGTTGGGTCCAGAACTCCATTGGCTATGGATCAATTTCCATACGTTGCT 240
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QY      301 TACTGTGTGTGTTAAGGGTAATTACAGAACTATTGCTGTTCTGCTGCTGCTAGATAC 360
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DB      301 TACTGTGTGTGGGTCAAGGGCACTACAGAACCATCGGTGTAAAGTGACAGCCGCCCTAC 360
QY      361 AATCAATGTAATTACTACTAGAGGTAAATGAACTTCTGTTATTAAATAGAGCTAAGAG 420
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DB      361 AATCAATGCAACAGACAGCGTGGGAATGAGTCACTGTGTATCAACCGGGCCAAGAAA 420
QY      421 GCTGTAAAGGCTGTGTGTGTTTACTACTACTAGAGTTCAACATGCTTCCAGCTGCT 480
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QY      961 CATCATGATGCTAAGGCTTATATGCTTGAAGCTGAAGCTATTAATGTTGAATGCTAT 1020
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DEFINITION      Sequence 1 from Patent EP1348760.
ACCESSION      AX840884
VERSION      AX840884.1  GI:39979031
KEYWORDS
SOURCE      Bos taurus (cow)
ORGANISM      Bos taurus
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              Bovinae; Bos.
REFERENCE      1
AUTHORS      Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W. and Kirschbaum,T.
TITLE      Production of inactive mutants or mutants with a low activity of an
              alkaline phosphatase and their expression in yeast
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JOURNAL Patent: EP 1348760-A 1 01-OCT-2003;
Roche Diagnostics GmbH (DE); F.HOFFMANN-LA ROCHE AG (CH)
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ORIGIN

Query Match 56.6%; Score 834.8; DB 6; Length 1464;
Best Local Similarity 73.2%; Pred. No. 1.8e-146;
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QY 8 TGATTCACAGTGAAGAAATCCAGCTTTTGGAAATAGACAAGCTCTCAAGCTTTGG 67
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DB 122 GGGATGGGATGGGGGTGCTACGGTACAGCACTCGGATCTTAAGGGGAGATGAATG 181
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DB 182 GCAAACTGGGACCTGAGACACCCCTGGCCATGAGCAAGTTCCCATACGTGGCTGTCCA 241
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QY 1028 CTAAATGAATTGACTTCTGAATTTGATACTTTGATTTGTTACTGCTGATCATAGTCATG 1087
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QY 1088 TTTTCTTTTGTGTTGTTACCTTTGAGAGGTACTTATTTTGGTTGGCTCCAGGTA 1147
DB 1082 TCTTCTCTTTGTGTTGCTTACACACTGCGTGGGACTCCATTTTCGGTCTGGCCCCGCA 1141
QY 1148 AGCTTTGGATAGTACGTTTCACTTCACTTCTATTTGTTATGTTATGTTCCAGTTATGCTT 1207
DB 1142 AGGCTTGAACAGCAAGTCTTCACTTCACTTCTTATGTTGCAATGAGCCAGGCTATGCGC 1201
QY 1208 TGGGTGTTGTTCTAGACAGATGTTAATGTTAGTACTAGTGAAGAACCATTTTACAGAC 1267
DB 1202 TTGGCGGGGCTGAGGCGCATGTTAATGTCAGACAAGCGAAGAACCTCTATACCGGC 1261
QY 1268 AACAAAGCTGCTGTTCCATTGGCTAGTGAAGCTCAAGGTGTAAGATGTTGCTTTTG 1327
DB 1262 AGCAGCGCGCGTGCCTGGCTAGCAGAGACCCAGGGGCGAAGAGCTGGCGGTTCG 1321
QY 1328 CTAGAGTCCACAAGCTCATTTGGTTCATGTTTCAAGAAAGAACTTTTGTCTCATTA 1387
DB 1322 CGCGAGGCGCGCAGCGGACCTGTGACAGCGCGGTGAGAGACCTTGTGCGGACCA 1381
QY 1388 TTATGCTTTTGTGTTGTTGTTGAACCATACACTGATTTGTAATTTGCCAGCTTCAAGCTA 1447
DB 1382 TCATGCTTTTGTGCGGCTGCGTGAAGCCCTACACCGAATCTGCAATCTGCCAGCCCCGCCA 1441
QY 1448 CTGCTACTAGTATTCCAGATTA 1469
DB 1442 CCGCCACAGCATCCCGACTA 1463

RESULT 11
E59950
LOCUS 1798 bp DNA linear PAT 13-AUG-2002
DEFINITION Highly active alkaline phosphatase.
ACCESSION E59950
VERSION E59950.1 GI:13017720
KEYWORDS JP 1999332586-A/1.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 1798)
AUTHORS Werner,H., Reina,M., Herumuto,B. and Jose,L.M.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: JP 1999332586-A 1 07-DEC-1999;
COMMENT ROCHE DIAGNOSTICS GMBH
OS Bovidae

PN JP 1999332586-A/1
PD 07-DEC-1999
PF 06-MAY-1999 JP 1999126494
PR 05-MAY-1998 DE 19819962:7
PI WERNER HOERUKU,REINA MULLER,HERUMUTTO BURUTOSHA, PI JOSE LOUIS MILAN
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/16, PC C12N15/00,C12N5/00
CC
FH Key Location/Qualifiers
FT source 1..1798 /organism='Bovidae'.
FT Location/Qualifiers
1..1798
/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
ORIGIN
Query Match 56.5%; Score 833.8; DB 6; Length 1798;
Best Local Similarity 73.2%; Pred. No. 2.7e-146;
Matches 1069; Conservative 0; Mismatches 392; Indels 0; Gaps 0;
QY 6 CTGATTCAGCTGAAGAAGAAATCCAGCTTTTGAATAGACAAGCTCTCAAGCTTT 65
DB 107 CCTCATCCAGCTGAGAGAGAAACCCCGCTTCTGAAACCGCCAGCGCAGCCCT 166
QY 66 GGATGTGCTAAGAGTTCACAACCAATTCAACTGCTGCTAAGAAATGTTATTTGTTT 125
DB 167 TGATGTAGCCAAGAGTTGACGCCGATCCAGACAGCTGCCAAGATGTCACTCTTCTT 226
QY 126 GGGTATGGTATGGGTGTTCCAACTGTACTGCTACTAGATTTTGAAGGTCGAATGAA 185
DB 227 GGGGATGGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCTTAAAGGGCAGATGAA 286
QY 186 TGGTAAGTTGGGTCCAGAAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGTG 245
DB 287 TGGCAAACTGGGACTGAGACACCCCTGGCCATGSAACCAAGTTCCCATACGTGGCTGTG 346
QY 246 TAAAGCTTACATGTTGATAGACAAGTTCCAGATTCTGCTGCTACTGCTTACTT 305
DB 347 CAAGACATACCAAGTGAAGACAGAGTGCCAGACAGCGAGGCACTGCACTGCTTACT 406
QY 306 GTGTGCTGTTAAGGTAATTACAGAACTATTGTTCTGCTGCTGCTAGATTAATCA 365
DB 407 GTGTGGGTCAAGGGCACTACAGAACCATCGGTGAAGTGACCGCGCGCTACAATCA 466
QY 366 ATGTATACTACTAGAGTAATGAAGTACTTCTGTTATTATAGAGTAAGAAGCTGG 425
DB 467 GTGCAACACGACACGTGGGAATGAGTCACTGTGATCAACCGGGCCAGAAAGCAGG 526
QY 426 TAAAGCTGTTGGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA 485
DB 527 GAAAGCCGTGGAGTGTGACCAACCAGGGTGACGATGCTCTCCCAAGCGGGGCTTA 586
QY 486 CGCTCATACTGTTAATAGAAATTGGTACTCTGATGCTGATTGGCAGCTGATGCTCAAAA 545
DB 587 CGCGCACACGGTGAACGAAACTGTACTCAGACGCCGACCTGCTGCTGATGACAGAA 646
QY 546 GAATGTTGTCAGATATTTGCTGCTCAATTGTTTACAATATGATATGATTTGATTTT 605
DB 647 GAATGCTGCCAGACATCGCCGACAGCTGTTCTACAACATGATATGATGATGATCT 706
QY 606 GGGTGGTGTAGATGATCATGTTTCCAGAGGTAATCCAGATCCAGAAATCCAGATGA 665
DB 707 GGGTGAAGCGCAATGATCATGTTTCTGAGGGGAGCCCAAGACCTGAAATCCAGATGA 766
QY 666 TGCTTCTGTTAATGCTGTAGAAAGATAGCAAAATTTGTTCAAGATGCGCAAGCTAA 725
DB 767 TGCCAGTGTGAATGAGTCCCGAAGACAGACAACTGTGTGCAAGGATGCGAGCCAA 826
QY 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGATGATTC 785

DB 827 GCACCAGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCCTTACGGCGCCGATGACTC 886
QY 786 TAGTGTACTCATTTGATGGGTTTGTGTAACCAAGCTGATATGAAGTAAATGTTCAACA 845
DB 887 CAGTGTAAACACCTCATGGGCTTGTGAGCCGCGACACATGAAGTAAATGTTACAGA 946
QY 846 AGATCATACTAAGGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTTTGTG 905
DB 947 AGACCACACCAAGAACCCGACCTGGCGAGATGACGAGCGCGCCCTGCAAGTGTGAG 1006
QY 906 TAGAATCCAGAGGTTTACTTGTGTTGTTGAAGGTGTAGAAATGATCATGCTCATCA 965
DB 1007 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGAGCGCCGATTGACCAAGCTCACCA 1066
QY 966 TGATGTAGGCTTATATGCTTTGACTGGAAGCTATATGTTGATATGCTATTGCTAA 1025
DB 1067 TGACGGCAAGCTTATATGCACTGACTGAGCGGATCATGTTGACAAATGCCATGCCAA 1126
QY 1026 GGCTAATGAATTGACTTCTGAATTGATCTTGAATTTGGTTACTGCTGATCATAGTCA 1085
DB 1127 GGCTAAGAGCTCACTAGCAAGTGAACGCTGATCCTTGTCACTGACAGACCACTCCCA 1186
QY 1086 TGTCTTTCTTTTGGTGTGTACACTTTGAGAGTACTTCTATTTTGGTTGGCTCCAGG 1145
DB 1187 TGTCTTCTTTTGGTGTGTACACATGCTGGGAGCTCCATTTTGGTCTGCCCCCGG 1246
QY 1146 TAAGCTTTGATAGTAACTTACACTTCTATTTGTATGTAATGCTCCAGTTATGC 1205
DB 1247 CAAGGCTTGAACAGCAAGTCTTACCTTCCATCTCTATGCGCAATGCGCCAGCTATGC 1306
QY 1206 TTTGGGTGGTGTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCTTACAG 1265
DB 1307 GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGACAAAGCGAGAACCTCATACCG 1366
QY 1266 ACAACAAGCTGCTGTTCATTGGCTAGTGAACCTCATGTGTGTTGATGTTGCTGTTT 1325
DB 1367 GCAGCAGCGCGCTGCCCCCTGCTAGCGAGACCAAGGGGCGAAGCGTGGCGGTGT 1426
QY 1326 TGCTAGAGTCCACAAGCTCATTTGTTCAATGTTTCAAGAAAGAACTTTGTTGCTCA 1385
DB 1427 CGCGCAGGCGCCGCAAGCGCACTGTTGCAAGCGGCTGACAGAGAGACCTTGTGGCGCA 1486
QY 1386 TATTATGGCTTTGCTGTTGTTGTTGAACCATACATGATTTGTAATTTGCCAGCTCCAGC 1445
DB 1487 CATCATGGCTTTTGGGGCTGCTGAGAGCTTACACCGACTGCAATCTGCGACCCCGCG 1546
QY 1446 TACTGCTACTAGTATTTCCAGA 1466
DB 1547 CACCGCACACGATCCCGGA 1567

RESULT 12
AR214214 1798 bp DNA linear PAT 25-SEP-2002
LOCUS AR214214 Sequence 1 from patent US 6406899.
DEFINITION AR214214
ACCESSION AR214214
VERSION AR214214.1 GI:23311768
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1798)
TITLES Hoelke,W., Muller,R., Burtcher,H. and Millan,J.L.
JOURNAL Highly active alkaline phosphatase
Patent: US 6406899-A 1 18-JUN-2002;
FEATURES Location/Qualifiers
1..1798
source /organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 56.5%; Score 833.8; DB 6; Length 1798;
Best Local Similarity 73.2%; Pred. No. 2.7e-146;

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|---|------|--|------|--|
| Matches 1069; Conservative 0; Mismatches 392; Indels 0; Gaps 0; | | | | |
| QY | 6 | CTTGATTCACGCTGAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTTT | 65 | |
| Db | 107 | CCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTGGAAACGCCAGGCAAGCCAGGCCCT | 166 | |
| QY | 66 | GGATGTTGCTAAGAAAGTTGCAACCAATTCAACTGCTGCTAAGAATGTTATTTGTTTTT | 125 | |
| Db | 167 | TGATGTAGCCAAGAAGTTGACGCCGATCCAGACAGCTGCCAAGAATGATCCTCTTCTT | 226 | |
| QY | 126 | GGGTGATGTAAGGGTGTCCAACTGTTACTGCTACTAGAATTTTGAAGGTCAAATGAA | 185 | |
| Db | 227 | GGGGATGGGATGGGGGTGCTTACGGTGACAGCCACTCGATCCTAAAGGGCAGATGAA | 286 | |
| QY | 186 | TGTAAGTTGGGTCCAGAACTCCATTTGGCTATGGATCAATTTCCATACGTTGCTTGTG | 245 | |
| Db | 287 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGGACCAAGTCCCATACGTGGCTGTG | 346 | |
| QY | 246 | TAAGACTTACATGTTGATAGACAAGTTCAGATTCTGCTGGTACTGCTACTGCTTACTT | 305 | |
| Db | 347 | CAAGACATACAACTGGACACAGACAGGTGCCAGACAGCGACGGCACTGCCCTTACCT | 406 | |
| QY | 306 | GTTGTGTTTAAAGGGTAATTACAGAACTATTGCTGTTTCTGCTGCTGCTAGATACAA | 365 | |
| Db | 407 | GTTGGGGTCAAGGGCACTACAGAACTCGGTGAAGTGACAGCCGCCCTACAAATCA | 466 | |
| QY | 366 | ATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAAATAGACTAAGAGGCTGG | 425 | |
| Db | 467 | GTCAACACGACACGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAGAAAGCAGG | 526 | |
| QY | 426 | TAAAGCTGTGTTGTTGTTACTACTACTAGATTCAACATGCTTCTCCAGCTGTGCTTA | 485 | |
| Db | 527 | GAAAGCCGTGGGAGTGTGTGACCAACCAAGGGTGCAGCATGCCCTCCCAAGCCGGGCTTA | 586 | |
| QY | 486 | CGCTCACTGTTAATAGAAATTGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAA | 545 | |
| Db | 587 | CGCGCACACGGTGAACCGAACTGTTACTCAGACGCCGACCTGCTGATGCACAGAA | 646 | |
| QY | 546 | GAATGTTGTCAGATATTTGCTGCTCAATTGCTTTACAATATGATATTGATGTTATTTT | 605 | |
| Db | 647 | GAATGGCTGCCAGGACATCGCCGCACAGCTGGTCTACAACATGGAATATTGACGTGATCT | 706 | |
| QY | 606 | GGGTGGTGTAGATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCCAGATGA | 665 | |
| Db | 707 | GGGTGAGGCCGAATGTACATGTTTCTGAGGGGACCCAGACCTGAATATCCAGATGA | 766 | |
| QY | 666 | TGCTTCTGTTAATGTTGTTAGAAAGATAAGCAAAATTTGTTCAAGAATGCCAAGCTAA | 725 | |
| Db | 767 | TGCCAGTGTGAATGAGTCCGGAAGSACAAGCAACCTGTTGCAAGGAATGCAGGCCAA | 826 | |
| QY | 726 | GCATCAAGGTGCTCAATATGTTTGAATAAGAACTGCTTGTGCAAGCTGCTGATGATTC | 785 | |
| Db | 827 | GCACCAGGGAGCCCAAGTATGTGGAACCGCACTGCGCTCCTTCAGGGCGCGATGACTC | 886 | |
| QY | 786 | TAGTGTACTCATTTGATGGGTTGTTTGAACCAAGCTGATATGAAGTATATGTTCAACA | 845 | |
| Db | 887 | CAGTGTAAACACACTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTCAAGCA | 946 | |
| QY | 846 | AGATCATACTAAGGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTGCAGGTTTGTTC | 905 | |
| Db | 947 | AGACCACACCAAGGACCCGACCTGGCGGAGATGACGGAGGCGGCCCTGCAAGTGTGAG | 1006 | |
| QY | 906 | TAGAAATCCAAAGGTTTTTACTTGTGTTGTTGAAGGTGTAGAAATGATCATGTCATCA | 965 | |
| Db | 1007 | CAGGAACCCCGGGGCTTCTACTCTTCTGTGAGGAGGAGCGGCATTGACCAAGTCAACA | 1066 | |
| QY | 966 | TGATGTAAAGGCTTATATGGCTTTGAAGTATATGTTGATATGCTATGCTTAA | 1025 | |
| Db | 1067 | TGACGGCAAAAGCTTATATGGCACTGAGGCGATCATGTTTGAACAATGCATGCGCAA | 1126 | |
| QY | 1026 | GGCTAATGAATTGACTTCTGAATTGGATACCTTTGATTTGGTTACTGCTGATCATAGTCA | 1085 | |
| Db | 1127 | GGCTAAGAGCTCACTAGCGAACTGGAACAGCTGATCCTTGTCACTGCAGACCACTCCCA | 1186 | |

| | | | | |
|----|------|---|------|--|
| QY | 1086 | TGTTTTTCTTTTGGTGTTACACTTTGAGAGGTACTTCTATTTTGGTTGGCTCCAGG | 1145 | |
| Db | 1187 | TGTTCTTCTTTTGGTGCTACACACTGCGTGGACCTTCAATTTTCGGTCTGGCCCCCGG | 1246 | |
| QY | 1146 | TAAAGCTTTGATAGTAAGTCTTACACTTCTATTTTGTATGTTATGTTCCAGGTTATGC | 1205 | |
| Db | 1247 | CAAGGCTTTAGACAGCAAGTCTTACACTTCATCTCTATGGAATGCGCCAGGCTATGC | 1306 | |
| QY | 1206 | TTTGGGTGGTGTCTTACAGCAGATGTTAATGTTAGTACTAGTGAAGAACCATCTTACAG | 1265 | |
| Db | 1307 | GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGACAAAGCAGAAACCTCATACCG | 1366 | |
| QY | 1266 | ACAACAAGCTGCTGTTCCATTTGCTAGTGAACCTCAATGCTGTAAGATGTTGCTGTTT | 1325 | |
| Db | 1367 | GCAGCAGCGCGCGTGCCTCGGCTAGCGAGACCCACGGGGCGAAGACGTGGCGGTGTT | 1426 | |
| QY | 1326 | TGCTAGAGGTCCACAAGCTCATTTGTTTCATGTTGTTCAAGAAGAACTTTGTTGCTCA | 1385 | |
| Db | 1427 | CGCGCAGAGCCCGCAGCGCACTGTGCACGGCGTGCAGAGAGACCTTGTGCGCGCA | 1486 | |
| QY | 1386 | TATTATGCTTTTGTGCTGTTGTTGTTGAACCATACACTGATTTGTAATTTGCCAGCTCAGC | 1445 | |
| Db | 1487 | CATCATGCGCTTTGCGGGCTGCGTGGAGCCCTACACCGACTGCAATCTGCGACGCCCGCC | 1546 | |
| QY | 1446 | TACTGCTACTAGTATTCCAGA | 1466 | |
| Db | 1547 | CACGCCACCAAGCATCCCGA | 1567 | |

RESULT 13
AX012341
LOCUS AX012341 1798 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent EP0955369.
ACCESSION AX012341
VERSION AX012341.1 GI:9998390
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1
AUTHORS Burtcher,H.D., Mueller,R.D., Hoelke,W.D. and Millan,J.L.
TITLE High active alkaline phosphatase
JOURNAL Patent: EP 0955369-A 1 10-NOV-1999;
ROCHE DIAGNOSTICS GMBH (DE)
FEATURES
source Location/Qualifiers
1..1798
/organism="Bos taurus"
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/db_xref="taxon:9913"

Query Match 56.5%; Score 833.8; DB 6; Length 1798;
Best Local Similarity 73.2%; Pred. No. 2.7e-146;
Matches 1069; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

| | | | | |
|----|-----|--|-----|--|
| QY | 6 | CTTGATTCACGCTGAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTTT | 65 | |
| Db | 107 | CCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTGGAACCGCCAGGAGCCAGGCCCT | 166 | |
| QY | 66 | GGATGTTGCTAAGAAAGTTGCAACCAATTCAACTGCTGCTAAGAAATGTTATTTGTTTTT | 125 | |
| Db | 167 | TGATGTAGCCAAGAAGTTGCAAGCCGATCCAGACAGCTGCCAAGAATGATCCTCTTCTT | 226 | |
| QY | 126 | GGGTGATGTAAGGCTGTTCCAAGTGTACTGCTACTAGAAATTTGAAGGTCAAATGAA | 185 | |
| Db | 227 | GGGGATGGGATGGGGGTGCTTACGGTGCACGCCAATCGGATCCTTAAAGGGCAGATGAA | 286 | |
| QY | 186 | TGTTAAGTTGGGTCCAGAACTCCATGGCTATGATCAATTTCCATACGTTGCTTGTG | 245 | |
| Db | 287 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGGACCAAGTTCCATACGTGGCTGTG | 346 | |

| | | | | | |
|----|--|------|---|----------------------------|------|
| OY | | 246 | TAAAGCTTACAATGTTGAATAGACAAAGTTCAGATTCTGTGTA | CTGCTACTGCTTACTT | 305 |
| Db | | 347 | CAAGACATACAACGTGGACAGACAGTGCCAGACAGCGCAC | CTGCCACTGCCTAACCT | 406 |
| OY | | 306 | GTTGTGTTAAGGGTAAATTACAGAATAATTGGTGTCTGCTG | CTGTAGATACATCA | 365 |
| Db | | 407 | GTGTGGGGTCAAAGGCACTACAGAACCATCCGTGTAA | GTGACAGCCCGCCTACATCA | 466 |
| OY | | 366 | ATGTAATCTACTAGAGTAATGAAGTTACTTCTGTATTA | TATAGAGTAAGAGCTGG | 425 |
| Db | | 467 | GTGCAACACGACACGTGGGAATGAGGTCAAGTCTGTGAT | CAACCGGGCCAAGAAACGAGG | 526 |
| OY | | 426 | TAAAGCTGTTGGTGTGTTACTACTAGAGTTCAACATGCT | TCTCCAGCTGGTCTTA | 485 |
| Db | | 527 | GAAAGCCGTGGAGTGTGATCAACCACGAGGTGACAGAT | CTCCCCAGCCGGGCTTA | 586 |
| OY | | 486 | CGCTCATCTGTTAATAGAAATTGGTACTCTGATGCTGAT | TTGCCAGCTGATCAAAA | 545 |
| Db | | 587 | CGCGCACACGGTGAACCGAAACTGGTACTCAGACGCGCA | CTGCTGTATGCACAGAA | 646 |
| OY | | 546 | GAATGTTGTCAAGATATGTGCTCATTTGTTTACAATAT | GGATATGTATTTT | 605 |
| Db | | 647 | GAATGGCTGCCAGGACATCGCCGACACAGCTGTTTACA | AATGGATATTGACGTGATCTT | 706 |
| OY | | 606 | GGGTGTTGTAGATGTACATGTTTCCAGAAAGTATCCAG | ATCCAGATACCCAGATGA | 665 |
| Db | | 707 | GGGTGAGGCCGAATGTACATGTTTTCTGAGGGGACCC | CAGACCCTGAATACCCAGATGA | 766 |
| OY | | 666 | TGCTTCTGTTAATGTTGTAGAAAGGATAGCAAAATTT | GGTTCAAGAAATGGCAAGCTAA | 725 |
| Db | | 767 | TGCCAGTGTGAATGAGTCCGGAAGACAAAGCAGAAC | CTGGTGACGAATGGCAGGCCAA | 826 |
| OY | | 726 | GCATCAAGGTGCTCAATATGTTTGGAAATAGAACTG | CTTGTGCAAGCTGTGATGATTC | 785 |
| Db | | 827 | GCACCAGGGAGCCCAATGTGTGGAACCGCACTGCG | CTCTCAGGGCGCGCATGACTC | 886 |
| OY | | 786 | TAGTCTTACTCATTTGATGGGTTTGTGGAACCAAG | CTGATATGAAGTATATGTTCAACA | 845 |
| Db | | 887 | CAGTGTACACACCTCATGTGGGCTCTTTGAGCCGG | CAGACATGAAGTATATGTTCAACA | 946 |
| OY | | 846 | AGATCATACTAAGGATCCAATTGGCTGAATGATGAAG | CTGCTTGGCAAGTTTGTCTC | 905 |
| Db | | 947 | AGACCACACCAAGGACCCGACCTGGCGAGATGACG | AGGCGGCTGCAAGTGTGAG | 1006 |
| OY | | 906 | TAGAAATCCAAGAGGTTTAACTTGTGTTGTTGAAG | GTGTAGAAATTTGATCATGTGATCA | 965 |
| Db | | 1007 | CAGGAACCCCGGGGCTTACCTCTTGTGAGGAGG | CGGCATTGACCAAGGTACCA | 1066 |
| OY | | 966 | TGATGTAGAGCTTATATGSGCTTGAAGCTATATAT | GTGATATGCTATTTGCTAA | 1025 |
| Db | | 1067 | TGACGGCAAGCTTATATGSCACTGACTGAGCGCAT | GTGTAACAATGCCATGSCCAA | 1126 |
| OY | | 1026 | GGCTAATGAATTGACTTCTGAATTGGACTCTTGAAT | TTTGGTTACTGCTGATCATAGTCA | 1085 |
| Db | | 1127 | GGCTAACGAGCTCACTAGCGAACTGGACACGCTGAT | CTGTCTCACTGCAGAACCACTGCCA | 1186 |
| OY | | 1086 | TGTTTTTTCTTTGGTGTGTACACTTGGAGAGTACT | TATTTTGGTTGGCTCCAGG | 1145 |
| Db | | 1187 | TGTTCTTCTTTTGGTGTACACACTGCGTGGAGCT | TCATTTTCGTTGCGCCCGG | 1246 |
| OY | | 1146 | TAAAGCTTTGATAGTAAGTCTTACACTTCTATTT | TGTATGGTAAATGTTCCAGGTTATGC | 1205 |
| Db | | 1247 | CAAGGCTTAGACAGCAAGTCTTACACCTCCATCC | TATGGCAATGGCCCAAGGCTATGC | 1306 |
| OY | | 1206 | TTTGGGTGTGTTCTAGACCAAGTGTTAATGTAAT | CTAGTGAAGAACCATCTTACAG | 1265 |
| Db | | 1307 | GCTTGGCGGGGGCTCGAGGCCGATGTTAATGG | CAGCACAAAGGAAACCTCATATCCG | 1366 |
| OY | | 1266 | ACAACAAGCTGCTGTTCCATTGGCTAGTAAACT | CTATGTTGTTGAAGATGTTGCTGTTT | 1325 |
| Db | | 1367 | GCAGCAGCGCGGCTGCTGCTAGCGAGACCCAG | CGGGCGGAAGACGTGGCGGTGTT | 1426 |

| | | | |
|-----------------------|---|---|-----------------|
| QY | 1326 | TGCTAGAGGTCACAACTCATTTGGTTCAAGTGTTCAGAGAAACTTTTGTGCTCA | 1385 |
| | | | |
| Db | 1427 | CGCGCGAGGCCCGCAGCGCACCTGGTGACAGCGCGTGACAGAGACCTTCGTGGCGCA | 1486 |
| | | | |
| QY | 1386 | TATATGCGCTTTTGTGCTGTGTGTGAACCATACACTGATTGTATTTGCCAGCTCCAGC | 1445 |
| | | | |
| Db | 1487 | CATCATGGCCTTTGCCGGCGTGGTGAGGCCCTACACCGACTGCATCTGCCAGCCCCCGC | 1546 |
| | | | |
| QY | 1446 | TACTGCTACTAGTATTCAGA | 1466 |
| | | | |
| Db | 1547 | CACCGCCACCAGCATCCCGA | 1567 |
| | | | |
| RESULT 14 | | | |
| LOCUS | AX741748 | 1650 bp | DNA |
| DEFINITION | Sequence 26 from Patent WO03002736. | | linear |
| ACCESSION | AX741748 | | PAT 10-MAY-2003 |
| VERSION | AX741748.1 | GI:30524393 | |
| KEYWORDS | | | |
| SOURCE | Bos taurus (cow) | | |
| ORGANISM | Bos taurus | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. | | |
| REFERENCE | 1 | | |
| AUTHORS | Shao,Z., Kratzsch,P., Schmuck,R., von der Eltz,H. and Kenklies,J. | | |
| TITLE | A walk-through technique for in vitro recombination of polynucleotide sequences | | |
| JOURNAL | Patent: WO 03002736-A 26 09-JAN-2003; | | |
| FEATURES | Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH) | | |
| source | location/Qualifiers | | |
| | 1. .1650 | | |
| | /organism="Bos taurus" | | |
| | /mol_type="genomic DNA" | | |
| | /db_xref="taxon:9913" | | |
| ORIGIN | | | |
| Query Match | 56.3%; | Score 831.6; | DB 6; |
| Best Local Similarity | 73.1%; | Pred. No. 7.2e-146; | length 1650; |
| Matches 1068; | Conservative | 0; | Mismatches 394; |
| | | Indels | 0; |
| | | Gaps | 0; |
| QY | 9 | GATTCACGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAAGCTGCTCAAGCTTTGGA | 68 |
| | | | |
| Db | 158 | GATCCACGCTGAGGAGGAAACCCTTCCTTGGAACCCGACAGGCGACGCCGCTTGA | 217 |
| | | | |
| QY | 69 | TGTTGCTAAGAAGTTGCAACCAATTCMAACTGCTGCTAAGAAATGTTATTGTTTGGG | 128 |
| | | | |
| Db | 218 | TGTAGCCAAGAAGTTGACGCCGATCCAGACAGCTGCCAAGAATGTCATCTTCTTGGG | 277 |
| | | | |
| QY | 129 | TGATGATAGGGTGTCCAACTGTTACTGCTACTAGAAATTTGAAGGGTCAAAATGAATGG | 188 |
| | | | |
| Db | 278 | GGATGGATGGGGGTGCTTACGGTGACAGCCACTCGATCCTAAAGGGGACAGATGATGG | 337 |
| | | | |
| QY | 189 | TAACTGGGTCAGAAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGTCTAA | 248 |
| | | | |
| Db | 338 | CAAACTGGGACCTGAGACACCCCTGGCCATGACCAAGTTCCCATACGTGGCTTGTCCAA | 397 |
| | | | |
| QY | 249 | GACTTACAATGTTGATAGCAAGTTCAGATTCTGCTGCTACTGCTACTGCTTACTTGTG | 308 |
| | | | |
| Db | 398 | GACATACAACGTGACAGACAGGTGCCAGACAGCGAGGCACTGCCACTGCTTACTGTG | 457 |
| | | | |
| QY | 309 | TGCTGTTAAGGTAATTACAGAACTATTGTTTCTGCTGCTGCTAGATACAATCAATG | 368 |
| | | | |
| Db | 458 | TGGGGTCAAGGCACTACAGAACCATCGGTGAAGTGCAGCGCGCCGCTACAATCACTG | 517 |
| | | | |
| QY | 369 | TAACTACTAGAGGTAATGAAGTTACTTCTGTATTAATAGAGCTAAGAGGCTGTAA | 428 |
| | | | |
| Db | 518 | CAACACGACACGTTGGGAATGAGGTCACGCTCTGTATCAACCGGGCCAAAGAAAGCAGGAA | 577 |
| | | | |
| QY | 429 | GGCTGTTGTTGTTTACTACTACTAGAGTTCAAATGCTTCTCCAGCTGGTGTTCAGC | 488 |
| | | | |
| Db | 578 | GGCCGTGGAGTGTGTGACCAACCCAGGGGTGACAGATGCTCCCGCAGCCGGGGCTTACGC | 637 |
| | | | |

| | | | | | | | | | | | | | | |
|----|------|---------|--------|--------|--------|--------|--------|-------|-------|-------|-------|-------|------|------|
| QY | 489 | TCATAC | TGTTA | TAGAA | ATTGG | TACTCT | GTAGT | GATTT | TGCC | AGCTG | ATGCT | CAAA | GAA | 548 |
| Db | 638 | GCACAC | GGTGA | ACCGAA | ACTGG | TACTCA | GACG | CCGAC | CTGCT | GATGC | ACAGA | GAA | 697 | |
| QY | 549 | TGGTGT | CAAGA | TATTC | GTCTC | TCAAT | TGGT | TTC | CAAT | TATG | GATAT | TGAT | TTT | 608 |
| Db | 698 | TGGCTG | CCAGG | ACATC | CGCCG | CACAG | CTGGT | CTA | CAAC | ATGAT | TGAC | GTAT | CT | 757 |
| QY | 609 | TGGTGT | AGATG | TACAT | GTTT | CCAGA | AGGTA | CTCC | AGAT | CCAGA | ATACC | AGAT | GAT | 668 |
| Db | 758 | TGGAGG | CCGA | TGTAT | CATG | TTTCT | GAGG | GGAC | CCCA | GA | CCCTG | AATAC | CCAG | 817 |
| QY | 669 | TTCTGT | AATGT | GTTAG | AAAG | ATAAG | CAAA | ATTGG | TTCA | AGA | TGGCA | AGCT | TA | 728 |
| Db | 818 | CAGTGT | AATGA | GTCCG | AAGACA | AGAC | AGAAC | CTGTG | CA | GAA | TGGC | AG | CC | 877 |
| QY | 729 | TCAAGG | TGCTCA | TATGT | TTGGA | TAGAA | CTGCT | TTG | TGA | AGCTG | CTGAT | GAT | TT | 788 |
| Db | 878 | CCAGGAG | CCCA | GTATG | TGGA | ACCG | CACTG | CGCT | CT | CA | GGCGG | CGATG | ACT | 937 |
| QY | 789 | TGTTAC | TCA | TGTGA | TGGG | TTGTT | GAA | CCA | CTG | ATAT | GATGA | ATAT | GT | 848 |
| Db | 938 | TGTA | CACAC | ACTCA | TGGG | CTCT | TGAG | CCG | CA | GACAT | GATGA | ATAT | GT | 997 |
| QY | 849 | TCATAC | TAA | GGAT | CCACT | TTGG | CTG | AAAT | GACT | GAA | GCTG | CTT | GC | 908 |
| Db | 998 | CCACAC | CAAG | ACC | CGAC | CCCTG | CGG | AGAT | GAC | GGG | CCCTG | CAAG | TG | 1057 |
| QY | 909 | AAATCC | AAGG | TTT | TACT | TGTT | GTG | TAA | GGT | GTA | ATTGA | TCAT | G | 968 |
| Db | 1058 | GAACCC | CCCCG | GGCTT | CTAC | CTTCT | G | TGA | GGG | AGG | CCG | CA | T | 1117 |
| QY | 969 | TGGTAA | GCTT | ATATG | GCTT | GACT | GAA | CTAT | TAT | GTTGA | TATG | CTA | T | 1028 |
| Db | 1118 | CGGCAA | AGCTT | ATATG | GCAC | TGAG | CGCAT | CTAT | TTG | ACAA | TGCC | AT | G | 1177 |
| QY | 1029 | TAA | TGA | ATG | CACTT | CTGA | ATTG | GA | ACTT | TG | ATTG | TG | T | 1088 |
| Db | 1178 | TAA | CGAG | CTCA | CTAG | CGAC | GTG | ATC | CTT | GT | CACTG | CA | CA | 1237 |
| QY | 1089 | TTTTCT | TTTGG | GT | TAC | ACTT | GAG | GA | CTT | CTA | TTTGG | TTG | G | 1148 |
| Db | 1238 | CTTCTC | CTTGG | TG | CTAC | ACACT | GCG | GA | CTC | CA | TTTGG | TTG | G | 1297 |
| QY | 1149 | GCGTTG | AGTA | GTA | AGT | CTTAC | CTTCTA | TTT | TG | ATG | GTA | AGT | CC | 1208 |
| Db | 1298 | GCGCTT | AGAC | AGCA | AGT | CTTAC | CTTCTA | TTT | TG | ATG | GTA | AGT | CC | 1357 |
| QY | 1209 | GCGTGT | GTCT | TA | GAC | CA | GATG | TAA | TG | TA | GTA | GA | CA | 1268 |
| Db | 1358 | TGGCGG | GGGCT | CGAG | CCGAT | GTTA | TGGC | AG | CA | CA | AG | CA | CA | 1417 |
| QY | 1269 | ACAA | GCTG | CTGT | CCATT | GGCTA | GAA | CTCA | TG | TG | TGA | GA | T | 1328 |
| Db | 1418 | GCA | GGG | GGC | CTG | CCCTG | CTAG | GAG | AC | CA | CG | GG | CG | 1477 |
| QY | 1329 | TAGA | GTC | CA | CAAG | CTCA | TTGG | TTC | ATG | TG | TCA | GA | GA | 1388 |
| Db | 1478 | GCGA | GGCC | CGCA | GGCC | CACTG | TG | CA | CG | GG | CG | GA | GA | 1537 |
| QY | 1389 | TATG | GCTT | TG | CTG | TG | TGA | AC | CA | TAC | TG | TA | TT | 1448 |
| Db | 1538 | CATG | GCTT | TG | CGG | GTG | CGT | GAG | CC | CTA | CA | CTG | CA | 1597 |
| QY | 1449 | TGCTA | CTA | GTAT | TCC | AGATT | AA | 1470 | | | | | | |
| Db | 1598 | CGCC | AC | CA | GCA | TCC | CG | ACT | G | 1619 | | | | |

RESULT 15
AF052226
LOCUS AF052226 2460 bp mRNA linear MAM 03-SEP-1998

| | | | | | | | | | | | | | | | | | | | | | |
|----------------------------|--|--------|-------|------|------|--------|-------|------|-----|------|-----|------|-----|-----|-------|----|-----|-----|-----|-----|-----|
| DEFINITION | Bos taurus intestinal alkaline phosphatase III mRNA, complete cds. | | | | | | | | | | | | | | | | | | | | |
| ACCESSION | AF052226 | | | | | | | | | | | | | | | | | | | | |
| VERSION | AF052226.1 GI:3510650 | | | | | | | | | | | | | | | | | | | | |
| KEYWORDS | | | | | | | | | | | | | | | | | | | | | |
| SOURCE | Bos taurus (cow) | | | | | | | | | | | | | | | | | | | | |
| ORGANISM | Bos taurus | | | | | | | | | | | | | | | | | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. | | | | | | | | | | | | | | | | | | | | |
| AUTHORS | 1 (bases 1 to 2460) Menes,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and Millan,J.L. | | | | | | | | | | | | | | | | | | | | |
| TITLE | Bovine alkaline phosphatases | | | | | | | | | | | | | | | | | | | | |
| JOURNAL | Unpublished | | | | | | | | | | | | | | | | | | | | |
| REFERENCE | 2 (bases 1 to 2460) Menes,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and Millan,J.L. | | | | | | | | | | | | | | | | | | | | |
| TITLE | Direct Submission | | | | | | | | | | | | | | | | | | | | |
| JOURNAL | Submitted (05-MAR-1998) Medical Genetics, Umea University, S-901 85 Umea, Sweden | | | | | | | | | | | | | | | | | | | | |
| FEATURES | Location/Qualifiers | | | | | | | | | | | | | | | | | | | | |
| source | 1..2460 | | | | | | | | | | | | | | | | | | | | |
| CDS | /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" 66..1658 /EC_number="3.1.3.1" /note="IAP III" /codon_start=1 /product="intestinal alkaline phosphatase III" /protein_id="AAC33853.1" /db_xref="GI:3510651" /translation="MQGACVLLLLGLWQLSLAFIPVEEDBPAFMNROAAQALDVAKK LPIQKAKNVILFLDGMGVPVTATRIKLGQMDKLGPEPLAMDQFPYVALSKTY NVDQVPDSAGTATAYLCGVKGNVRIIGVSAARYNQNTTRGNEVTSVMNRKAKAG SVGVTTTRVQHASPAGAYAHVNRDWSADADLPADAQTYGCCDIALQLVNMDIDIV LGGGRKVMPEGTDPDEYPHDASVNGVRKDKRNILVQEMAKHGOAQYVMNRTELLQAA NDSVTHLMGLFEPADMKYNVQDPTKDPTEEMTEALQVLSNPGFYLFVEGGRI DHGHDSKAYMALTEAVMFDNALIAKANELTSGLDILVTAHDHSHVFSFGGYTLRGTS IFGLAPSKASDKSYTSILYNGPGYVLGGSRPDVNDISIDPSYRQAAVPLSSET HGEDVAVFARGPQAHLVHGOEETFVAHVMAFAGCVEPYTDCNLPAPSGLSDAHLA ASAPSLALLAGAMLLLLAPALY" | | | | | | | | | | | | | | | | | | | | |
| ORIGIN | | | | | | | | | | | | | | | | | | | | | |
| Query Match | 52.6%; Score 777; DB 4; Length 2460; | | | | | | | | | | | | | | | | | | | | |
| Best Local Similarity | 71.2%; Pred. No. 1.1e-135; | | | | | | | | | | | | | | | | | | | | |
| Matches 1026; Conservative | 0; Mismatches 415; Indels 0; Gaps 0; | | | | | | | | | | | | | | | | | | | | |
| QY | 6 | CTTGAT | TCCAG | CTG | AGAA | AAATCC | AGCTT | TTT | GGA | TAG | ACA | AGCT | GCT | CA | AGCTT | 65 | | | | | |
| Db | 122 | CTTCAT | CCAG | TG | AGAG | GAAG | ACC | CCG | CTT | CTG | GA | AC | CG | CA | GGC | CA | AGC | CTT | 181 | | |
| QY | 66 | GGATG | TGCT | AGAG | TTG | CAAC | CAATT | CAAA | CTG | CTG | CTA | AGA | ATT | TGA | AGG | GT | CA | AA | TG | 125 | |
| Db | 182 | TGATG | TGG | CTA | AGAG | CTG | AC | CC | CA | TC | CA | GA | AA | CC | CG | CA | GA | AT | G | 241 | |
| QY | 126 | GCGT | ATG | TAT | G | GGT | TT | CCA | AGT | GTT | ACT | GCT | ACT | AGA | ATT | T | TGA | AG | G | 185 | |
| Db | 242 | GGA | GAT | G | GG | AT | G | GG | AT | G | GG | AT | G | GG | AT | G | GG | AT | G | 301 | |
| QY | 186 | TGGT | AGT | TGG | GT | CCAG | AACT | CCAT | TGG | CTAT | GAT | CA | ATT | TC | CA | TG | CT | T | G | 245 | |
| Db | 302 | TGAC | AA | GCT | GG | AC | CTG | AG | AC | ACC | CTG | CA | TG | AC | CA | G | T | T | C | 361 | |
| QY | 246 | TAA | GACT | TAC | ATG | TG | TAG | ACA | AGT | TC | CA | GA | T | T | CT | G | T | CA | T | 305 | |
| Db | 362 | CA | AG | CA | TAC | AA | CTG | G | AC | AG | GT | CC | CA | GA | CA | G | CG | CA | CT | 421 | |
| QY | 306 | G | TG | TG | T | G | T | A | G | G | T | A | T | T | A | G | G | T | A | T | 365 |
| Db | 422 | G | TG | TG | G | G | T | A | G | G | T | A | T | T | A | G | G | T | A | T | 481 |
| QY | 366 | ATG | TAT | ACT | ACT | AG | GTA | TGA | AGT | TACT | TCT | GTT | ATT | ATA | TGA | AG | CTA | GA | AG | 425 | |

Db 482 GTGCAACACGACGCTGGGAATGAGTCACTGCTGTGATGAACCGGGCCAGAAAGCAGG 541
QY 426 TAAGGCTGTGGTGTGTTTACTACTACTAGTTCACATGCTTCTCCAGCTGTGCTTA 485
Db 542 GAAGTCAGTGGGAGTGTGACCAACCAACGAGGTGACGACGCTCCCGAGCGGTGCTTA 601
QY 486 CGCTCATCTGTTAATAGAAATGGTACTCTGATGCTGATTGGCCAGCTGATGCTCAAA 545
Db 602 TGACACACGCGTGAACCGTGAATGCTGACTGCTGACGCGGACCTGCTGCGATGACAGAC 661
QY 546 GAATGCTGTCAAGATATGCTGCTCAATGCTTTACATATGATGATGATGATGATTTT 605
Db 662 GTATGCTGCCAGACATCGCCACACAACCTGGTCAACACATGATGATGATGATGATCCT 721
QY 606 GGGTGGTGAATGATCATGTTCCAGAGGTAATCCAGATCCAGATCCAGATCCAGATGA 665
Db 722 GGGTGAAGCGCGAAGTACATGTTCTGAGGGGAGCCCGAGACCTGAAATACCCACAGCA 781
QY 666 TGCTTCTGTTAATGCTGTGAAGAGATAGCAAAATTTGTTCAAGATGGCAAGCTAA 725
Db 782 TGCCAGTGTGAATGAGTCCGGAAGACAGCGGAATCTGTTGACAGAGTGGCAGGCCAA 841
QY 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGATGATTC 785
Db 842 GCACCAAGGAGCCAGTATGTGGAACCGCACGAGCTCCTTCAGGACCAATGACTC 901
QY 786 TAGTGTACTCTATTGATGGGTTGTTGAACCACTGATATGAAGTAAATGTTCAACA 845
Db 902 CAGTGTACACATCTCATGGGCTCTTGAAGCGGACAGACATGAATGAATGTTCAACA 961
QY 846 AGATCATACTAAGATCCAATTTGGCTGAATGACTGAAGCTGCTTGAAGTTTGTGTC 905
Db 962 AGACCCCAACCAAGACCCGACCTGAGAGATGACGAGCGCGCCCTGCAAGTGTGAG 1021
QY 906 TAGAATCCAGAGCTTTTACTTGTGTTGAAGGTGTTGAATGATGATGATGATGATCA 965
Db 1022 CAGGAACCCCAAGGCTTCTACTCTTGTGAGGAGGAGCGCCGATGATGATGATGATCA 1081
QY 966 TGATGTAAGGCTTATATGCTTGTGATGATGATGATGATGATGATGATGATGATGAT 1025
Db 1082 TGATAGCAAGCTTATATGCGCTGATGAGGCGGTATGTTGACATGCTATGCTATGCTAA 1141
QY 1026 GGCTAATGAATGACTTCTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
Db 1142 GGCTAAGAGCTCACTAGCAACTGACAGCTGATCCTGTGCTGACGACCACTCCA 1201
QY 1086 TGTGTTTCTTTGGTGGTTACACTTGAAGGTAATCTTATTTTGGTTGGCTCCAGG 1145
Db 1202 TGTCTTCTTTTGGTGGTACACACTGCGTGGGAACTCCATTTTGGTGGCTCCAGG 1261
QY 1146 TAAGCTTTGATAGTAACTTACACTTCTATTTTGTATGTAATGATGATGATGATGATG 1205
Db 1262 CAAGGCTTCAAGCAAGAGTCTTACACTCTCTATGGAATGCTGCTGCTACGT 1321
QY 1206 TTTGGGTGGTGTCTAGACCAAGATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1265
Db 1322 GCTTGTGGGCTCAAGGCGCGATGTAATGACAGCATGAAGCGAGGACCCCTCATACCG 1381
QY 1266 ACAACAAGCTGCTGTCTCATGCTAGTGAATCTCATGCTGCTGTAAGATGCTGCTTTT 1325
Db 1382 GCAGCAGGCGGCGTGCCTCTGTACGAGACCCACGCGGCGAAGCGTGGCGTGT 1441
QY 1326 TGCTAGAGTCCACAAGCTCATTTGTTCAATGTTCAAGAGAACTTTTGTGCTCA 1385
Db 1442 CGCGGAGGCGCGCAGCGCACCTGTGCAAGCGCTGACAGAGAGACCTTCTGCGCGCA 1501
QY 1386 TATTATGGCTTTTGTGCTGTGTGTTGAACCATACACTGATTTGTAATTTGCCAGCTCAAGC 1445
Db 1502 CGTCATGGCTTTTGGCGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCGCGCCCTC 1561
QY 1446 T 1446

Db 1562 T 1562

Search completed: October 19, 2004, 14:44:36
Job time: 6527.86s

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 20, 2004, 00:09:03 ; Search time 768 Seconds
(without alignments)
10088.731 Million cell updates/sec

Title: US-09-911-132A-5
Perfect score: 1476
Sequence: 1 gaattcttgattccagctga.....gtattccagatcaaggtacc 1476

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

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| 1: | geneseqn1980s:* |
| 2: | geneseqn1990s:* |
| 3: | geneseqn2000s:* |
| 4: | geneseqn2001as:* |
| 5: | geneseqn2001bs:* |
| 6: | geneseqn2002as:* |
| 7: | geneseqn2002bs:* |
| 8: | geneseqn2003as:* |
| 9: | geneseqn2003bs:* |
| 10: | geneseqn2003cs:* |
| 11: | geneseqn2003ds:* |
| 12: | geneseqn2004s:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------------|---------------------|
| 1 | 1476 | 100.0 | 1476 | 6 ADI26515 | Adi26515 Optimised |
| 2 | 1476 | 100.0 | 1476 | 10 ADE53386 | Ades53386 Bovine al |
| 3 | 1474.4 | 99.9 | 1476 | 10 ADE53391 | Ades53391 Bovine al |
| 4 | 1472.8 | 99.8 | 1476 | 10 ADE53392 | Ades53392 Bovine al |
| 5 | 1471.2 | 99.7 | 1476 | 10 ADE53393 | Ades53393 Bovine al |
| 6 | 1469.6 | 99.6 | 1476 | 10 ADE53394 | Ades53394 Bovine al |
| 7 | 845.6 | 57.3 | 1476 | 6 ADI26549 | Adi26549 Bovine bi |
| 8 | 834.8 | 56.6 | 1464 | 10 ADE53384 | Ades53384 Bovine al |
| 9 | 831.6 | 56.3 | 1650 | 8 ABZ22773 | Abz22773 Calf inte |
| 10 | 616 | 41.7 | 2523 | 4 AAK51495 | Aak51495 Human pol |
| 11 | 613.8 | 41.6 | 1702 | 12 ADN43057 | Adn43057 Human sec |
| 12 | 611.2 | 41.4 | 1587 | 2 AAQ78135 | Aaq78135 Human ent |
| 13 | 611.2 | 41.4 | 1587 | 2 AAT27384 | Aat27384 Human alk |
| 14 | 611.2 | 41.4 | 2516 | 12 ADF45468 | Adf45468 Human vas |
| 15 | 611.2 | 41.4 | 2516 | 12 ADO28592 | Ado28592 Human PPB |
| 16 | 610.2 | 41.3 | 1491 | 2 AAQ90640 | Aaq90640 Human ent |
| 17 | 609.2 | 41.3 | 3076 | 2 AAT27391 | Aat27391 Human Igg |
| 18 | 609.2 | 41.3 | 3127 | 2 AAT27392 | Aat27392 Human Igg |
| 19 | 603.4 | 40.9 | 1966 | 4 AAK52479 | Aak52479 Human pol |
| 20 | 603 | 40.9 | 2372 | 2 AAT27393 | Aat27393 Human Igg |
| 21 | 603 | 40.9 | 2484 | 2 AAT27386 | Aat27386 Human Igg |

| | | | | | |
|----|-------|------|------|-------------|--------------------|
| 22 | 603 | 40.9 | 3022 | 2 AAT27390 | Aat27390 Human Igg |
| 23 | 603 | 40.9 | 3147 | 2 AAT27389 | Aat27389 Human Igg |
| 24 | 602.2 | 40.8 | 1464 | 2 AAQ90639 | Aaq90639 Human ent |
| 25 | 583.6 | 39.5 | 2445 | 2 AAT27387 | Aat27387 Human Igg |
| 26 | 583.6 | 39.5 | 3108 | 2 AAT27388 | Aat27388 Human Igg |
| 27 | 582.8 | 39.5 | 1422 | 2 AAQ90638 | Aaq90638 Human ent |
| 28 | 573 | 38.8 | 1649 | 8 ABZ22774 | Abz22774 Human pla |
| 29 | 572.8 | 38.8 | 1515 | 12 ADQ80224 | Adq80224 Human gen |
| 30 | 572.8 | 38.8 | 1597 | 10 ADH10077 | Adh10077 Human SEA |
| 31 | 572.8 | 38.8 | 1634 | 2 AAV42729 | Aav42729 Human pla |
| 32 | 572.8 | 38.8 | 1675 | 10 ADH10079 | Adh10079 Human SEA |
| 33 | 572.8 | 38.8 | 1697 | 12 ADQ80223 | Adq80223 Human SEA |
| 34 | 572.8 | 38.8 | 1728 | 6 ABL49916 | Ab149916 SEAP, ins |
| 35 | 572.8 | 38.8 | 1748 | 10 ADH10087 | Adh10087 Human SEA |
| 36 | 572.8 | 38.8 | 1777 | 10 ADH10083 | Adh10083 Human SEA |
| 37 | 572.8 | 38.8 | 1904 | 12 ADQ80225 | Adq80225 Human gen |
| 38 | 572.8 | 38.8 | 1915 | 10 ADH10091 | Adh10091 Human SEA |
| 39 | 572.8 | 38.8 | 1918 | 10 ADH10073 | Adh10073 Human sec |
| 40 | 572.8 | 38.8 | 1975 | 10 ADH10095 | Adh10095 Human SEA |
| 41 | 572.8 | 38.8 | 2239 | 10 ADD67946 | Add67946 HIV seque |
| 42 | 572.8 | 38.8 | 2239 | 10 ABX10618 | Abx10618 HIV-SEAP |
| 43 | 572.8 | 38.8 | 5264 | 8 ACC43141 | Acc43141 Nucleotid |
| 44 | 572.8 | 38.8 | 5408 | 8 ACC43140 | Acc43140 Nucleotid |
| 45 | 572.8 | 38.8 | 7469 | 4 AAH47042 | Aah47042 Nucleotid |

ALIGNMENTS

| | | | | | |
|----------|---|------------------------------|--|--|--|
| RESULT 1 | | | | | |
| ADI26515 | AD126515 | standard; DNA; 1476 BP. | | | |
| XX | XX | | | | |
| AC | ADI26515; | | | | |
| DT | 22-APR-2004 | (first entry) | | | |
| XX | XX | | | | |
| DE | Optimised bovine bIAPII DNA. | | | | |
| XX | XX | | | | |
| KW | alkaline phosphatase; resistance gene; zeomycin; G418; heat stability; | | | | |
| KM | bovine; bIAPII; yeast; gene; ds. | | | | |
| XX | XX | | | | |
| OS | Bos taurus. | | | | |
| OS | Synthetic. | | | | |
| XX | XX | | | | |
| FH | Key | Location/Qualifiers | | | |
| FT | CDS | 7..1470 | | | |
| FT | | /*tag= a | | | |
| FT | | /product= "optimised bIAPII" | | | |
| FT | | /partial | | | |
| FT | | /note= "no start codon" | | | |
| XX | XX | | | | |
| PN | EP1176205-A2. | | | | |
| XX | XX | | | | |
| PD | 30-JAN-2002. | | | | |
| XX | XX | | | | |
| PF | 21-JUL-2001; 2001EP-00117822. | | | | |
| XX | XX | | | | |
| PR | 25-JUL-2000; 2000DE-01036491. | | | | |
| XX | XX | | | | |
| PA | (HOFF) ROCHE DIAGNOSTICS GMBH. | | | | |
| PA | (HOFF) HOFFMANN LA ROCHE & CO AG F. | | | | |
| XX | XX | | | | |
| PI | Mueller R, Thalhofer J, Geipel F, Hoelke W, Glaser S, Eckstein H; | | | | |
| PI | Kirschbaum T, Bommarius B; | | | | |
| XX | XX | | | | |
| DR | WPI; 2002-173123/23. | | | | |
| DR | P-PSDB; ADI26514. | | | | |
| XX | XX | | | | |
| PT | Preparing eukaryotic alkaline phosphatase, useful as diagnostic reagent | | | | |
| PT | and for dephosphorylation, by recombinant expression in yeast selected | | | | |
| PT | for high gene copy number. | | | | |
| XX | XX | | | | |

PS Claim 3; SEQ ID NO 5; 23pp; German.

XX This invention describes a novel method of preparing eukaryotic alkaline
CC phosphatase in yeast cells, comprising cloning an alkaline phosphatase
CC gene sequence into different vectors, transforming, and expressing and
CC purifying. A first vector is used containing a resistance gene against a
CC selection marker and transformants that have integrated resistance gene
CC and alkaline phosphatase gene into the genome are selected by growth on
CC medium containing a low concentration of selection marker. The gene copy
CC number is increased by multiple transformation and multiple transformants
CC selected on growth medium under high selection pressure. A second vector
CC containing the alkaline phosphatase gene and a second resistance gene
CC against a second marker is introduced, its copy number increased as for
CC the first resistance gene and clones selected that have many copies of
CC the alkaline phosphatase gene and of both resistance genes, integrated
CC into the genome. The vectors used in the method are pHAP10-3 and pHAP10-
CC 3/9K. Preferred cells include methylotrophic yeast, particularly *Pichia*
CC *pastoris* and *Hansenula polymorpha* and specifically *P. pastoris* X-33
CC transformed with pHAP10-3 and pHAP10-3/9K. The amino acid sequence of
CC bovine alkaline phosphatase is known and, working back from this, an
CC optimised codon sequence was designed. This was assembled conventionally
CC from 28 synthetic oligonucleotides to give a sequence having *Eco*RI and
CC *Asp*718 recognition sites at the ends to facilitate cloning. The selection
CC markers are particularly zeomycin and G418, respectively. The alkaline
CC phosphatase is used as diagnostic reagent, as part of a conjugate and for
CC dephosphorylation of DNA. This method produces very active, glycosylated
CC alkaline phosphatase with specific activity over 3000, preferably 10000,
CC units/mg and heat stability comparable with that for commercial enzymes.
CC The expression system is resistant and stable and provides high-level
CC expression without any selection pressure. This sequence represents an
CC optimised bovine *hAP*1 polynucleotide.

XX
SQ Sequence 1476 BP; 387 A; 223 C; 346 G; 520 T; 0 U; 0 Other;

Query Match 100.0%; Score 1476; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTTGATTCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
Db 1 GAATTCCTTGATTCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
QY 61 GCTTTGGATGTTGCTAAGAGTTCGCAACCAATTCAACTGCTGCTAAGATGTTATTTTG 120
Db 61 GCTTTGGATGTTGCTAAGAGTTCGCAACCAATTCAACTGCTGCTAAGATGTTATTTTG 120
QY 121 TTTTGGGATGATGATGATGGTTCACACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
Db 121 TTTTGGGATGATGATGATGGTTCACACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
QY 181 ATGAATGGTAAGTTGGGTCAGAAACTCCATTGGCTATGATCAATTTCCATACGTTGCT 240
Db 181 ATGAATGGTAAGTTGGGTCAGAAACTCCATTGGCTATGATCAATTTCCATACGTTGCT 240
QY 241 TTGTTCTAAGACTTACAAATGTTGATAGCAAGTTCAGATTCTGCTGTAAGTCTACTGCT 300
Db 241 TTGTTCTAAGACTTACAAATGTTGATAGCAAGTTCAGATTCTGCTGTAAGTCTACTGCT 300
QY 301 TACTTGTGTGTTAAGGGTAATTAAGAACTATTGGTGTCTGCTGCTAGATAC 360
Db 301 TACTTGTGTGTTAAGGGTAATTAAGAACTATTGGTGTCTGCTGCTAGATAC 360
QY 361 AATCAATGTAATACTACTAGAGGTATGAAGTTACTTCTGTTAATATAGAGCTAAGAG 420
Db 361 AATCAATGTAATACTACTAGAGGTATGAAGTTACTTCTGTTAATATAGAGCTAAGAG 420
QY 421 GCTGGTAAGGCTGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
Db 421 GCTGGTAAGGCTGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
QY 481 GCTTACGCTCATACTGTTAATATAGAAATTTGGTACTCTGATGCTGATTGGCAGCTGATGCT 540
Db 481 GCTTACGCTCATACTGTTAATATAGAAATTTGGTACTCTGATGCTGATTGGCAGCTGATGCT 540

QY 541 CAAAAGATGTTGTCAAGATATTTGCTGCTCAATTTGTTTACATATGATATGATGTT 600
Db 541 CAAAAGATGTTGTCAAGATATTTGCTGCTCAATTTGTTTACATATGATATGATGTT 600
QY 601 ATTTTGGGTGTTGATAGATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCCA 660
Db 601 ATTTTGGGTGTTGATAGATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCCA 660
QY 661 GATGATGCTTCTGTTAATGGTGTAGAAAGGATTAAGCAAAATTTGGTCAAGAAATGCCAA 720
Db 661 GATGATGCTTCTGTTAATGGTGTAGAAAGGATTAAGCAAAATTTGGTCAAGAAATGCCAA 720
QY 721 GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGTTTGGTCAAGCTGCTGAT 780
Db 721 GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGTTTGGTCAAGCTGCTGAT 780
QY 781 GATTCTAGTGTACTCATTTGATGGGTTGTTTGAACCAAGCTGATATGAAGTAATATGTT 840
Db 781 GATTCTAGTGTACTCATTTGATGGGTTGTTTGAACCAAGCTGATATGAAGTAATATGTT 840
QY 841 CAACAAGATCATACTAAGATCCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCCAAGTT 900
Db 841 CAACAAGATCATACTAAGATCCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCCAAGTT 900
QY 901 TTGTTCTAGAAATCCAAAGGTTTCTTACTGTTTGTGTTGAAGGTGTTAGAAATGATCATGCT 960
Db 901 TTGTTCTAGAAATCCAAAGGTTTCTTACTGTTTGTGTTGAAGGTGTTAGAAATGATCATGCT 960
QY 961 CATCATGATGTTAAGGCTTATATGCTTTGACTGTAAGCTATTATGTTGATTAATGCTATT 1020
Db 961 CATCATGATGTTAAGGCTTATATGCTTTGACTGTAAGCTATTATGTTGATTAATGCTATT 1020
QY 1021 GCTAAGGCTAATGAATGACTTCTGAAATGGAATCTTGAATTTTGGTACTGCTGATCAT 1080
Db 1021 GCTAAGGCTAATGAATGACTTCTGAAATGGAATCTTGAATTTTGGTACTGCTGATCAT 1080
QY 1081 AGTCATGTTTCTTTGGTGGTTACACTTTGAGAGTACTTCTATTTTGGTTGGCT 1140
Db 1081 AGTCATGTTTCTTTGGTGGTTACACTTTGAGAGTACTTCTATTTTGGTTGGCT 1140
QY 1141 CCAGGTAAGGCTTTGGATAGTAAGCTTACACTTCTATTTTGTATGTAATGGTCCAGGT 1200
Db 1141 CCAGGTAAGGCTTTGGATAGTAAGCTTACACTTCTATTTTGTATGTAATGGTCCAGGT 1200
QY 1201 TATGCTTTGGGTGGTGTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACATCT 1260
Db 1201 TATGCTTTGGGTGGTGTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACATCT 1260
QY 1261 TACAGACAACAAGCTGCTGTTCATTGGCTAGTGAACCTCATGTGTTGAAGATGTTGCT 1320
Db 1261 TACAGACAACAAGCTGCTGTTCATTGGCTAGTGAACCTCATGTGTTGAAGATGTTGCT 1320
QY 1321 GTTTTGGCTAGAGGTCACAAGCTCATTTGGTTCATGTTTCAAGAAGAACTTTTGGT 1380
Db 1321 GTTTTGGCTAGAGGTCACAAGCTCATTTGGTTCATGTTTCAAGAAGAACTTTTGGT 1380
QY 1381 GCTCATATTATGGCTTTTGTGCTGTTGTGTTGAACCATACACTGATTGTAATTTGCCAGCT 1440
Db 1381 GCTCATATTATGGCTTTTGTGCTGTTGTGTTGAACCATACACTGATTGTAATTTGCCAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTAATTCAGATTAAAGTTACC 1476
Db 1441 CCAGCTACTGCTACTAGTAATTCAGATTAAAGTTACC 1476

RESULT 2
ADE53386
ID ADE53386 standard; DNA; 1476 BP.
XX
AC ADE53386;
XX
DT 29-JAN-2004 (first entry)

XX DE Bovine alkaline phosphatase variant DNA.
XX KW alkaline phosphatase; mutation; immunoassay; antigen;
XX KM interference suppressor; bovine; ds; gene.
OS Synthetic.
OS Bos taurus.
XX PN EP1348760-A2.
XX PD 01-OCT-2003.
XX PF 21-MAR-2003; 2003EP-00006426.
XX PR 25-MAR-2002; 2002DE-01013201.
XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX PA (HOFF) HOFMANN LA ROCHE & CO AG F.
XX PI Mueller R, Thalhofer J, Geipel F, Hoelke W, Kirschbaum T;
XX DR WPI; 2003-769844/73.
XX PT New mutants of alkaline phosphatase (AP) where enzymatic activity is
PT reduced a hundred fold, are useful as blocking reagents in AP-based
XX immunoassays.
PS Claim 1; SEQ ID NO 3; 35bp; German.
XX CC This invention describes a novel mutant of eukaryotic alkaline
CC phosphatase where the wild-type sequence is at least 77% homologous with
CC ADE53385 and where the alkaline phosphatase activity is reduced by at
CC least 100-fold, relative to the wild type. The mutations described are
CC Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly,
CC Val or Leu; Glu311 for Glu, Asn, Leu, Ile or Met; His320, 358 or 432 for
CC Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp.
CC Conjugates of the novel mutant with antibodies are useful in alkaline
CC phosphatase-based immunoassays for antigens as interference suppressors,
CC i.e. they prevent non-specific binding of active alkaline phosphatase-
CC based conjugates to vessel walls or first antibodies, a phenomenon that
CC may result in false positive results. The mutants have almost the same
CC tertiary and quaternary structures as wild-type alkaline phosphatase, so
CC are very specific interference suppressors. This sequence represents a
CC variant bovine alkaline phosphatase which includes an EcoRI site
CC described in the disclosure of the invention.
XX SQ Sequence 1476 BP; 387 A; 223 C; 346 G; 520 T; 0 U; 0 Other;
Query Match 100.0%; Score 1476; DB 10; Length 1476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCCTGATTCAGCTGAAGAAGAAAATCCAGCTTTTGGATAGACAAGCTGCTCAA 60
DB 1 GAATTCCTGATTCAGCTGAAGAAGAAAATCCAGCTTTTGGATAGACAAGCTGCTCAA 60
QY 61 GCTTTGAGTGTGCTAAGAAGTGCACCAATTCAAACTGCTGCTAAGATGTTATTTTG 120
DB 61 GCTTTGAGTGTGCTAAGAAGTGCACCAATTCAAACTGCTGCTAAGATGTTATTTTG 120
QY 121 TTTTGGGTGATGCTATGGGTGTTCCAACTGTTACTGCTACTAGATTTGAAGGTCAA 180
DB 121 TTTTGGGTGATGCTATGGGTGTTCCAACTGTTACTGCTACTAGATTTGAAGGTCAA 180
QY 181 ATGAATGCTAGTGGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACTGCT 240
DB 181 ATGAATGCTAGTGGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACTGCT 240
QY 241 TTGCTAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTAAGTCTACTGCT 300
DB 241 TTGCTAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTAAGTCTACTGCT 300

QY 301 TACTGTGTGTGTTAAGGGTAATTACAGAACTATTGGTGTCTGCTGCTAGATAC 360
DB 301 TACTGTGTGTGTTAAGGGTAATTACAGAACTATTGGTGTCTGCTGCTAGATAC 360
QY 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTATTATAAGACTAAGAAG 420
DB 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTATTATAAGACTAAGAAG 420
QY 421 GCTGTAAGGCTGTGGTGTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGGT 480
DB 421 GCTGTAAGGCTGTGGTGTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGGT 480
QY 481 GCTTACGCTCATCTGTTAATAGAAATGGTACTCTGATGCTGATTGGCCAGCTGATGCT 540
DB 481 GCTTACGCTCATCTGTTAATAGAAATGGTACTCTGATGCTGATTGGCCAGCTGATGCT 540
QY 541 CAAAAGATGCTGTCAAGATATTGCTGCTCAATTGTTTACAAATAATGATATGATGTT 600
DB 541 CAAAAGATGCTGTCAAGATATTGCTGCTCAATTGTTTACAAATAATGATATGATGTT 600
QY 601 ATTTGGGTGCTAGATATGATGTTCCAGAAAGTACTCCAGATCCAGATAACCA 660
DB 601 ATTTGGGTGCTAGATATGATGTTCCAGAAAGTACTCCAGATCCAGATAACCA 660
QY 661 GATGATGCTTCTGTTAATGCTGTAGAAAGGATTAAGCAAAATTTGGTTCAAGAATGGCAA 720
DB 661 GATGATGCTTCTGTTAATGCTGTAGAAAGGATTAAGCAAAATTTGGTTCAAGAATGGCAA 720
QY 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAATAGAACTGCTTTGTCAGAGCTGCTGAT 780
DB 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAATAGAACTGCTTTGTCAGAGCTGCTGAT 780
QY 781 GATTCATGCTTACTCATTTGATGAGGTTGTTTGAACCAAGCTGATATGAATATATGTT 840
DB 781 GATTCATGCTTACTCATTTGATGAGGTTGTTTGAACCAAGCTGATATGAATATATGTT 840
QY 841 CAACAAGATCACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGCAGATT 900
DB 841 CAACAAGATCACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGCAGATT 900
QY 901 TTGCTAGAAATCCAAAGAGTTTCTGTTTGTGTAAGGTGCTGAATATGATCATGCT 960
DB 901 TTGCTAGAAATCCAAAGAGTTTCTGTTTGTGTAAGGTGCTGAATATGATCATGCT 960
QY 961 CATCATGATGCTAAGGCTTATATGCTTTGACTGAAGCTATATTTGATATATGCTATT 1020
DB 961 CATCATGATGCTAAGGCTTATATGCTTTGACTGAAGCTATATTTGATATATGCTATT 1020
QY 1021 GCTAAGGCTAATGAATGACTTCTGAATGAGATCACTTGAATTTGGTTACTGCTGATCAT 1080
DB 1021 GCTAAGGCTAATGAATGACTTCTGAATGAGATCACTTGAATTTGGTTACTGCTGATCAT 1080
QY 1081 AGTCATGTTTTTCTTTTGGTGTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
DB 1081 AGTCATGTTTTTCTTTTGGTGTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
QY 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGCTAATGCTCCAGGT 1200
DB 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGCTAATGCTCCAGGT 1200
QY 1201 TATGCTTTGGGTGCTGTTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCT 1260
DB 1201 TATGCTTTGGGTGCTGTTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCT 1260
QY 1261 TACAGACAACAAGCTGCTGTTCCATTGCTAGTGAAACTCATGGGTGAAGATGTTGCT 1320
DB 1261 TACAGACAACAAGCTGCTGTTCCATTGCTAGTGAAACTCATGGGTGAAGATGTTGCT 1320
QY 1321 GTTTTGTAGAGGTCCACAAGCTCATTTGGTTCATGCTGCTGTTCAAGAAACTTTTGT 1380
DB 1321 GTTTTGTAGAGGTCCACAAGCTCATTTGGTTCATGCTGCTGTTCAAGAAACTTTTGT 1380
QY 1381 GCTCATATTATGCTTTTGTGCTGCTGTTGTTGAACCATACACTGATTTGTAATTGCGCAGCT 1440

Db 1381 GCTCATATTATGGCTTTTGTGCTGTGTGTAACCATACATGATTTGATTTGCCAGCT 1440

Qy 1441 CCAGCTACTGCTACTAGTATTCAGATTAAAGGTACC 1476

Db 1441 CCAGCTACTGCTACTAGTATTCAGATTAAAGGTACC 1476

RESULT 3

ID ADE53391 standard; DNA; 1476 BP.

XX ADE53391;

AC ADE53391;

XX 29-JAN-2004 (first entry)

XX Bovine alkaline phosphatase DNA encoding S92A.

XX

KW alkaline phosphatase; mutation; immunoassay; antigen; interference suppressor; bovine; ds; mutant.

XX Synthetic.

OS Bos taurus.

XX EP1348760-A2.

XX 01-OCT-2003.

XX 21-MAR-2003; 2003EP-00006426.

XX 25-MAR-2002; 2002DE-01013201.

XX (HOF) ROCHE DIAGNOSTICS GMBH.

PA (HOF) HOFMANN LA ROCHE & CO AG F.

XX Mueller R, Thalhofer J, Geipel F, Hoelke W, Kirschbaum T;

XX WPI; 2003-769844/73.

XX

PT New mutants of alkaline phosphatase (AP) where enzymatic activity is reduced a hundred fold, are useful as blocking reagents in AP-based immunoassays.

PT

XX Claim 8; SEQ ID NO 8; 35bp; German.

XX

CC This invention describes a novel mutant of eukaryotic alkaline phosphatase where the wild-type sequence is at least 77% homologous with ADE53385 and where the alkaline phosphatase activity is reduced by at least 100-fold, relative to the wild type. The mutations described are Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly, Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp. Conjugates of the novel mutant with antibodies are useful in alkaline phosphatase-based immunoassays for antigens as interference suppressors, i.e. they prevent non-specific binding of active alkaline phosphatase-based conjugates to vessel walls or first antibodies, a phenomenon that may result in false positive results. The mutants have almost the same tertiary and quaternary structures as wild-type alkaline phosphatase, so are very specific interference suppressors. This sequence encodes a CC variant bovine alkaline phosphatase which contains an S92A mutation and an EcoRI site described in the disclosure of the invention.

CC

XX

Sequence 1476 BP; 387 A; 223 C; 347 G; 519 T; 0 U; 0 Other;

Query Match 99.9%; Score 1474.4; DB 10; Length 1476;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAATTCCTTGATTCAGCTGAAGAGAAATCCAGCTTTTGGATAGACAAGCTGCTCAA 60

Db 1 GAATTCCTTGATTCAGCTGAAGAGAAATCCAGCTTTTGGATAGACAAGCTGCTCAA 60

Qy 61 GCTTTGATGTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGATGTATTG 120

Db 61 GCTTTGATGTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGATGTATTG 120

Qy 121 TTTTGGGTGATGATGGGTGTTCCAACTGTTACTGCTACTAGAATTTGAAGGCTCAA 180

Db 121 TTTTGGGTGATGATGGGTGTTCCAACTGTTACTGCTACTAGAATTTGAAGGCTCAA 180

Qy 181 ATGAATGTAAGTTGGGTCAGAAACTCCATTGGCTATGATCAATTTCCATACGTTGCT 240

Db 181 ATGAATGTAAGTTGGGTCAGAAACTCCATTGGCTATGATCAATTTCCATACGTTGCT 240

Qy 241 TTGCTTAAGACTTACAAATGTTGATAGACAAGTTCCAGATTCTGCTGCTGCTAGATAC 300

Db 241 TTGCTTAAGACTTACAAATGTTGATAGACAAGTTCCAGATTCTGCTGCTGCTAGATAC 300

Qy 301 TACTGTGTGTTGTTAAGGTTAATTACAGAACTATTGTTCTGCTGCTGCTAGATAC 360

Db 301 TACTGTGTGTTGTTAAGGTTAATTACAGAACTATTGTTCTGCTGCTGCTAGATAC 360

Qy 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTATTATAGAGCTAAGAA 420

Db 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTATTATAGAGCTAAGAA 420

Qy 421 GCTGTAAGGCTGTGTTGTTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480

Db 421 GCTGTAAGGCTGTGTTGTTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480

Qy 481 GCTTACGCTCATACTGTTAATAGAAATTGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540

Db 481 GCTTACGCTCATACTGTTAATAGAAATTGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540

Qy 541 CAAAAGATGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGATATTGATGTT 600

Db 541 CAAAAGATGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGATATTGATGTT 600

Qy 601 APTTGGGTGTTGTTAGAAATGTACATGTTTCCAGAGTAATCCAGATCCAGAAATGCCAA 660

Db 601 APTTGGGTGTTGTTAGAAATGTACATGTTTCCAGAGTAATCCAGATCCAGAAATGCCAA 660

Qy 661 GATGATGCTTCTGTTAATGTTGTTAGAAAGATAGCAAAATTTGGTTCAAGAAATGCCAA 720

Db 661 GATGATGCTTCTGTTAATGTTGTTAGAAAGATAGCAAAATTTGGTTCAAGAAATGCCAA 720

Qy 721 GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTCAGAGCTGCTGAT 780

Db 721 GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTCAGAGCTGCTGAT 780

Qy 781 GATTTAGTGTACTCATTTGATGGGTTTGTGTTGAACAGCTGATATGAATATATGTT 840

Db 781 GATTTAGTGTACTCATTTGATGGGTTTGTGTTGAACAGCTGATATGAATATATGTT 840

Qy 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGAAGCTGCTTTGCAAGTT 900

Db 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGAAGCTGCTTTGCAAGTT 900

Qy 901 TTGCTAGAATCCAAAGGTTTACTTGTGTTGAAGGTGAGATTTGATGATGATGAT 960

Db 901 TTGCTAGAATCCAAAGGTTTACTTGTGTTGAAGGTGAGATTTGATGATGATGAT 960

Qy 961 CATCATGATGTGAAGGCTTATATGCTTTGACTGAAGCTATATGTTGATATGCTAT 1020

Db 961 CATCATGATGTGAAGGCTTATATGCTTTGACTGAAGCTATATGTTGATATGCTAT 1020

Qy 1021 GCTAAGGCTAATGAATGATCTTGAATTTGATGATGATTTGTTGTTGTTGTTGTTGTT 1080

Db 1021 GCTAAGGCTAATGAATGATCTTGAATTTGATGATGATTTGTTGTTGTTGTTGTTGTT 1080

Qy 1081 AGTCATGTTTTTTCTTTTGGTGTACACTTTGAGAGTAATTTGTTGTTGTTGTTGTT 1140

Db 1081 AGTCATGTTTTTTCTTTTGGTGTACACTTTGAGAGTAATTTGTTGTTGTTGTTGTT 1140

Qy 1141 CCAGTAAAGGCTTTGATAGTAAGTCTTACACTTCTAATTTGTATGTAATGTTGCAAGT 1200

Db 1141 CCAGTAAAGGCTTTGATAGTAAGTCTTACACTTCTAATTTGTATGTAATGTTGCAAGT 1200

Db 1141 CCAGTAAAGGCTTTGGATAGTAACTTACACTTCTATTGTTGTAAGTGTCCAGGT 1200
QY 1201 TATGCTTTGGGTGGTCTTAGACACAGATGTTAAGTAGTACTAGTGAAGACCATCT 1260
Db 1201 TATGCTTTGGGTGGTCTTAGACACAGATGTTAAGTAGTACTAGTGAAGACCATCT 1260
QY 1261 TACAGACAACAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGTGTAAGATGTTGCT 1320
Db 1261 TACAGACAACAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGTGTAAGATGTTGCT 1320
QY 1321 GTTTTGTAGAGGTCCACAAGCTCATTTGGTTCAATGCTGTTCAGAAGAACTTTGTT 1380
Db 1321 GTTTTGTAGAGGTCCACAAGCTCATTTGGTTCAATGCTGTTCAGAAGAACTTTGTT 1380
QY 1381 GCTCATATTATGGCTTTGCTGTTGTTGAACCATACACTGATTGTAATTGCGAGCT 1440
Db 1381 GCTCATATTATGGCTTTGCTGTTGTTGAACCATACACTGATTGTAATTGCGAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTATTCCAGATTAAAGGTACC 1476
Db 1441 CCAGCTACTGCTACTAGTATTCCAGATTAAAGGTACC 1476
RESULT 4
ADE53392 standard; DNA; 1476 BP.
XX AC ADE53392;
XX DT 29-JAN-2004 (first entry)
XX DE Bovine alkaline phosphatase DNA encoding G322F.
XX KM alkaline phosphatase; mutation; immunoassay; antigen;
XX KW interference suppressor; bovine; ds; mutant.
XX OS Synthetic.
XX OS Bos taurus.
XX PN EP1348760-A2.
XX PD 01-OCT-2003.
XX PF 21-MAR-2003; 2003EP-00006426.
XX PR 25-MAR-2002; 2002DE-01013201.
XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX PI Mueller R, Thalhofer J, Geipel F, Hoelke W, Kirschbaum T;
XX DR WPI; 2003-769844/73.
XX PT New mutants of alkaline phosphatase (AP) where enzymatic activity is
PT reduced a hundred fold, are useful as blocking reagents in AP-based
PT immunoassays.
XX PS Claim 8; SEQ ID NO 9; 35bp; German.
XX CC This invention describes a novel mutant of eukaryotic alkaline
CC phosphatase where the wild-type sequence is at least 77% homologous with
CC ADE53385 and where the alkaline phosphatase activity is reduced by at
CC least 100-fold, relative to the wild type. The mutations described are
CC Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly,
CC Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for
CC Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp.
CC Conjugates of the novel mutant with antibodies are useful in alkaline
CC phosphatase-based immunoassays for antigens as interference suppressors,
CC i.e. they prevent non-specific binding of active alkaline phosphatase-
CC based conjugates to vessel walls or first antibodies, a phenomenon that
CC may result in false positive results. The mutants have almost the same
CC tertiary and quaternary structures as wild-type alkaline phosphatase, so

CC are very specific interference suppressors. This sequence encodes a
CC variant bovine alkaline phosphatase which contains an G322F mutation and
CC an E30R site described in the disclosure of the invention.
XX
SQ Sequence 1476 BP; 387 A; 223 C; 344 G; 522 T; 0 U; 0 Other;
Query Match 99.8%; Score 1472.8; DB 10; Length 1476;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAATCTTGATTCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
Db 1 GAATCTTGATTCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
QY 61 GCTTGGATGTGCTAAGAGTTGCAACCAATTCAACTGCTGCTAAGATGTTATTG 120
Db 61 GCTTGGATGTGCTAAGAGTTGCAACCAATTCAACTGCTGCTAAGATGTTATTG 120
QY 121 TTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
Db 121 TTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
QY 121 TTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
Db 121 TTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
QY 181 ATGAATGTAAGTTGGGTCCAGAAATCCATTGGCTATGATCAATTTCCATACGTTGCT 240
Db 181 ATGAATGTAAGTTGGGTCCAGAAATCCATTGGCTATGATCAATTTCCATACGTTGCT 240
QY 241 TTGCTAAGACTTACAATGTGATAGACAAGTTCCAGATTCTGCTGCTACTGCTACTGCT 300
Db 241 TTGCTAAGACTTACAATGTGATAGACAAGTTCCAGATTCTGCTGCTACTGCTACTGCT 300
QY 301 TACTTGTGTGTTAAGGGTAATTACAGAACTATTGGTGTTCGTGCTGCTAGATAC 360
Db 301 TACTTGTGTGTTAAGGGTAATTACAGAACTATTGGTGTTCGTGCTGCTAGATAC 360
QY 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAAAGACTAAGAAG 420
Db 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAAAGACTAAGAAG 420
QY 421 GCTGTAAGGCTGTGTTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGGT 480
Db 421 GCTGTAAGGCTGTGTTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGGT 480
QY 481 GCTTACGCTACTACTGTTAATAGAAATGCTACTGATGCTGATTTGCCAGCTGATGCT 540
Db 481 GCTTACGCTACTACTGTTAATAGAAATGCTACTGATGCTGATTTGCCAGCTGATGCT 540
QY 541 CAAAAGATGTTGTCAAGATATTGCTCAATTGCTTTTACAAATATGATATTGATGTT 600
Db 541 CAAAAGATGTTGTCAAGATATTGCTCAATTGCTTTTACAAATATGATATTGATGTT 600
QY 601 ATTTGGGTGCTAGATGTATGTTCCAGAAAGTACTCCAGATCCAGAAATACCCA 660
Db 601 ATTTGGGTGCTAGATGTATGTTCCAGAAAGTACTCCAGATCCAGAAATACCCA 660
QY 661 GATGATGCTTCTGTTAATGTTAGTAAGCAAAATTTGTTCAAGAATGGCAA 720
Db 661 GATGATGCTTCTGTTAATGTTAGTAAGCAAAATTTGTTCAAGAATGGCAA 720
QY 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAATAGAACTGCTTTGTTCAAGCTGCTGAT 780
Db 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAATAGAACTGCTTTGTTCAAGCTGCTGAT 780
QY 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGAACCAAGCTGATATGAATATATGTT 840
Db 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGAACCAAGCTGATATGAATATATGTT 840
QY 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGCAGATT 900
Db 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGCAGATT 900
QY 901 TTGCTAGAAATCCAAGAGTTTCTGTTGTTGTTGAAGGTGATGAATGATCATGAT 960
Db 901 TTGCTAGAAATCCAAGAGTTTCTGTTGTTGTTGAAGGTGATGAATGATCATGAT 960

QY 961 CATCATGATGGTAAGGCTTATATGCTTGAAGCTATATATGTTTGATATGCTATT 1020
Db 961 CATCATGATTTTAAGGCTTATATGCTTGAAGCTATATATGTTTGATATGCTATT 1020
QY 1021 GCTAAGGCTAATGAATGACTTCTGAATGGAATCTTTGATTTGGTTACTGCTGATCAT 1080
Db 1021 GCTAAGGCTAATGAATGACTTCTGAATGGAATCTTTGATTTGGTTACTGCTGATCAT 1080
QY 1081 AGTCATGTTTTTCTTTGGTGTTACACTTTGAGAGGTACTCTTAATTTTGGTTGGCT 1140
Db 1081 AGTCATGTTTTTCTTTGGTGTTACACTTTGAGAGGTACTCTTAATTTTGGTTGGCT 1140
QY 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTAACACTTCTATTTTGTATGGTAATGGTCCAGGT 1200
Db 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTAACACTTCTATTTTGTATGGTAATGGTCCAGGT 1200
QY 1201 TATGCTTTGGGTGGTGTTCTAGACCAAGTGTATGTAGTACTAGTGAAGAACCATCT 1260
Db 1201 TATGCTTTGGGTGGTGTTCTAGACCAAGTGTATGTAGTACTAGTGAAGAACCATCT 1260
QY 1261 TACAGACAACAAGCTGCTGTTCCATTTGGCTAGTGAACACTCATGTGGTGAAGATGTTGCT 1320
Db 1261 TACAGACAACAAGCTGCTGTTCCATTTGGCTAGTGAACACTCATGTGGTGAAGATGTTGCT 1320
QY 1321 GTTTTGTAGAGGTCACACAGCTCATTTGTTTCATGTGTGTCAAGAAAGAACTTTTGT 1380
Db 1321 GTTTTGTAGAGGTCACACAGCTCATTTGTTTCATGTGTGTCAAGAAAGAACTTTTGT 1380
QY 1381 GCTCATATTTATGGCTTTTGCTGTTGTGTGAACCATACACTGATTTGTAATTTGCCAGCT 1440
Db 1381 GCTCATATTTATGGCTTTTGCTGTTGTGTGAACCATACACTGATTTGTAATTTGCCAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTATTCAGATTTAAGGTACC 1476
Db 1441 CCAGCTACTGCTACTAGTATTCAGATTTAAGGTACC 1476

RESULT 5
ADE53393
ID ADE53393 standard; DNA; 1476 BP.
XX ADE53393;
AC ADE53393;
XX 29-JAN-2004 (first entry)
DT 29-JAN-2004 (first entry)
XX Bovine alkaline phosphatase DNA encoding H320N/G322F.
DE alkaline phosphatase; mutation; immunoassay; antigen;
XX interference suppressor; bovine; ds; mutant.
KM Synthetic.
XX Bos taurus.
OS EP1348760-A2.
XX 01-OCT-2003.
PD 21-MAR-2003; 2003EP-00006426.
XX 25-MAR-2002; 2002DE-01013201.
PR (HOFF) ROCHE DIAGNOSTICS GMBH.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA Mueller R, Thalhofer J, Geipel F, Hoelke W, Kirschbaum T;
XX WPI; 2003-769844/73.
DR New mutants of alkaline phosphatase (AP) where enzymatic activity is
XX reduced a hundred fold, are useful as blocking reagents in AP-based
PT immunoassays.
XX

PS Claim 8; SEQ ID NO 10; 35bp; German.
XX This invention describes a novel mutant of eukaryotic alkaline
CC phosphatase where the wild-type sequence is at least 77% homologous with
CC ADE53385 and where the alkaline phosphatase activity is reduced by at
CC least 100-fold, relative to the wild type. The mutations described are
CC Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly,
CC Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for
CC Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp.
CC Conjugates of the novel mutant with antibodies are useful in alkaline
CC phosphatase-based immunoassays for antigens as interference suppressors,
CC i.e. they prevent non-specific binding of active alkaline phosphatase-
CC based conjugates to vessel walls or first antibodies, a phenomenon that
CC may result in false positive results. The mutants have almost the same
CC tertiary and quaternary structures as wild-type alkaline phosphatase, so
CC are very specific interference suppressors. This sequence encodes a
CC variant bovine alkaline phosphatase which contains an H320N/G322F
CC mutation and an EcoRI site described in the disclosure of the invention.
XX
SQ Sequence 1476 BP; 388 A; 222 C; 344 G; 522 T; 0 U; 0 Other;

Query Match 99.7%; Score 1471.2; DB 10; Length 1476;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTTCTTGATTTCCAGCTGAAGAAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
Db 1 GAATTTCTTGATTTCCAGCTGAAGAAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
QY 61 GCTTTGATGTTGCTAAGAAAGTTGCCAACCAATTCAACTGCTGCTAAGAAATGTTATTTTG 120
Db 61 GCTTTGATGTTGCTAAGAAAGTTGCCAACCAATTCAACTGCTGCTAAGAAATGTTATTTTG 120
QY 121 TTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGGTCAA 180
Db 121 TTTTGGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGGTCAA 180
QY 181 ATGAATGTAAGTTGGGTCAGAAACTCCATTTGGCTATGATCATATTTCCATACGTTGCT 240
Db 181 ATGAATGTAAGTTGGGTCAGAAACTCCATTTGGCTATGATCATATTTCCATACGTTGCT 240
QY 241 TTGCTAAGACTTACAATGTTGATAGACAAGTCCAGATTTCTGCTGCTACTGCTACTGCT 300
Db 241 TTGCTAAGACTTACAATGTTGATAGACAAGTCCAGATTTCTGCTGCTACTGCTACTGCT 300
QY 301 TACTTGTGTGTTAAGGGTAATTACAGAACTAATTTGGTCTTCTGCTGCTGCTAGATAC 360
Db 301 TACTTGTGTGTTAAGGGTAATTACAGAACTAATTTGGTCTTCTGCTGCTGCTAGATAC 360
QY 361 AATCAATGTAATACTAGAGGTAATGAAGTACTTCTGTTATTAATAGACTAAGAAG 420
Db 361 AATCAATGTAATACTAGAGGTAATGAAGTACTTCTGTTATTAATAGACTAAGAAG 420
QY 421 GCTGTAAGGCTGTGGTGTGTTTACTACTAGAGTTCACACATGCTTCCAGCTGGT 480
Db 421 GCTGTAAGGCTGTGGTGTGTTTACTACTAGAGTTCACACATGCTTCCAGCTGGT 480
QY 481 GCTTACGCTCATACTGTTAATAGAAATTTGTTACTGCTGATGCTGATTTGCCAGCTGATGCT 540
Db 481 GCTTACGCTCATACTGTTAATAGAAATTTGTTACTGCTGATGCTGATTTGCCAGCTGATGCT 540
QY 541 CAAAAGAATGTTGTCAGATATTTGCTGCTCAATTTGTTTACAATATGATATTGATGTT 600
Db 541 CAAAAGAATGTTGTCAGATATTTGCTGCTCAATTTGTTTACAATATGATATTGATGTT 600
QY 601 ATTTTGGGTGTTGTAAGATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCCA 660
Db 601 ATTTTGGGTGTTGTAAGATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCCA 660
QY 661 GATGATGCTTCTGTTAATGTTGTTAGAAAGATTAAGCAAAATTTGTTCAAGAATGGCAA 720
Db 661 GATGATGCTTCTGTTAATGTTGTTAGAAAGATTAAGCAAAATTTGTTCAAGAATGGCAA 720

QY 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780
Db 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780
QY 781 GATTCTAGTGTACTCATTTGATGGGTTTGTTGAACCAAGCTGATATGAAGTATATGTT 840
Db 781 GATTCTAGTGTACTCATTTGATGGGTTTGTTGAACCAAGCTGATATGAAGTATATGTT 840
QY 841 CAACAAGATCACTAAGGATCCAAGTTGGCTGAATGACTGAAGCTGCTTTGCAAGTT 900
Db 841 CAACAAGATCACTAAGGATCCAAGTTGGCTGAATGACTGAAGCTGCTTTGCAAGTT 900
QY 901 TTGCTAGAAATCCAAGAGGTTTACTTGTGTTGTTGAAGGTGTTGAATGATCATGCT 960
Db 901 TTGCTAGAAATCCAAGAGGTTTACTTGTGTTGTTGAAGGTGTTGAATGATCATGCT 960
QY 961 CATCATGATGGTAAGGCTTATATGGCTTTGACTGAAGCTATATGTTGATTAATGCTATT 1020
Db 961 CATATGATTTTAAGGCTTATATGGCTTTGACTGAAGCTATATGTTGATTAATGCTATT 1020
QY 1021 GCTAAGGCTAATGAATGACTTCTGAATGGAATCTTTGATTTGGTTACTGCTGATCAT 1080
Db 1021 GCTAAGGCTAATGAATGACTTCTGAATGGAATCTTTGATTTGGTTACTGCTGATCAT 1080
QY 1081 AGTCATGTTTTTTCTTTGGTGTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
Db 1081 AGTCATGTTTTTTCTTTGGTGTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
QY 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTGTTATGGTAATGGTCCAGGT 1200
Db 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTGTTATGGTAATGGTCCAGGT 1200
QY 1201 TATGCTTTGGTGGTGTCTTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCT 1260
Db 1201 TATGCTTTGGTGGTGTCTTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCT 1260
QY 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTTGGTGAAGATGTTGCT 1320
Db 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTTGGTGAAGATGTTGCT 1320
QY 1321 GTTTTGGCTAGAGTCCACAAGCTCATTTGGTTCAATGTTCAAGAGAACTTTTGT 1380
Db 1321 GTTTTGGCTAGAGTCCACAAGCTCATTTGGTTCAATGTTCAAGAGAACTTTTGT 1380
QY 1381 GCTCATATTTATGGCTTTTGGCTGTTGTTGAACCATACACTGATTTGTAATTTGCCAGCT 1440
Db 1381 GCTCATATTTATGGCTTTTGGCTGTTGTTGTTGAACCATACACTGATTTGTAATTTGCCAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTATTCAGATTTAAGGTACC 1476
Db 1441 CCAGCTACTGCTACTAGTATTCAGATTTAAGGTACC 1476

RESULT 6
ADE53394
ID ADE53394 standard; DNA; 1476 BP.
XX ADE53394;
AC ADE53394;
XX 29-JAN-2004 (first entry)
DT 29-JAN-2004 (first entry)
XX Bovine alkaline phosphatase DNA encoding S92A/H320N/G322F.
DE Bovine alkaline phosphatase DNA encoding S92A/H320N/G322F.
XX alkaline phosphatase; mutation; immunoassay; antigen;
KW interference suppressor; bovine; ds; mutant.
XX
OS Synthetic.
OS Bos taurus.
XX
PN EP1348760-A2.
XX
PD 01-OCT-2003.
XX

PF 21-MAR-2003; 2003EP-00006426.
XX
PR 25-MAR-2002; 2002DE-01013201.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Mueller R, Thalhofer J, Geipel F, Hoelke W, Kirschbaum T;
XX
DR WPI; 2003-769844/73.
XX
PT New mutants of alkaline phosphatase (AP) where enzymatic activity is
PT reduced a hundred fold, are useful as blocking reagents in AP-based
PT immunoassays.
XX
PS Claim 8; SEQ ID NO 11; 35pp; German.
XX
CC This invention describes a novel mutant of eukaryotic alkaline
CC phosphatase where the wild-type sequence is at least 77% homologous with
CC ADE53385 and where the alkaline phosphatase activity is reduced by at
CC least 100-fold, relative to the wild type. The mutations described are
CC Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly,
CC Val or Leu; Glu311 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for
CC Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp.
CC Conjugates of the novel mutant with antibodies are useful in alkaline
CC phosphatase-based immunoassays for antigens as interference suppressors,
CC i.e. they prevent non-specific binding of active alkaline phosphatase-
CC based conjugates to vessel walls or first antibodies, a phenomenon that
CC may result in false positive results. The mutants have almost the same
CC tertiary and quaternary structures as wild-type alkaline phosphatase, so
CC are very specific interference suppressors. This sequence encodes a
CC variant bovine alkaline phosphatase which contains an S92A/H320N/G322F
CC mutation and an EcoRI site described in the disclosure of the invention.
XX
SQ Sequence 1476 BP; 388 A; 222 C; 345 G; 521 T; 0 U; 0 Other;

Query Match 99.6%; Score 1469.6; DB 10; Length 1476;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAATCTTGATTTCCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
Db 1 GAATCTTGATTTCCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
QY 61 GCTTTGATGTTGCTAAGAAGTTGCAACCAATTCAAACCTGCTGTAAGAATGTTATT 120
Db 61 GCTTTGATGTTGCTAAGAAGTTGCAACCAATTCAAACCTGCTGTAAGAATGTTATT 120
QY 121 TTTTGGGATGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
Db 121 TTTTGGGATGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
QY 181 ATGAATGGTAAGTTGGTCCAGAACTCCATTGGCTATGGATCAATTTCCATACGTTGCT 240
Db 181 ATGAATGGTAAGTTGGTCCAGAACTCCATTGGCTATGGATCAATTTCCATACGTTGCT 240
QY 241 TTGTTAAGACTTTACAATGTTGATAGACAAGTTCCAGATGCTGCTGTAAGTCTGCT 300
Db 241 TTGTTAAGACTTTACAATGTTGATAGACAAGTTCCAGATGCTGCTGTAAGTCTGCT 300
QY 301 TACTTGTGTGTTAAGGGTAATTAACAAGACTATTGGTGTCTGCTGCTAGATAC 360
Db 301 TACTTGTGTGTTAAGGGTAATTAACAAGACTATTGGTGTCTGCTGCTAGATAC 360
QY 361 AATCAATGTAATACTACTAGAGGTAAAGTACTTCTGTTAATAAGAGCTAAGAAG 420
Db 361 AATCAATGTAATACTACTAGAGGTAAAGTACTTCTGTTAATAAGAGCTAAGAAG 420
QY 421 GCTGTAAGGCTGTTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
Db 421 GCTGTAAGGCTGTTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
QY 481 GCTTACGCTCACTGTTAATAGAAATGGTACTGATGCTGATTTGCCAGCTGATGCT 540

Db 481 GCTTACGCTCATACTGTTAATAGAAATGGTACTCTGATGCTGATTTGGCAGCTGATGCT 540
QY 541 CAAAAGAAATGGTGTGCAAGATATTGCTGCTCAATTTGGTTACAAATATGGATATTGATGTT 600
Db 541 CAAAAGAAATGGTGTGCAAGATATTGCTGCTCAATTTGGTTACAAATATGGATATTGATGTT 600
QY 601 ATTTGGGTGGTGTAGAAATGTACATGTTCCAGAAGGTACTCCAGATCCAGAATACCCA 660
Db 601 ATTTGGGTGGTGTAGAAATGTACATGTTCCAGAAGGTACTCCAGATCCAGAATACCCA 660
QY 661 GATGATGCTTCTGTTAATGTTAGTGAAGATTAAGCAAAATTGGTTCAAGAATGGCAA 720
Db 661 GATGATGCTTCTGTTAATGTTAGTGAAGATTAAGCAAAATTGGTTCAAGAATGGCAA 720
QY 721 GCTAAGCATCAAGGTGCTCAATATGTTTGGATAGAACTGCTTTGTCGAAGCTGCTGAT 780
Db 721 GCTAAGCATCAAGGTGCTCAATATGTTTGGATAGAACTGCTTTGTCGAAGCTGCTGAT 780
QY 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGTAACCAAGCTGATATGAAGTATATGTT 840
Db 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGTAACCAAGCTGATATGAAGTATATGTT 840
QY 841 CAACAAGATCATACTAAGGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCAAGTT 900
Db 841 CAACAAGATCATACTAAGGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCAAGTT 900
QY 901 TTGCTAGAAATCCAAAGAGTTTCTGTTGTTGTTGAAGGTGTTGAATGATCATGCT 960
Db 901 TTGCTAGAAATCCAAAGAGTTTCTGTTGTTGTTGAAGGTGTTGAATGATCATGCT 960
QY 961 CATCATGATGCTAAGGCTTATATAGGCTTTGACTGAAGCTATATGTTGATATGCTATT 1020
Db 961 CATATGATTTTAAAGCTTATATAGGCTTTGACTGAAGCTATATGTTGATATGCTATT 1020
QY 1021 GCTAAGGCTAATGAATTGACTTCTGAATTGGATACTTTGATTTGGTTACTGCTGATCAT 1080
Db 1021 GCTAAGGCTAATGAATTGACTTCTGAATTGGATACTTTGATTTGCTTACTGCTGATCAT 1080
QY 1081 AGTCATGTTTTTTCTTTTGGTGTTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
Db 1081 AGTCATGTTTTTTCTTTTGGTGTTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
QY 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGTTAGTGTCCAGGT 1200
Db 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGTTAGTGTCCAGGT 1200
QY 1201 TATGCTTTGGGTGGTGTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCT 1260
Db 1201 TATGCTTTGGGTGGTGTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCT 1260
QY 1261 TACAGACAACAAGCTGCTGTTCCATGGCTAGTGAAGTCAATGGTGTGAAGATGTGCT 1320
Db 1261 TACAGACAACAAGCTGCTGTTCCATGGCTAGTGAAGTCAATGGTGTGAAGATGTGCT 1320
QY 1321 GTTTTGCTAGAGGTCCACAAGCTCAATTGGTTCATGTTGTTCAAGAAAGAACTTTTGT 1380
Db 1321 GTTTTGCTAGAGGTCCACAAGCTCAATTGGTTCATGTTGTTCAAGAAAGAACTTTTGT 1380
QY 1381 GCTCATATTATGGCTTTTGTGCTGTTGTTGAACCATACACTGATTTGATTTGGCAGCT 1440
Db 1381 GCTCATATTATGGCTTTTGTGCTGTTGTTGAACCATACACTGATTTGATTTGGCAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTATTCCAGATTAAGGTACC 1476
Db 1441 CCAGCTACTGCTACTAGTATTCCAGATTAAGGTACC 1476

RESULT 7
ADI26549
ID ADI26549 standard; DNA; 1476 BP.
XX
AC ADI26549;

XX 22-APR-2004 (first entry)
DT Bovine b1APII DNA.
XX
DE alkaline phosphatase; resistance gene; zeomycin; G418, heat stability;
KW bovine; b1APII; yeast; gene; ds.
XX
OS Bos taurus.
XX
PN EP1176205-A2.
XX
PD 30-JAN-2002.
XX
PF 21-JUL-2001; 2001EP-00117822.
XX
PR 25-JUL-2000; 2000DE-01036491.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI Mueller R, Thalhofer J, Geipel F, Hoelke W, Glaser S, Eckstein H;
PI Kirschbaum T, Bommaritus B;
XX
DR WPI; 2002-173123/23.
XX
PT Preparing eukaryotic alkaline phosphatase, useful as diagnostic reagent
PT and for dephosphorylation, by recombinant expression in yeast selected
PT for high gene copy number.
XX
PS Claim 2; SEQ ID NO 1; 23pp; German.

This invention describes a novel method of preparing eukaryotic alkaline phosphatase in yeast cells, comprising cloning an alkaline phosphatase gene sequence into different vectors, transforming, and expressing and purifying. A first vector is used containing a resistance gene against a selection marker and transformants that have integrated resistance gene and alkaline phosphatase gene into the genome are selected by growth on medium containing a low concentration of selection marker. The gene copy number is increased by multiple transformation and multiple transformants selected on growth medium under high selection pressure. A second vector containing the alkaline phosphatase gene and a second resistance gene against a second marker is introduced, its copy number increased as for the first resistance gene and clones selected that have many copies of the alkaline phosphatase gene and of both resistance genes, integrated into the genome. The vectors used in the method are pHAP10-3 and pHAP10-3/9K. Preferred cells include methylotrophic yeast, particularly Pichia pastoris and Hansenula polymorpha and specifically P. pastoris X-33 transformed with pHAP10-3 and pHAP10-3/9K. The amino acid sequence of bovine alkaline phosphatase is known and, working back from this, an optimised codon sequence was designed. This was assembled conventionally from 28 synthetic oligonucleotides to give a sequence having EcoRI and Asp718 recognition sites at the ends to facilitate cloning. The alkaline markers are particularly zeomycin and G418, respectively. The alkaline phosphatase is used as diagnostic reagent, as part of a conjugate and for dephosphorylation of DNA. This method produces very active, glycosylated alkaline phosphatase with specific activity over 3000, preferably 10000, units/mg and heat stability comparable with that for commercial enzymes. The expression system is resistant and stable and provides high-level expression without any selection pressure. This sequence represents the bovine b1APII gene.

Seq Sequence 1476 BP; 337 A; 449 C; 441 G; 249 T; 0 U; 0 Other;
Query Match 57.3%; Score 845.6; DB 6; Length 1476;
Best Local Similarity 73.3%; Pred. No. 8.6e-193;
Matches 1082; Conservative 0; Mismatches 394; Indels 0; Gaps 0;
QY 1 GAATTCCTGATTCAGCTGTAAGAAAGAAATCCAGCTTTTGGATATAGACAAGCTGCTCAA 60
Db 1 GAATTCCTCATCCAGCTGAGAGAGAAACCCTTCCTTTGGAACCGCCAGGACGCCAG 60
QY 61 GCTTTGGATGTTGCTAAGAAAGTTGCCAACCAATTCAAACTGCTGCTAAGAAATGTTATT 120


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Db      61  GCCCTTGATGTAGCCAAGAGTGCAGCCGATCCAGACAGCTGCCAAGATGTCATCCTC
Qy      121  TTTTGGGTGATGTATGGGTGTTCCAACTGTACTCTACTAGAAATTTGAAGGTCAA
Db      121  TTTTGGGTGATGTATGGGTGTTCCAACTGTACTCTACTAGAAATTTGAAGGTCAA
Qy      181  ATGAATGGTAAGTTGGGTCCAGAACTCCATTGGCTATGGATCAATTTCCATACGTTGCT
Db      181  ATGAATGGCAAACTGGGACCTGAGACACCCCTGGCCATGGACCAAGTCCATACGTTGCT
Qy      241  TTGCTTAAGCTTACAATGTGATAGACAAGTTCCAGATTCTGCTGCTGCTACTGCT
Db      241  CTGTCCAAGACATACAACGTGACAGACAGGTGCCAGACGCGCAGGCACTGCCACTGCC
Qy      301  TACTGTGTGTGTTAAGGTAATTACAGAACTATTGGTGTCTGCTGCTAGATAC
Db      301  TACCTGTGTGGGTCAAGGGCACTACAGAACCATCGGTGTAGTGCAAGCCGCCGCTAC
Qy      361  AATCAATGTATACTACTAGAGTAATGAAGTTACTTCTGTATTATATAGACTAAGAG
Db      361  AATCAAGTCAACAACAACGACGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAAGAA
Qy      421  GCTGTAGGCTGTGTGGTGTGTACTACTACTAGAGTCAACATGCTTCTCCAGCTGGT
Db      421  GCAGGGAAGCCGTGGAGTGTGACCAACAGGGTGCAGCATGCTCCCAAGCCGGG
Qy      481  GCTTACGCTCATCTGTATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT
Db      481  GCCTACGCGCACACGCTGAACCGAACTGGTACTCAGACGCCGACCTGCTGCTGATGCA
Qy      541  CAAAAGATGGTTGTCAAGATATGCTGCTCAATTGGTTTACAATATGATATGATGTT
Db      541  CAGAAAGATGGCTGCCAGGACATCGCCGACAGCTGCTACAAACATGATATGACGTG
Qy      601  ATTTGGGTGTGTAGATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAAATACCA
Db      601  ATCCTGGGTGAGGCCGAATGTACATGTTTCTCGAGGGGACCCAGACCTCGAATACCA
Qy      661  GATGATGCTTCTGTATATGCTGTAGAAAGGTAAGCAAAATTGGTTCAAGAATGGCAA
Db      661  GATGATGCCAGTGTGAATGAGTCCGGAAGGCAAGAACCTGGTGCAGGAATGGCAG
Qy      721  GCTAAGCATCAAGGTGCTCATATATGTTGGAATAGAACTGCTTGTGCAAGCTGCTGAT
Db      721  GCCAAGCACCAAGGAGCCAGTATGTGTGAACCGCACTGCGCTCTTCAGGCGCGCAT
Qy      781  GATTCTAGTGTACTCATTTGATGGGTTGTTGAACCAAGCTGATATGATATATGTT
Db      781  GACTCCAGTGTACACACCTCATGGGCTCTTTGAGCCGGCAGACATGATATATGTT
Qy      841  CAACAAGATCATATAAGGATCCAACTTGGCTGAATGACTGAAGCTGCTTGCAAGTT
Db      841  CAGCAAGACCAACAAGGACCCGACCTGGCGGAGATGACGAGGCGGCTGCAAGTG
Qy      901  TTGCTTAAAAATCCAAGAGGTTTCTTACTTGTGTTGTAAGGTGTAGAAATGATCATGCT
Db      901  CTGAGCAGGAACCCCGGGCTTCTACTCTTCTGTGAGGAGGCGGCATGTAACCAAGGT
Qy      961  CATCATGATGTGAAGCTTATATGCTTGAAGCTATATGTTGATTAATGCTATT
Db      961  CACCATGACGCGCAAGCTTATATGCACTGACTGAGCGCATCATGTTGACAAATGCCATC
Qy      1021  GCTAAGGCTAATGAATGACTTGAATGGAATCTTGAATTTGGTTACTGCTGATCAT
Db      1021  GCCAAGGCTAAGAGCTCACTAGCAACTGACAGCTGATCCTGTCTCACTGACAGACCAC
Qy      1081  AGTCATGTTTTTTCTTTGGTGTGTACACTTTGAGAGTACTTCTATTTTGGTTGGCT
Db      1081  TCCCATGTCTTCTTTTGGTGTGTACACTGCGTGGGACCTCCATTTTGGTCTGGCC
Qy      1141  CCAGGTAAGGCTTTGGATAGTAACTTACACTTCTATTTTGTATGTAATGCTCCAGGT

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Db      1141  CCGGCAAGGCTTAGACAGCAAGTCTTACACCTCCATCCTTATGSCAATGCCCCAGGC
Qy      1201  TATGCTTTGGGTGGTGTGTTCTAGACCAAGTGTAAATGTTAGTACTAGTGAAGAACCATCT
Db      1201  TATGCGCTTGGCGGGGCTCGAGGCCGATGTAAATGGCAGACAGAGAAACCTCA
Qy      1261  TACAGACAACAAGCTGCTGTTCCATGTGCTAGTGAAACTCATGGTGTGAAGATGTTGCT
Db      1261  TACCGCAGCAGCGCGCGTGCCTTGGCTAGCAGAACCCACGGGCGAAGACGTGGCG
Qy      1321  GTTTTGTAGAGGTCACAGCTCATTTGGTTCATGTTGTTCAAGAAACTTTTGT
Db      1321  GTGTTCCGCGAGGCCCCGACGCGCATGTTGCACGCGGTGCAGAGAGAACCTTGTG
Qy      1381  GCTCATATATGCTTTGCTGCTGTTGTTGAACCATACACTGATTTGTAATTTGCCAGCT
Db      1381  GCGCACATCATGGCTTTGCGGGCTGCTGAGACCCCTACACCGACTGCAATCTGCCAGCC
Qy      1441  CCAGTACTGCTACTAGTATTCCAGATTAAAGTACC
Db      1441  CCGGCAAGGCTTACAGCAAGTCTTACACCTCCATCCTTATGSCAATGCCCCAGGC

RESULT 8
ADE53384
ID      ADE53384 standard; DNA; 1464 BP.
XX
AC      ADE53384;
XX
DT      29-JAN-2004 (first entry)
XX
DE      Bovine alkaline phosphatase DNA.
XX
KW      alkaline phosphatase; mutation; immunoassay; antigen;
XX      interference suppressor; bovine; ds; gene.
XX
OS      Bos taurus.
XX
FH      Key
FT      CDS
FT      1..1464
FT      /*tag= a
FT      /product= "alkaline phosphatase"
FT      /partial
FT      /note= "no start codon given"
XX
PN      EP1348760-A2.
XX
PD      01-OCT-2003.
XX
PF      21-MAR-2003; 2003EB-00006426.
XX
PR      25-MAR-2002; 2002DE-01013201.
XX
PA      (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI      Mueller R, Thalhofer J, Geipel F, Hoelke W, Kirschbaum T;
XX
DR      MPI; 2003-769844/73.
XX      P-PSDB; ADE53385.
XX
PT      New mutants of alkaline phosphatase (AP) where enzymatic activity is
PT      reduced a hundred fold, are useful as blocking reagents in AP-based
PT      immunoassays.
XX
PS      Disclosure; SEQ ID NO 1; 35pp; German.
XX
CC      This invention describes a novel mutant of eukaryotic alkaline
CC      phosphatase where the wild-type sequence is at least 77% homologous with
CC      ADE53385 and where the alkaline phosphatase activity is reduced by at
CC      least 100-fold, relative to the wild type. The mutations described are
CC      Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly,
CC      Val or Leu; Glu11 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for

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CC Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp.
CC Conjugates of the novel mutant with antibodies are useful in alkaline
CC phosphatase-based immunoassays for antigens as interference suppressors,
CC i.e. they prevent non-specific binding of active alkaline phosphatase-
CC based conjugates to vessel walls or first antibodies, a phenomenon that
CC may result in false positive results. The mutants have almost the same
CC tertiary and quaternary structures as wild-type alkaline phosphatase, so
CC are very specific interference suppressors. This sequence encodes the
CC wild-type bovine alkaline phosphatase described in the disclosure of the
CC invention.

XX Sequence 1464 BP; 334 A; 446 C; 438 G; 246 T; 0 U; 0 Other;

Query Match 56.6%; Score 834.8; DB 10; Length 1464;
Best Local Similarity 73.2%; Pred. No. 3.4e-190;
Matches 1070; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

QY 8 TGATTCGAGCTGAAGAGAAAATCCAGCTTTTGGATAGACAGCTGCTCAAGCTTTGG 67
DB 2 TCATCCCACTGAGGAGGAAAAACCCGCTTCTGGAACCCGCGAGGAGCCGAGCCCTTG 61
QY 68 ATGTTGCTAAGAAGTTGCAACCAATTCAAACTGCTGTAAGATGTTATTTTGGT 127
DB 62 ATGTAGCCCAAGAAGTTGCAAGCCGATTCAGACAGCTGCCAAGATGTCTCTTTGG 121
QY 128 GTGATGATGGGTGTTCCAACTGTTACTGCTACTAGAATTTGAAGGGTCAATGAATG 187
DB 122 GGGATGGGATGGGGGTGCTTACGGTGAACAGCCACTCGATCTTAAAGGGGCAGATGAATG 181
QY 188 GTAAGTTGGGTCCAGAAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGTCTA 247
DB 182 GCAAACTGGGACCTGAGACACACCCTGGCCATGGACCAAGTCCCATACGTGGCTCTGTCCA 241
QY 248 AGACTTACAATGTTGATAGACAAAGTTCCAGATTCTGCTGTACTGCTACTGCTTACTTGT 307
DB 242 AGACATACAACGTGACACAGAGTGCACAGACGCGAGGCACTGCCACTGCCTACCTGT 301
QY 308 GTGGTGTAAAGGTAAATTACAGAACTATTGGTCTTCTGCTGCTGCTAGATACAATCAAT 367
DB 302 GTGGGGTCAAGGGCACTACAGAACCATCGGTGTAAGTCAAGCCGCCGCTACAATCAGT 361
QY 368 GTAATACTACTAGAGTAATGAAGTTACTTCTGTTATTATAGAGCTAAGAAAGGCTGTA 427
DB 362 GCAACACGACACGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAAGAACAGGGA 421
QY 428 AGGCTGTGGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTGTACG 487
DB 422 AGGCCGTGGGAGTGTGACCAACCAAGGGTGCAGCATGCTTCCCCAGCCGGGGCTTACG 481
QY 488 CTGATACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAA 547
DB 482 CGCACACGGTGAACCGAACTGTACTCAGACGCCGACCTGCTGATGACACAGAA 541
QY 548 ATGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGATATTGATTTTGG 607
DB 542 ATGGCTGCCAGACATCGCCGACAGCTGTCTACAACATGATATTGACGTGATCCTGG 601
QY 608 GTGGTGTAGAAATGATCATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCCAGATGATG 667
DB 602 GTGGAGGCCGGAATGTACATGTTTCTGAGGGGAGCCCCAGACCTGAATACCCAGATGATG 661
QY 668 CTTCGTTAATGTTAGAAAGGATAAGCAAAATTTGGTTCAAGAATGGCAAGCTTAAGC 727
DB 662 CCAAGTGAATGAGTCCGGAAGGACAAAGCAAGAACCTGGTGCAGGAATGGCAGGCCAAGC 721
QY 728 ATCAAGGTGCTCAATATGTTGGAAATAGAACTGCTTTGTTGCAAGCTGCTGATGATCTA 787
DB 722 ACCAGGGAAGCCAGTATGTGGAACCGCACTGCGCTCTTCAGGGCGCGGATGACTCA 781
QY 788 GTGTACTCATTTGATGGGTTGTTGAACCAAGCTGATATGAGTATAATGTTCAACAG 847
DB 782 GTGTAAACACCTCATGGGCTCTTTGAGCCGCGAGACATGAAGTATAATGTTCAAG 841

QY 848 ATCATACTAAGATCCAACTTTGGCTGAATAGTACTGAAGCTGTTGCAAGTTTGTCTA 907
DB 842 ACCACACCAAGAGACCCGACCTGGCGGAGATGACGAGGCGGCCCTGCAAGTGTGACGA 901
QY 908 GAAATCCAAGAGTTTCTTACTGTTTGTGGAAGGTGTAAGAAATGATCATGTGTCATG 967
DB 902 GGAACCCCCGGGCTTCACTCTTCTGAGGAGGAGCGGACATGACCAAGTCAACATG 961
QY 968 ATGTAAGGCTTATATGGCTTGAAGCTATATATTTGATATATGCTATGCTAAG 1027
DB 962 ACGCAAGCTTATATGGCACTGAGGCGATCATGTTTGACAAATGCCATCGCCAAG 1021
QY 1028 CTATGAATTGACTTCTGAATTGGATACTTGAATTTGGTTACTGCTGATCATAGTCATG 1087
DB 1022 CTAAAGAGCTCACTAGCGAACTGGACACAGCTGATCCTTGTCACTGACAGACCACTCCATG 1081
QY 1088 TTTTCTTTTGGTGTACACTTTGAGAGGTACTTATTTTGGTTTGGTTCAGGTA 1147
DB 1082 TCTTCTCTTTGGTGTACACACTGCGGTGGACCTTCATTTTGGTCTGGCCCCGCA 1141
QY 1148 AGGCTTTGATAGTAAGCTTACACTTCTATTTTGTATGTAATGTCAGAGTTAGCTT 1207
DB 1142 AGGCTTAGACAGCAAGTCTTACACTCCATCCTTATGGCAATGGCCAGGCTATGCGC 1201
QY 1208 TGGGTGTGTTCTTAGACAGATGTTAATGTAAGTCTAGTGAAGAACCATCTTACAGAC 1267
DB 1202 TTGGCGGGGCTCGAGGCCGATGTTAATGCGACGACAAAGCAAGCAAGCAAGCAAG 1261
QY 1268 AACAGCTGCTGTTCATTTGGCTAGTGAACCTCATGGTGTGAAGATGTTGCTTTTG 1327
DB 1262 AGCAGCGCGCGCTGCTGCTGCTAGCGAGACCCAGCGGGCGGAAGACGTGGCGGTTCG 1321
QY 1328 CTAGAGGTCCACAAGCTATTGGTTCATGTTGTTCAAGAAACTTTGTTGCTCAT 1387
DB 1322 CGGAGGCGCGCAGGCGCACTGTGTGACCGGCGTGCAGAGAGAGACCTTGTGGCGACA 1381
QY 1388 TTATGCTTTTGTGTTGTGTGAACCATATACATGATTTGTAATTTGCCAGCTCAGCTA 1447
DB 1382 TCATGGCTTTGCGGCTGTGTGAGCCCTACACGCACTGCAATCTGCCAGCCCCGCCA 1441
QY 1448 CTGCTACTAGTATTCAGATT 1469
DB 1442 CCGCCACCAAGCATCCCGCACTA 1463

RESULT 9
ABZ22773
ID ABZ22773 standard; DNA; 1650 BP.
XX
AC ABZ22773;
XX
DT 02-APR-2003 (first entry)
XX
DE Calf intestinal alkaline phosphatase DNA sequence SEQ ID NO:26.
XX
KW Recombination; mutagenesis; sarcosine oxidase; phosphatase; human;
KW human placental alkaline phosphatase; hpap; ciap; gene; ds;
KW calf intestinal alkaline phosphatase.
XX
OS Bos taurus.
XX
PN WO2003002736-A2.
XX
PD 09-JAN-2003.
XX
PF 26-JUN-2002; 2002WO-EP007060.
XX
PR 27-JUN-2001; 2001EP-00115424.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI Shao Z, Kratzsch P, Schmuck R, Von Der Eltz H, Kenkies J;

XX WPI; 2003-201503/19.
DR
XX
PT Forming a polynucleotide sequence for optimizing biomolecules and enzymes
PT by generating a nucleic acid fragment ladder, removing the chain-
PT terminating molecules and reassembling the polynucleotide.
XX
PS Example 2; Fig 5; 64pp; English.
XX
CC The present invention describes a method of forming a polynucleotide
CC sequence, comprising: (a) generating a nucleic acid fragment ladder by
CC nucleic acid synthesis; (b) removing the chain-terminating molecules or
CC changing them into non-terminating molecules; and (c) reassembling the
CC polynucleotide. Also described is a method for providing mutant
CC polypeptides or proteins. The methods of forming a polynucleotide
CC sequence and providing mutant polypeptides or proteins are useful for
CC optimising biomolecules and enzymes. The present sequence represents a
CC calf intestinal alkaline phosphatase (ciap) DNA sequence, which is used
CC in an example from the present invention for the recombination of human
CC placental alkaline phosphatase (hnap) and ciap genes
XX
SQ Sequence 1650 BP; 382 A; 495 C; 483 G; 290 T; 0 U; 0 Other;

Query Match: 56.3%; Score 831.6; DB 8; Length 1650;
Best Local Similarity 73.1%; Pred. No. 2e-189;
Matches 1068; Conservative 0; Mismatches 394; Indels 0; Gaps 0;

QY 9 GATTCAGCTGAGAGAAGAAATCCAGCTTTTGAATAGACAAGCTGCTCAAGCTTTGA 68
DB 158 GATCCAGCTGAGAGAAACCCCGCTTCTGGAACCGCAGCAGCCAGCCCTTGA 217
QY 69 TGTGCTAAGAGTTGCCAACCAATTCAACTGCTGCTAAGAATGTTATTTTGGG 128
DB 218 TGTAGCCAAGAGTTGCCAGCCGATCCAGACAGCTGCCAAGATGTCATCTCTTGGG 277
QY 129 TGATGGTATGGGTTCCTCACTGTACTGTACTAGAAATTTGAAGGGTCAATGAATGG 188
DB 278 GGATGGGATGGGGTGCTTACCGGTGACAGCCACTCGGATCCTAAGGGGCGAGATGAATGG 337
QY 189 TAAGTTGGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTAA 248
DB 338 CAACTGGGACTGAGACACCCCTGGCCATGACAGTTCCTATGCTGCTCTGCTCAA 397
QY 249 GACTTACAATGTGATAGACAAGTTCCAGATTTGCTGTGCTGCTACTGCTTACTTGTG 308
DB 398 GACATACAACGTGGAAGACAGAGTGCAGACGCGCAGCACTGCGCTTAACTGCTG 457
QY 309 TGGTGAAGGTAATTACAGAACTATTGGTCTCTGCTGCTGCTAGATACAATCAATG 368
DB 458 TGGGCTCAAGGGAATACAGAACCATCGGTGAAGTGACAGCCCGCTTACAATCAGTG 517
QY 369 TAATACTACTAGAGTAATGAAGTACTCTGTTATTAATAGAGCTAGAGAGCTGTTAA 428
DB 518 CAACACGACACGTGGGAATGAGGTCACTGTGTATCAACCGGGCCAAAGAGCAGGGAA 577
QY 429 GGCTGTTGGTGTGTACTACTACTAGATTCAACATGCTTCTCAGCTGCTTACGC 488
DB 578 GGCCGTGGAGTGTGACCAACCAAGGTGACATGCTCCCGAGCCGGGCTTACGC 637
QY 489 TCATACTGTAAAGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
DB 638 GCACACGCTGAACCGAAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 697
QY 549 TGGTGTCAAGATATGCTGCTCAATGGTTTACAATATGATATGATATGATATTTGGG 608
DB 698 TGGCTGCCAGACATCGCCGACACAGCTGCTTACACATGATATGATGATCTCTGGG 757
QY 609 TGGTGTAGATGATCATGTTTCCAGAGGTTCTCCAGATCCAGAAATCCAGATGATGC 668
DB 758 TGGAGGCCGAATGATCATGTTTCTGAGGGGACCCCAAGACCTGAATACCCAGATGATGC 817
QY 669 TTCTGTTAATGGTGTGAAGAGTAAGCAAAATTTGTTCAAGAAATGGCAAGCTTAAGCA 728

DB 818 CAGTGTGAATGAGTCCGGAGGACAGCAAGAACTGTGTGACGAATGGCAGCCAAAGCA 877
QY 729 TCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGATGATTTAG 788
DB 878 CCAGGAGCCAGATATGTGTGAACCGCACTGCGCTCTTACGGCGCGATGACTCCAG 937
QY 789 TGTACTGATTTGATGGGTTGTTGAACCAAGCTGATATGAAGTAATGTTCAACAAGA 848
DB 938 TGTACACACCTCATGGGCTCTTGAGCCGGCAGACATGAATGTAATGTTACGAAGA 997
QY 849 TCATACTAAGATCCCACTTTGGCTGAATAGACTGAAGCTGCTTGCAAGTTTGTCTAG 908
DB 998 CCACACCAAGAACCCGACCTGCGGAGATGACGGAGCGGCCCTGCAAGTGTGAGCAG 1057
QY 909 AAATCCAAGAGTTTCTTACTGTTGTTGAAGGTGTGAATGATGATGATCATCATGA 968
DB 1058 GAACCCCGGGGCTTCTACCTCTTGTGAGGAGGCCGCAATGACCAAGGTACCATGA 1117
QY 969 TGGTAAGCTTATATGCTTTGATGAGCTATTAATGTTGATTAATGCTATGCTAAGGC 1028
DB 1118 CGCAAGCTTATATGCACTGAGGCGATCATGTTGACAAATGCCATGCGCAAGGC 1177
QY 1029 TAATGAATGACTTCTGAATTTGATTTGATTTGTTACTGCTGATCATAGTATGT 1088
DB 1178 TAACGAGCTCACTAGCGAAGTGAACGCTGATCTTGTCACTGACAGACCACTCCATGT 1237
QY 1089 TTTTCTTTTGGTGTGTACACTTTGAGAGTACTTCTATTTTGGTTGGCTCCAGGTAA 1148
DB 1238 CTCTCTCTTTGGTGTGTACACACTGCTGGGACCTCCATTTTGGTCTGCCCCGCA 1297
QY 1149 GGCTTGAATAGTAAGTCTTACACTTCTATTTGTATGTAATGTTCCAGGTTATGCTTT 1208
DB 1298 GGCTTGAAGCAAGTCTTACACTTCTATTTGTATGTAATGTTCCAGGTTATGCTTT 1357
QY 1209 GGCTGTTGTTCTAGACCAAGATTTAATGTAATGTAATGTAATGTAATGTAATGTA 1268
DB 1358 TGGCGGGGCTGAGGCCGATGTTAATGAGCAGACCAAGCGAGAACCTTCTGACCGCA 1417
QY 1269 ACAAGCTGCTTCCATTTGCTAGTGAACCTCATGTTGTTGAAGTGTGCTGTTTGGC 1328
DB 1418 GCAGGCGGCGTCCCTGCTAGCGAGACCCAGGGGGAAGCGTGGCTGTTGCG 1477
QY 1329 TAGAGTCCACAAGCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1388
DB 1478 GCGAGGCCCGCAGCGCACCTGTTGCAAGCGGCTGCAAGAGAACCTTCTGCGGCACAT 1537
QY 1389 TATGGCTTTTCTGCTGTTGTTGTAACCATACACTGATTTGTAATTTGCCAGCTCAC 1448
DB 1538 CATGGCTTTTGGGCTGCGTGAAGCCTTACACCGAAGTCAATCTGCAAGCCCTCCAC 1597
QY 1449 TGCTACTAGTATTCAGATTAA 1470
DB 1598 CGCCACCAAGCATCCCGACTGA 1619

RESULT 10
AAK51495
ID AAK51495 standard; cDNA; 2523 BP.
XX
AC AAK51495;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 40.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.

XX 09-AUG-2001.
PD
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR P-PSDB; AAM78362.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 1; Page 603-606; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 2523 BP, 521 A; 856 C; 713 G; 433 T; 0 U; 0 Other;

Query Match 41.7%; Score 616; DB 4; Length 2523;
Best Local Similarity 64.2%; Pred. No. 1.4e-137;
Matches 925; Conservative 0; Mismatches 515; Indels 0; Gaps 0;

QY 6 CTTGATTCAGCTGAGAGAAGAAATCCAGCTTTTGAATAGACAAGCTGCTCAAGCTTT 65
DB 107 CGTCATCCCAAGCTGAGAGAGAACCCGGCTTCTGAAACGCCAGGACGCTGAGGCCCT 166
QY 66 GGATGTTGCTAAGAAGTTGCAACCAATTCAACTGCTGCTAAGAATGTTATTTGTTT 125
DB 167 GGATGCTGCCAAGAAGCTGCAGCCCATCCAGAAGTCCGCAAGAACTCATCTTCT 226
QY 126 GGGTGATGCTATGGGTGTTCCAAGTCTTACTGCTACTAGAAATTTGAAGGGTCAAAATGAA 185
DB 227 GGGGATGGGTGGGGGTGCCCCAGGTGACAGACCAAGATCCTAAAGGGGACAGAGAA 286
QY 186 TGGTAAGTTGGGTCCAGAACTTCATTTGGCTATGGATCAATTTCCATACGTTGCTTGT 245
DB 287 TGGCAAACTGGGGCTGAGACGCCCTTGCCATGACCGCTTCCCATACCTGGCTGTCTC 346
QY 246 TAAAGCTTACAATGTTGATAGACAAGTTCAGATTCCTGCTGTAAGTCTACTGCTTAATT 305
DB 347 CAAGACATACATGTGACAGACAGGTGCAGACAGCGCACAGCCACGCGCTTAAGT 406
QY 306 GTGTGCTGTTAAGGTAATTAACAAGAACTATTGCTGTTCTGCTGCTAGATACAAATCA 365
DB 407 GTGCGGGGTCAAGGCCAACTTCCAGACCATCGCTTGAAGTGACAGCCCGCTTAAACA 466
QY 366 ATGTAATACTACTAGAGGTAATGAAGTACTTCTGTATTATAAGACTAAGAGCGCTGG 425

DB 467 GTGCAACACGACACGCGGCAATGAGGTCAATCTCCGTGATGAACCGGGCCAAAGACAGAG 526
QY 426 TAAAGCTGTTGGTGTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGTGCTTA 485
DB 527 AAAGTCAGTAGAGTGTGACCAACACACGCGGTGACACGCTCGCCAGCGGCACTTA 586
QY 486 CGCTCATCTGTTAATAGAAATTTGCTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAA 545
DB 587 CGCACACACAGTGAACCGCAACTGTGTAAGTGTGATGATGCTGCTGCTGAGCCGCCA 646
QY 546 GAATGTTGTCAAGATATGCTGCTCAATTGTTTACAATATGATATGATGTTATTTT 605
DB 647 GAGGGGGTGCCAGACATGCGCACTCAGCTCATCTCCAACATGACATTGACGTGATCCT 706
QY 606 GGGTGTGCTAGATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCAATGA 665
DB 707 TGGCGGAGGCGCGCAATACATGTTTCCCATGCGGAGCCCAAGACCTGAGTACCACTGA 766
QY 666 TGCTTCTGTTAATGCTGTGTTAGAAAGATAAGCAAAATTTGTTCAAGAATGCGAAGCTAA 725
DB 767 TGCCAGCCAGAAATGAATCAGGCTGACCGGAAGAACTGTGACGAATGCTGGCAAA 826
QY 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGTTGTTGCAAGCTGCTGATGATTC 785
DB 827 GCACCAAGGTGCTGTGATGTGTGAACCGCACTGAGCTCATGCAAGCGTCTCGACCA 886
QY 786 TAGTGTACTCATTTGATGAGGTTTGTGTTGAACCAAGCTGATATGAATATATGTTCAACA 845
DB 887 GTCTGTGACCCATCTCATGAGGCTCTTTGAGCCCGGAGACACGAATATGATCCACCG 946
QY 846 AGATCATACTAAGATCCAACTTTGCTGAATGAAGCTGCTTGAAGTTTGTGTC 905
DB 947 AGACCCACACACTGAGACCCCTCCCTGATGAGATGACAGAGCTGCCCTGCTGTAG 1006
QY 906 TAGAAATCCAAAGGTTTTTACTGTTGTTGTAAGGTGTAGATGATGATGTCATCA 965
DB 1007 CAGGAACCCCCCGGCTTCTACCTCTTTGTGAGAGGCGCGCCGATCGACCATGTCATCA 1066
QY 966 TGATGTAAGCTTATATGCTTTGACTGAGACTATATGTTGATATATGCTATTGCTAA 1025
DB 1067 TGAAGGTGTGCTTACCAAGGCACTCATGAGCGGCTCATGTTGACGACGCCATTGAGAG 1126
QY 1026 GGCTAATGAATGACTTCTGAATTGATGATCTTTGTTACTGCTGATCATAGTCA 1085
DB 1127 GGGGGGCAAGCTACCAAGAGAGAGACAGCTGACCTGTCACCGCTGACCACTCCA 1186
QY 1086 TGTTTTCTTTTGGTGTGTTACACTTGAAGGTACTTCTATTTTGGTTGGCTCCAGG 1145
DB 1187 TGTCTTCTCTTTGGTGTGTTACACTTGGGAGGAGCTCCATCTTGGGTTGGCCCCAG 1246
QY 1146 TAAAGCTTGAATGTAAGTCTTACACTTCTATTTGTATGTAATGTCAGGTTATGC 1205
DB 1247 CAAGGCTCAGGACAGCAAAAGCTTACAGTCCATCTGTACGGCAATGGCCCCGCTACGT 1306
QY 1206 TTTGGGTGTTGTTCTAGACCAGATGTTAAGTACTAGTGAAGAACCATCTTACAG 1265
DB 1307 GTTCAACTCAGGCGTGCACCAAGCTGATGAGAGCGAGCGGAGCCCCGATTACCA 1366
QY 1266 ACAACAAGCTGCTGTTCCATTTGGCTAGTGAACCTCATGCTGTGTAAGATGTTGCTGTTT 1325
DB 1367 GCAGAGCGCGCGGCTGCCCTGTGCTCCGAGAACCCAGGAGCGGAAGCTGGCGGTGT 1426
QY 1326 TGCTAGAGGTCCACAAGCTCATTTGCTTCATGTTGTTCAAGAGAAACTTTTGTGCTCA 1385
DB 1427 TGGCGCGGCGCGCAGCGCACCTGTGATGTGTGACAGAGAGAGCTTGTGAGCGCA 1486
QY 1386 TATTATGCTTTTGTGCTGTTGTGTGAACCATACACTGATGTAATTTGCCAGCTCCAGC 1445
DB 1487 TGTATGCTTGTGCTGCTGTGTGTGAGCCCTTACACGCGCTGCGACCTGGCGCTCCCGC 1546

ADN43057
ID ADN43057 standard; cDNA; 1702 BP.
XX
AC ADN43057;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human secreted protein SECP-43 cDNA.
XX
KW cytosolic; anorectic; immunosuppressive; gene therapy; SECP-antagonist;
KW SECP-agonist; secreted protein; SECP; autoimmune disorder; obesity;
KW cancer; human; SECP-43; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004037987-A2.
XX
PD 06-MAY-2004.
XX
PF 22-OCT-2003; 2003WO-US033491.
XX
PR 22-OCT-2002; 2002US-0420720P.
PR 07-NOV-2002; 2002US-0425207P.
PR 15-NOV-2002; 2002US-0426679P.
PR 19-NOV-2002; 2002US-0427871P.
PR 06-JAN-2003; 2003US-0438551P.
PR 17-JAN-2003; 2003US-0441144P.
PR 27-JAN-2003; 2003US-0443135P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Baughn MR, Becha SD, Bhatia UG, Blake JJ, Burrill JD, Chawla NK;
PI Chien D, Elliott VS, Emerling BM, Favero KD, Hafalia AJA;
PI Harmesen BW, Ho A, Ison CH, Khare R, Lee S, Lee SY, Lu DAM;
PI Marquis JP, Murage J, Nguyen DB, Ramkumar J, Richardson TW;
PI Swarnakar A, Tang TY, Tran UK, Wang JT, Yue H, Zheng W;
XX
DR MPI; 2004-365505/34.
DR P-PSDB; ADN42982.
XX
PT New human secreted protein (SECP) polypeptide, useful for preparing a
PT composition for treating a disease associated with decreased expression
PT or overexpression of functional SECP e.g., autoimmune disorders, obesity
PT or cancer.
XX
PS Claim 5; SEQ ID NO 118; 289pp; English.
XX
CC The invention describes an isolated human secreted protein (SECP)
CC polypeptide. Also described are: an isolated polynucleotide encoding the
CC polypeptide; a recombinant polynucleotide comprising a promoter sequence
CC operably linked to the polynucleotide; a cell transformed with the
CC recombinant polynucleotide; a transgenic organism comprising the
CC recombinant polynucleotide; a method of producing the polypeptide; an
CC isolated antibody that specifically binds to the polypeptide; a method of
CC detecting a target polynucleotide in a sample; a method for treating a
CC disease or condition associated with decreased expression or
CC overexpression of functional SECP; a method of screening a compound for
CC effectiveness as an agonist or antagonist of the polypeptide or in
CC altering expression of the target polynucleotide; a method of screening a
CC compound that specifically binds to, or that modulates the activity of,
CC the polypeptide; a method of assessing toxicity of a test compound; a
CC diagnostic test for a condition or disease associated with the expression
CC of SECP in a biological sample; a method of diagnosing a condition or
CC disease associated with the expression of SECP in a subject; a
CC composition comprising the antibody and a carrier, or the polypeptide, or
CC agonist or antagonist compound and an excipient a method of preparing a
CC polyclonal or monoclonal antibody; a method of detecting the polypeptide
CC in a sample; a method of purifying the polypeptide; a method of
CC generating an expression profile of a sample that contains
CC polynucleotides; and an array comprising different nucleotide molecules
CC affixed in distinct physical locations on a solid substrate, where at
CC least one of the nucleotide molecules comprises a first oligonucleotide
CC or polynucleotide sequence specifically hybridizable with at least 30

CC contiguous nucleotides of the target polynucleotide. The polypeptide is
CC useful for preparing a composition for diagnosing or treating a disease
CC or condition associated with decreased expression or overexpression of
CC functional SECP e.g. autoimmune disorders, obesity or cancer. This
CC sequence encodes a human secreted protein.
XX
SQ Sequence 1702 BP; 339 A; 562 C; 513 G; 288 T; 0 U; 0 Other;
Query Match 41.6%; Score 613.8; DB 12; Length 1702;
Best Local Similarity 64.3%; Pred. No. 4e-137;
Matches 921; Conservative 0; Mismatches 512; Indels 0; Gaps 0;
QY 13 CCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTTTGATGTT 72
DB 150 CCAGCTGAGGAGAGAACCCGGCTTCTGGAAACCGCCAGGAGCTGAGGCCCTGGATGCT 209
QY 73 GCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGAAATGTTATTTTGGGTGAT 132
DB 210 GCCAAGAGCTGCAGCCCATCCAGAGGTGCGCAAGAACCTCATCTCTTCTGGCGAT 269
QY 133 GGTATGGGTTCCTCAACTGTTACTGCTACTAGATTGGAATTTGAAGGGTCAATGATGTAAG 192
DB 270 GGGTTGGGGTGGCCACGCTGACAGCCACAGATCTTAAGGGGCAAGATGGCAAA 329
QY 193 TTGGGTCCAGAACTCCATTGGCTATGATGATCAATTTCCATACGTTGCTTGTCTAAGACT 252
DB 330 CTGGGGCTTGAGACGCCCCCTGGCCATGAGCCGCTTCCATACCTGGCTCTGTCCAAGACA 389
QY 253 TACAATGTTGATAGACAAGTCCAGATTCTGCTGCTACTGCTACTGCTTACTTGTGTGT 312
DB 390 TACAATGTGACAGACAGAGTGCCAGACAGCGCACAGCCACAGCCAGGCTTACTGTGCGGG 449
QY 313 GTTAAGGGTAATTACAGAACTATTTGTTCTGCTGCTGCTAGATACAATCAATGTAAT 372
DB 450 GTCAAGGCCAATTCCAGACCATCGGCTTGAGTGACGCCGCCGCTTTTAAACAGTGCAAC 509
QY 373 ACTACTAGAGTAAATGAAGTTACTTCTGTATTATAGAGCTAAGAGGCTGTAAGGCT 432
DB 510 ACGACACGGCGCAATGAGTCACTCCGATGATGAAGTGGCCAAAGCAAGAAAGTCA 569
QY 433 GTTGTGTTGTTACTACTACTAGATTCAACATGCTTCTCCAGCTGGTCTTACGCTCAT 492
DB 570 GTAGGAGTGTGACCAACCAACCGGGTGACGACAGCCCTCGCCAGCCGACCTACGACAC 629
QY 493 ACTGTTAATAGAAATTGCTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAAAGATGCT 552
DB 630 ACAGTGAACCGCAACTGTGTAATCTGATGCTGATGCTGCTCCTCAGCCGCCAGAGAGGGG 689
QY 553 TGTCAAGATATTTGCTGCTCAATTGGTTTACAATATGATATGATGTTATTTGGGTGCT 612
DB 690 TGCCAGGACATCGCCACTCAGCTCATCTCAACATGACATGACATGATCTTGGCGGA 749
QY 613 GGTAAGATGATCATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCCAGATGATGCTTCT 672
DB 750 GGCCGCAAGTACATGTTTCCATGGGAGCCCAAGACCTGAGTACCCAGCTGATGCCAGC 809
QY 673 GTTAATGTTGTTAGAAAGATAGCAAAATTGTTTCAAGATGGCAAGCTTAAGCATCAA 732
DB 810 CAGAATGGAATCAGGCTGACCGGAGAACCTGTGCAAGAAATGGCTGGCAAAAGCACCAAG 869
QY 733 GGTGCTCATATGTTTGGAAATAGAACTGTTGTTGCAAGCTGCTGATGATTTAGTGTT 792
DB 870 GGTGCTGTGATGTGTGAACCGCACTGAGCTCATGCAAGGCGTCTCTGAGCCAGTCTGTG 929
QY 793 ACTCATTTGATGGGTTTGTGTAACAGCTGATATGAAGTATATGTTCAACAAGATCAT 852
DB 930 ACCCATTCATGGGCTCTTTGAGCCGGAAGACAGAAATATGATTCACCGAGACCCC 989
QY 853 ACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTTTGTCTAGAAAT 912
DB 990 ACACGTGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCTGAGCAGGAAC 1049
QY 913 CCAAGAGTTTCTTACTTGTGTTGTAAGGTGTGAATTGATCATGTCATCATGATGCT 972

Db 1050 CCCCAGGCTTCTACCTTTGTGAGGGCGCCGATCGACCATGTCATCATGAGGCT 1109
QY 973 AAGCTTATATGCTTGTACTGAGGCTATATGTTGATAATGCTATTGCTAAGGCTAAT 1032
Db 1110 GTGGCTTACGAGGACTCACTGAGGGGTATGTCGACGACCATTGAGAGGGCGGGC 1169
QY 1033 GAATTGACTTCTGAATTGATCTTGAATTTGGTACTGCTGATCATAGTCATGTTTTT 1092
Db 1170 CAGCTCACGACGAGGAGGACACGCTGACCCCTCGTACCCGCTGACCACTCCCATGTCTTC 1229
QY 1093 TCTTTGGTGGTTACACTTGTAGAGGTACTTCTATTTTGGCTTGGCTCCAGGTAAGGCT 1152
Db 1230 TCCTTTGGTGGCTACACCTTGCAGGGAGCTCCATCTTCCGGTTGGCCCCCAGCAAGGCT 1289
QY 1153 TTGGATAGTAAGTCTTACACTTCTATTTTGTATGTTAATGTTCCAGGTTATGCTTTGGGT 1212
Db 1290 CAGGACAGCAAGCCTACACGCTCATCTGTACGGCAATGGCCGGGCTACGTTTCAAC 1349
QY 1213 GGTGTTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCTTACAGACAACAA 1272
Db 1350 TCAGGCGTGCAGCAGACGTAATGAGCGAGAGCGGAGCCCGAATTACAGACAGCAG 1409
QY 1273 GCTGCTGTTCCATTGGCTAGTGAACCTCATGGTGTGAAGATGTTCTGTTTGTGCTAGA 1332
Db 1410 GCGGCGGTGCCCCCTGTCTCGTCCGAGACCCAGGAGCGGAGCGGTGTTGCGCGC 1469
QY 1333 GGTCCACAAGCTCATTTGGTTCATGTTTCAAGAAGAACTTTGTTGCTCATATATAG 1392
Db 1470 GGGCCGCGAGCGCACTGTGTCATGTTGTCAGAGACAGAGCTTCGTAAGCATGTCTATG 1529
QY 1393 GCTTTTGGTGGTTGTGTTGAACCATACACTGATTGTAATTTGCCAGCTCCAGC 1445
Db 1530 GCCTTCGCTGCTGTCTGTGAGGCCCTACACGCGCTGCGACCTGGCGCTCCCGC 1582

RESULT 12

AAQ78135

ID AAQ78135 standard; cDNA to mRNA; 1587 BP.

XX AAQ78135;

DT 24-JUL-1995 (first entry)

XX Human enteric alkaline phosphatase cDNA.

XX Human enteric alkaline phosphatase; homogeneous quality production;

KW clinical diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1587

FT CDS /*tag= a

PN JF06284885-A.

XX 11-OCT-1994.

PD 02-APR-1993; 93JP-00076883.

XX 02-APR-1993; 93JP-00076883.

XX (TOYU) TOSOH CORP.

XX WPI; 1994-362592/45.

DR P-PSDB; AAR63438.

PT Recombinant human enteric alkaline phosphatase - for cheap and large
scale prodn. of homogeneous HIP.

XX Disclosure; Page 3-5; 9pp; Japanese.

CC AAQ78135 encodes AAR63438 human enteric alkaline phosphatase (HIP), using
CC the mutagenic primers described in AAQ78137-Q78140 the 1422, 1464 and
CC 1491 bp mutants described in AAQ90638-Q90640 were produced. Using
CC recombinant DNA techniques homogeneous quality HIP mutants could be
CC produced, avoiding the problems associated with poor quality labelled
CC enzymes in clinical diagnosis

XX Sequence 1587 BP; 317 A; 514 C; 491 G; 265 T; 0 U; 0 Other;

Query Match 41.4%; Score 611.2; DB 2; Length 1587;

Best Local Similarity 64.0%; Pred. No. 1.6e-136;

Matches 922; Conservative 0; Mismatches 518; Indels 0; Gaps 0;

QY 6 CTTGATTCACGCTGAGAGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTTT 65
Db 57 CGTCATCCAGCTGAGAGAGAGAACC CGGCTTCTGGAACCGCAGGAGCTGAGGCCCT 116
QY 66 GGAATGTTGCTAAGAGTTGCCAACCAATTCAAACTGCTGTAAGAATGTTATTTGTTTTT 125
Db 117 GGATGCTGCCAAGAGAGCTGCAGCCCATCCAGAGAGTCCGCAAGAACCTCATCTCTTCCT 176
QY 126 GGGTATGTTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGGTCAAAATGAA 185
Db 177 GGGGATGGGTGTTGGGGTGCACCGGTGACAGCCACAGATCTTAAGGGGCGAAGAA 236
QY 186 TGGTAAATTTGGGTCCAGAACTCCATTTGGCTATGATCAATTTCCATACGTTGCTTGTTC 245
Db 237 TGGCAAACTGGGCGCTGAGACGCCCTGCGCATGAGCCGCTTCCATACCTGGCTCTGTC 296
QY 246 TAAGACTTACAATGTTGATAGACAAGTTCCAGATTTCTGCTGTAAGTCTGCTTACTT 305
Db 297 CAAGACATACAATGTGACAGACAGTGCAGACAGCGACAGCCACAGCGCTTACT 356
QY 306 GTGTGTTGTTAAGGGTAAATTAACAAGTATGTTTCTGCTGCTGCTAGATTAACAATCA 365
Db 357 GTGGGGGTCAAGGCCCACTTCCAGACCATTGGCTTGAATGACAGCGCGCTTAAACA 416
QY 366 ATGTAATACTACTAGAGCTAATGAAGTACTTCTGTTATTAATAGAGCTAAGAGGCTGG 425
Db 417 GTGCAACACGACACCGCGCAATGAGTCACTCCGTGATGAACCGGCAAGACAGAG 476
QY 426 TAAAGCTGTGTTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA 485
Db 477 AAGTCAGTAGAGTGTGACCAACACAGGGTGCAGCAGGCCCTCGCAAGCCGACCTA 536
QY 486 CGCTCATACTGTTAATAGAAATTTGTTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAA 545
Db 537 CGCACACACAGTGAACCGCACTGTTACTCAGATGCTGACATGCTTGCCTCAGCCGCCA 596
QY 546 GAAATGTTGCAAGATATTTGCTGCTCAATTTGTTTACAATATGATATGATGTTATTTT 605
Db 597 GAGGGGTGCCAGACATGCGCACTCAGCTCATCTCCAACATGACATTGACGTGATCTT 656
QY 606 GGGTGTGTAGATGATGATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGA 665
Db 657 TGGCGAGGCGCGAAGTACATGTTTCCCATGGGAGCCCAAGACCTGAGTACCCAGCTGA 716
QY 666 TGCTTCTGTTAATGTTGTTAAGATAAGCAAAATTTGTTCAAGAATGGCAAGCTTAA 725
Db 717 TGCCAGCCAGAATGAGATCAGGCTGAGCGGAAGAACCTGTCAGAAATGGCTGGCAAA 776
QY 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGATATTC 785
Db 777 GCACCAAGGTGCTGTTATGTTGAAACCGCACTGAGCTCATGCAAGGCGTCCCTGGACCA 836
QY 786 TAGTGTACTCATTTGATGGGTTTGTGTAACCAAGCTGATATGAGTATATGTTCAACA 845
Db 837 GTCTGTGACCCATCTCATGGGCTCTTGTAGCCCGGAGACACGAATATAGATCTCTCCG 896
QY 846 AGATCATTAAGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTGCAGATTTTGTTC 905
Db 897 AGACCCCACTGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTGAG 956

QY 906 TAGAATCCAGAGTTTACTTGTGTTGAAGGTGTAGAAATGATCATGTCATCA 965
DB 957 CAGGAACCCCGCGCTTCTACTCTTGTGTGAGGCGCGCATGACCAATGTCATCA 1016
QY 966 TGATGTAAGGCTTATATGCTTTGACTGAAGCTATATGTTGATAATGCTATGCTAA 1025
DB 1017 TGAGGCTGTGCTTACAGAGCACTGACTGAGCGGCTATGTCGACGACCAATGAGAG 1076
QY 1026 GGCTAATGATGACTTCTGAATTGGATCTTGAATTTGCTTACTGCTGATCATAGTCA 1085
DB 1077 GCGGGCCAGCTCACACGAGGAGGACACGCTGACCTCTGACCGCTGACCACTCCA 1136
QY 1086 TGTCTTCTTTGTTGGTGTGTTACACTTTGAGAGTACTTCTATTTTGGTTGGCTCCAGG 1145
DB 1137 TGTCTTCTTTGTTGGTGTGTTACACTTTGAGAGTACTTCTATCTTGGGTTGGCTCCAG 1196
QY 1146 TAAGGCTTTGATAGTACTTCTTACACTTCTATTTGTATGTTAATGTTCCAGGTTATGC 1205
DB 1197 CAAGGCTCAGACAGCAAGCTTACACGTCATCTGTACGCAATGCGCGGCTTACGT 1256
QY 1206 TTTGGGTGTGTTCTAGACAGATGTTAATGTTAGTACTAGTGAAGACCACTTACAG 1265
DB 1257 GTTCAACTCAGGCGGTGCGACCAAGCTGATGAGCGAGAGCGGAGCCCGATTAACA 1316
QY 1266 ACAACAAGCTGCTTCTTCCATTGGCTAGTGAATCTATGCTGTGTGAAGATGCTGTTT 1325
DB 1317 GCAGCAGGCGGCGGTGCGCTTGTGTCGAGACCCACGAGGCGAAGACGTGCGGTTT 1376
QY 1326 TGCTAGAGGTCACAAAGCTCATTTGTTGATGTTCAAGAAACTTTTGTGCTCA 1385
DB 1377 TGGCGCGGCGCGGCGGCGGACCTGTGTGATGTTGTGAGAGCAGAGCTTGTAGCGCA 1436
QY 1386 TATTATGCTTTGCTGTGTGTGTGAACCATACAGTGTGTAATTTGCCAGCTCCAGC 1445
DB 1437 TGTCTAGGCTTGTGCTGTGTGTGTGAGCCCTTACAGGCTGCGACCTGCGCTCCCGC 1496

RESULT 13
AAT27384
ID AAT27384 standard, DNA, 1587 BP.
XX AAT27384;
AC AAT27384;
XX 20-SEP-1996 (first entry)
DT 20-SEP-1996 (first entry)
XX Human alkaline phosphatase coding sequence.
DE Human alkaline phosphatase coding sequence.
XX alkaline phosphatase; label; antibody; IgG; fusion protein; chimera;
KW immunoassay; ds.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1..1587
FT /*tag= a
FT /product= "Alkaline_phosphatase"
XX JP08070875-A.
PN 19-MAR-1996.
XX 05-SEP-1994; 94JP-00211035.
PF 05-SEP-1994; 94JP-00211035.
XX 05-SEP-1994; 94JP-00211035.
PR (TOYJ) TOSOH CORP.
XX
PA WPI; 1996-203155/21.
XX P-PSDB; AAR91805.
DR Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprises
PT AP fused downstream of antibody heavy or light chain, useful as
PT immunoassay reagent.

XX Example 1; Page 10-12; 44pp; Japanese.
PS The gene coding for human alkaline phosphatase is fused downstream of a
XX gene coding for either the variable and CH1 regions of an antibody heavy
CC chain or an antibody light chain. Coexpression of the H- and L-chain
CC sequences, one of which is fused to the AP gene, results in production of
CC AP-labelled antibodies suitable for use in immunoassays. The present
CC sequence codes for human AP
XX
SQ Sequence 1587 BP; 317 A; 515 C; 490 G; 265 T; 0 U; 0 Other;
Query Match 41.4%; Score 611.2; DB 2; Length 1587;
Best Local Similarity 64.0%; Pred. No. 1.6e-136;
Matches 922; Conservative 0; Mismatches 518; Indels 0; Gaps 0;
QY 6 CTGATTCAGCTGAAGAAGAAATCCAGCTTTTGAATAGACAAGCTCTCAAGCTTT 65
DB 57 CGTCATCCAGCTGAGAGAGAGAAACCGGCTTCTGGAACCGCAGGCACTGAGGCCCT 116
QY 66 GGATGTTGCTAAGAAAGTTGCAACCAATTCAACTGCTGTAAGAATGTTATTTGTTTTT 125
DB 117 GGATGCTGCCAAGAAAGCTGCAAGCCATCCGAAGGTGCGCAAGAACTTCCTTCTCT 176
QY 126 GGGTGTGCTAAGAGTTGCAACCAATTCAACTGCTGTAAGAATGTTATTTGTTTTT 185
DB 177 GGGCGATGGGTTGGGGGTGCGCCACGCTGACAGCCACCAAGATCTTAAAGGGGCAAGAA 236
QY 186 TGCTAAGTTGGGTCAGAAACTCCATTGCTATGATCAATTTCCATACGTTGCTTGTG 245
DB 237 TGGCAACTGGGCGCTGAGAGCGCCCTGGCATGGAACCGCTTCCATACCTGGCTCTGTC 296
QY 246 TAAGACTTACATGTTGATAGACAAGTTCCAGATTCTGCTGTGACTGCTACTTACTT 305
DB 297 CAAGACATACATGTGACAGACAGAGTGCAGACAGCGCACACAGCAAGGCTTACCT 356
QY 306 GTGTGTTAAGGTTAATTACAGAACTATTGTTGTTCTGCTGCTGCTAGATACAATCA 365
DB 357 GTGCGGGGTCAAGGCCCAACTTCCAGACCATCGGCTTGAAGTGAAGCGCGCTTAAACA 416
QY 366 ATGTAATCTACTAGAGTATGAGTTACTTCTGTTATTAATAGCTAAGAAGGCTGG 425
DB 417 GTCAACACGACACCGCGCAATGAGGTACTCTCCGTGATGAACCGGCGCAAGCAAGCAGG 476
QY 426 TAAGGCTGTGTTGTTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGTGCTTA 485
DB 477 AAAGTCACTAGAGTGTGACCAACAGCGGTGACAGCAGCGCTGCGCACCGGCACTTA 536
QY 486 CGCTCATCTGTTAATAGAAATGTTACTCTGATGCTGATTTGCCAGCTGATCTCAAAA 545
DB 537 CGCACACACAGTGAACCGCAACTGTGTTACAGATGTCATGCTGCTCAGCCGCCA 596
QY 546 GAATGTTGTCAGATATTTGCTGCTCAATTTGTTTACAATATGATATGATGTTATTTT 605
DB 597 GGAAGGCTGCCAGAGACATCGCCACTCACTCATCTCCAACATGAGATTGACGTGATCCT 656
QY 606 GGGTGTGTTAGAAATGATCATGTTTCCAGAAGGTAAGTCTCCAGATCCAGAAATCCAGATGA 665
DB 657 TGGCGAGGCGGCAAGTACATGTTTCCATGGGGAACCCAGAACCTTGAATACCCAGCTGA 716
QY 666 TGCTTCTGTTAATGTTGTTAGAAAGATTAAGCAAAATTTGTTCAAGAAATGCAAGCTAA 725
DB 717 TGCCAGCCAGAAATGAAATCAGGCTGGAAGGGAAGAACTGTGTGAGAAATGGCTGGCAAA 776
QY 726 GCATCAAGGCTCAATATGTTTGAATGAAGTCTGTTTGAAGTCTGATGATTC 785
DB 777 GCACCAAGGCTGCTGTATGTGTGAACCGCACTGAGCTCATGAGCGCTCCCTGAGACCA 836
QY 786 TAGTGTACTCATTTGATGAGGTTGTTTGAACCAAGCTGATATGATATGATGTTCAACA 845
DB 837 GTCTGTGACCATCTCATGAGGCTTTTGAAGCCGAGACACAGAAATATGAGATCTCCG 896
QY 846 AGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTCAGATTGTC 905

Db 882 GTCTGTGACCCATCTCAATGGGCTCTTTGAGCCCGAGACACGAAATATGATCCTCCG 941
QY 846 AGATCATACTAAGATCCAACTTGGCTGAATGACTGAAGCTGCTTGCAGTTTGTGTC 905
Db 942 AGACCCACACTGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCTGTGAG 1001
QY 906 TAGAATCCAGAGTTTCTTACTTGTGTGTAAGGTGTGTAATGTATGATGATGATCA 965
Db 1002 CAGGAACCCCGCGCTTCTAACCCTTTGTGAGGGCGCGCCGATCGACCATGTGATCA 1061
QY 966 TGATGTAAGCTTATATGCTTGAAGCTTGAAGCTATATGTTGATTAATGCTATTGCTAA 1025
Db 1062 TGAGGCTGTGCTTACAGGACGCTGAGGCGGTGATGTTGACGACGCAATGAGAG 1121
QY 1026 GGCTAATGAATGACTTCTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
Db 1122 GGGCGGCGAGCTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1181
QY 1086 TGTCTTCTTCTTGTGCTTACACTTGAAGGCTTCTATTTTGTGCTGCTCCAGG 1145
Db 1182 TGTCTTCTTCTTGTGCTTACACTTGAAGGCTTCTATTTTGTGCTGCTCCAGG 1241
QY 1146 TAAGGCTTTGATAGTACTTACACTTCTATTTTGTATGTAATGTAATGTAATGTAATGTA 1205
Db 1242 CAAAGCTCAGGACAGCAAGCCTACACGCTCCTGTACGGAATGCGCGGCTACGT 1301
QY 1206 TTGGGCTGTGCTTCTAGACAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1265
Db 1302 GTTCAACTCAGGCTGCGACAGCAGATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1361
QY 1266 ACAACAAGCTGCTGTCTTCCATTTGGCTAGTGAACCTATGCTGTGTAAGATGTTGCTGTTT 1325
Db 1362 GCAGCAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421
QY 1326 TGCTAGAGTCCACAGCTCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1385
Db 1422 TGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1481
QY 1386 TATATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1445
Db 1482 TGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541

RESULT 15

ADO28592
ID ADO28592 standard; cDNA; 2516 BP.

AC ADO28592;

DT 12-AUG-2004 (first entry)

DE Human PPBI encoding cDNA SEQ ID NO:21.

KW high-grade dysplasia; HGD; oesophageal adenocarcinoma;

KW neo-plastic transformation; cancer; cytostatic; gene therapy; human;

KW alkaline phosphatase intestinal precursor; PPBI; chromosome 2; gene; ss.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

PA (GETH) GENENTECH INC.

XX Smith V;

XX WPI; 2004-420319/39.

DR P-PSDB; ADO28593.

XX Detecting of high-grade dysplasia in cells of a mammalian tissue sample

PT comprises establishing the level of expression in the test tissue sample

XX of the genes.

XX Claim 1; SEQ ID NO 21; 256bp; English.

XX The present invention describes a method for detecting high-grade

XX dysplasia (HGD) in cells of a mammalian tissue sample. Also described:

XX (1) identifying an oesophageal tissue susceptible to oesophageal

XX adenocarcinoma; (2) determining the predisposition of a mammalian tissue

XX to a neo-plastic transformation by detecting HGD in cells of the tissue;

XX and (3) detecting cancer in a patient. The method can be used in

XX detecting HGD and cancer in cells of a mammalian tissue sample. The

XX methods and compositions of the present invention can be used in treating

XX CC and preventing HGD and cancer, and in gene therapy. The present in sequence

XX CC encodes human alkaline phosphatase intestinal precursor (PPBI), which is

XX CC used in the exemplification of the present invention. The human PPBI gene

XX is located on chromosome 2.

XX Sequence 2516 BP; 517 A; 853 C; 712 G; 434 T; 0 U; 0 Other;

XX Query Match 41.4%; Score 611.2; DB 12; Length 2516;

XX Best Local Similarity 64.0%; Pred. No. 1.9e-136;

XX Matches 922; Conservative 0; Mismatches 518; Indels 0; Gaps 0;

QY 6 CTGATCCAGCTGAAGAAGAAATCCAGCTTTTGAATGACAAAGCTGCTCAAGCTTTT 65

Db 102 CGTATCCAGCTGAGAGAGAACCCGCTTCTGAAACCGCAGGAGCTGAGGCTT 161

QY 66 GGATGTTGCTAAGAAGTTGCAACCAATTCAACTGCTGCTAAGAATGTTATTTGTTT 125

Db 162 GGATGTTGCTAAGAAGTTGCAACCAATTCAACTGCTGCTAAGAATGTTATTTGTTT 221

QY 126 GGGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185

Db 222 GGGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 281

QY 186 TGGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245

Db 282 TGGTGAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 341

QY 246 TGAAGCTTCAATGTTGATAGACAGTTCCAGATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305

Db 342 TGAAGCTTCAATGTTGATAGACAGTTCCAGATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 401

QY 306 GTGTGCTTGAAGGTAATTAAGAACTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365

Db 402 GTGTGCTTGAAGGTAATTAAGAACTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 461

QY 366 ATGTATACTACTAGAGGTAATGAAGTTACTCTGTTATTAATGAAGCTAAGAGGCTGG 425

Db 462 GTGCAACACGACACGCGGCAATGAGGTCTCTCGTATGAACCGGGCCAAAGCAAGCAGG 521

QY 426 TGAAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485

Db 522 TGAAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581

QY 486 CGCTCATCTGTTAATAGAAATGCTACTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 545

Db 582 CGCTCATCTGTTAATAGAAATGCTACTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 641

QY 546 GAAATGTTGCAAGATATGCTGCTCAATGTTGTTAATATGATATGATGTTATTTT 605

Db 642 GAAATGTTGCAAGATATGCTGCTCAATGTTGTTAATATGATATGATGTTATTTT 701

QY 606 GGGTGTGTTGAATGTTATGTTTCCAGAGGTAATCCAGATCCAGATCA 665

Db 702 TGGCGGAGGCGCCAGATACATGTTTCCCATGGGGAGACCCAGACCTTGAGTACCCAGCTGA 761
QY 666 TGCTTCGTGTTAATGGTGTAGAAAGGATAAGCAAAATTGGTTCAAGATGGCAAGCTAA 725
Db 762 TGCCAGCCAGAAATGGAATCAGGCTGGACGGGAAGAAACCTGGTGCAGGAATGGCTGGCAAA 821
QY 726 GCATCAAGGTGCTCAATATGTTGGAAATGAATGCTGTTGTTGCAAGCTGCTGATGATTC 785
Db 822 GCACCAAGGTGCTGATGATGTAACCGCACTGAGCTCATGCAAGGCTGCCCTGGACCA 881
QY 786 TAGTGTACTCATTTGATGGGTTGTTGAACCAAGCTGATATGAGTAAATGTTCAACA 845
Db 882 GTCTGTACCATCTCATGGGCTCTTGAGCCCGAGACACGAATAATGAGATCCTCCG 941
QY 846 AGATCACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGCAAGTTTGTG 905
Db 942 AGACCCCACTGGAGCCCTCCTGATGAGATGACAGAGGCTGCCCTGCCCTGTGAG 1001
QY 906 TAGAAATCCAGAAGTTTCTTACTGTTGTTGTAAGGTGTAAGTGAATGATCATGTGTCATCA 965
Db 1002 CAGGAACCCCGCGGCTTCTACTCTTTGTTGGAAGGGCGGCGCCGCAATGATGTCATCA 1061
QY 966 TGATGGTAAGGCTTATATGGCTTTGACTGAAGCTATATGTTGTAATGCTATTTGCTAA 1025
Db 1062 TGAGGGTGTGGCTTACCAAGGCACTGAGGCGGTGATGTTGACGACGCCATTTGAGAG 1121
QY 1026 GGCTAATGAATGACTTCTGAATTGAACTTTGATTGTTGTTACTGTCATAGTCA 1085
Db 1122 GCGGGCCAGCTCACCAAGAGAGACAGCTGACCCCTGTCACGCTGACCACTCCCA 1181
QY 1086 TGTTTTCTTTTGGTGTACACTTTGAGAGTACTTCTATTTTGGTTGGCTCCAGG 1145
Db 1182 TGTCTTCTCTTGGTGGCTACACCTTGGAGGAGCTCCATCTTGGGGTTGGCCCCCAG 1241
QY 1146 TAAGGCTTGGATAGTAAGTCTTACACTTCTATTTTGTATGTAATGGTCCAGTTATGC 1205
Db 1242 CAAGGCTCAGGACAGCAAGCCTACACGCTCATCTGTACGSCAATGGCCCGGCTACGT 1301
QY 1206 TTTGGGTGGTCTTCTAGACCAGATGTTAATGGTAGTACTAGTGAAGAACCATCTTACAG 1265
Db 1302 GTTCAACTCAGGCGGTGCGACCAGACGTGAATGAAGCGAGAGCGGAGCCCCGATTACCA 1361
QY 1266 ACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTGTGTGAAGATGTTGCTGTTT 1325
Db 1362 GCAGCAGGCGGCGGTGCCCTGTGTCGAGAGCCACGAGGCGAAGACGTGGCGGTGTT 1421
QY 1326 TGCTAGAGGTCCACAAGCTCATTTGGTTGATGGTGTCAAGAAGAACTTTGTTGCTCA 1385
Db 1422 TGCGCGCGGCGCGCAGCGCACCTGTGTGTCAGAGCAAGACTTGTAGCGCA 1481
QY 1386 TATTATGGCTTTTGGCTGTTGTGTGAACATACACTGATTGTAATTGGCAGCTCCAGC 1445
Db 1482 TGTCAATGGCTTGGCTGCTGTGTGAGAGCCCTACACGGCCTGCGACTGGCGCTCCCCGC 1541

Search completed: October 20, 2004, 06:32:36
Job time : 774 secs

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OM nucleic - nucleic search, using sw model

Run on: October 19, 2004, 10:21:12 ; Search time 138.5 Seconds
(without alignments)
7574.905 Million cell updates/sec

Title: US-09-911-132A-5

Perfect score: 1476

Sequence: 1 gaattcttgattccagctga.....gtattccagattaaggtacc 1476

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 - 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 - 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 - 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 - 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------------------------|
| 1 | 833.8 | 56.5 | 1798 | 4 | US-09-305-681-1 Sequence 1, Appli |
| 2 | 777 | 52.6 | 2460 | 4 | US-09-305-681-3 Sequence 3, Appli |
| 3 | 772.2 | 52.3 | 2542 | 4 | US-09-305-681-5 Sequence 5, Appli |
| 4 | 572.8 | 38.8 | 1956 | 3 | US-08-867-352-20 Sequence 20, Appli |
| 5 | 572.8 | 38.8 | 13910 | 3 | US-09-263-933-1 Sequence 1, Appli |
| 6 | 572.8 | 38.8 | 13910 | 3 | US-09-263-933-8 Sequence 8, Appli |
| 7 | 572.8 | 38.8 | 13910 | 3 | US-09-263-933-15 Sequence 15, Appli |
| 8 | 572.8 | 38.8 | 13910 | 4 | US-09-919-901-1 Sequence 1, Appli |
| 9 | 572.8 | 38.8 | 13910 | 4 | US-09-919-901-8 Sequence 8, Appli |
| 10 | 572.8 | 38.8 | 13910 | 4 | US-09-919-901-15 Sequence 15, Appli |
| 11 | 572.8 | 38.8 | 13910 | 4 | US-10-191-966-1 Sequence 1, Appli |
| 12 | 572.8 | 38.8 | 13910 | 4 | US-10-191-966-8 Sequence 8, Appli |
| 13 | 572.8 | 38.8 | 13910 | 4 | US-10-191-966-15 Sequence 15, Appli |
| 14 | 571.2 | 38.7 | 4989 | 4 | US-09-693-011-12 Sequence 12, Appli |
| 15 | 571.2 | 38.7 | 5083 | 4 | US-09-693-011-11 Sequence 11, Appli |
| 16 | 571.2 | 38.7 | 5928 | 4 | US-09-932-581-25 Sequence 25, Appli |
| 17 | 571.2 | 38.7 | 6314 | 4 | US-09-693-011-10 Sequence 10, Appli |
| 18 | 571.2 | 38.7 | 6408 | 4 | US-09-693-011-9 Sequence 9, Appli |
| 19 | 571.2 | 38.7 | 7076 | 4 | US-09-837-863-20 Sequence 20, Appli |
| 20 | 571.2 | 38.7 | 7076 | 4 | US-09-837-863-21 Sequence 21, Appli |
| 21 | 571.2 | 38.7 | 7092 | 4 | US-09-837-863-19 Sequence 19, Appli |
| 22 | 571.2 | 38.7 | 7092 | 4 | US-09-837-863-22 Sequence 22, Appli |
| 23 | 571.2 | 38.7 | 7573 | 4 | US-09-837-863-27 Sequence 27, Appli |
| 24 | 570.8 | 38.7 | 4951 | 2 | US-08-752-307B-1 Sequence 1, Appli |
| 25 | 570.8 | 38.7 | 4951 | 3 | US-09-707-802-1 Sequence 1, Appli |
| 26 | 570.8 | 38.7 | 4951 | 3 | US-09-991-326-1 Sequence 1, Appli |
| 27 | 566.4 | 38.4 | 1467 | 3 | US-09-330-317B-17 Sequence 17, Appli |

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|----|-------|------|-------|---|---------------------|--------------------|
| 28 | 566.4 | 38.4 | 1467 | 4 | US-09-808-589A-17 | Sequence 17, Appli |
| 29 | 560 | 37.9 | 8299 | 1 | US-08-462-014-2 | Sequence 2, Appli |
| 30 | 560 | 37.9 | 8299 | 3 | US-08-923-137-3 | Sequence 3, Appli |
| 31 | 560 | 37.9 | 8299 | 3 | US-08-973-334-5 | Sequence 5, Appli |
| 32 | 560 | 37.9 | 8299 | 3 | US-09-563-869A-5 | Sequence 5, Appli |
| 33 | 118.8 | 8.0 | 5399 | 1 | US-08-368-071-9 | Sequence 9, Appli |
| 34 | 118.8 | 8.0 | 5399 | 1 | US-08-458-181-9 | Sequence 9, Appli |
| 35 | 118.8 | 8.0 | 5399 | 4 | PCT-US93-02172-9 | Sequence 9, Appli |
| 36 | 95.8 | 6.5 | 5293 | 5 | US-09-900-708-1 | Sequence 1, Appli |
| 37 | 86.8 | 5.9 | 3489 | 2 | US-08-728-323A-1 | Sequence 1, Appli |
| 38 | 86.8 | 5.9 | 3489 | 3 | US-09-298-568-1 | Sequence 1, Appli |
| 39 | 86.8 | 5.9 | 3489 | 4 | US-09-410-399-1 | Sequence 1, Appli |
| 40 | 86.8 | 5.9 | 3489 | 4 | US-09-894-273-1 | Sequence 1, Appli |
| 41 | 86.8 | 5.9 | 32207 | 2 | US-08-770-379-20 | Sequence 20, Appli |
| 42 | 86.8 | 5.9 | 32207 | 3 | US-08-757-669A-20 | Sequence 20, Appli |
| 43 | 86.8 | 5.9 | 32207 | 3 | US-09-230-371A-20 | Sequence 20, Appli |
| 44 | 77.2 | 5.2 | 884 | 4 | US-09-270-767-11859 | Sequence 11859, A |
| 45 | 70.8 | 4.8 | 220 | 3 | US-09-263-933-22 | Sequence 22, Appli |

ALIGNMENTS

RESULT 1
US-09-305-681-1

Sequence 1, Application us/09305681

Patent No. 6406899

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Highly active alkaline phosphatase

NUMBER OF SEQUENCES: 54

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/305,681

FILING DATE:

CLASSIFICATION:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1798 base pairs

TYPE: nucleotide

STRANDEDNESS: single strand

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

Query Match 56.5%; Score 833.8; DB 4; Length 1798;
Best Local Similarity 73.2%; Pred. No. 2.9e-211;
Matches 1069; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 6 | CTTGATTCAGCTGAAGAAATTCAGCTTTTGGATAGACAGCTGCTCAAGCTT | 65 |
| DB | 107 | CCTCATCCAGCTGAGGAAACCCTTCTGAAACCGCCAGGAGCCAGCCCT | 166 |
| QY | 66 | GGATGTTGTAAGAGTTGCAACCAATTCAACTGCTGCTAAGATGTAATTTGTTT | 125 |
| DB | 167 | TGATGTGCAAGAGTTGCAAGCACTGCAAGAGCTGCCAAGATGTCATCTCTCT | 226 |
| QY | 126 | GGGTGATGATGGGTGTTCCAACTGTAAGTCTAGTGAATTTGAAGGTCGAATGAA | 185 |
| DB | 227 | GGGGGATGGATGGGGTGCTACGCTGACAGCCACTCGATCCTAAAGGGCAGATGAA | 286 |
| QY | 186 | TGCTAAGTTGGGTCAGAACTCCATTGGCTATGATCAATTTCCATACGTGCTTGT | 245 |
| DB | 287 | TGGCAACTGGGACCTGAGACACCCCTGGCCATGACCAAGTTCCATACGTGCTGT | 346 |
| QY | 246 | TAAGACTTACAATGTTGATAGACAGTTCCAGATTCTGCTGCTACTGCTACTT | 305 |
| DB | 347 | CAAGACATCAACGTGACAGACAGAGGTGCCAGACGCGCAGGCACTGCTCACT | 406 |

| | | | |
|----|------|---|------|
| QY | 306 | GTGTGTGTTAAGGGTAAATTACAGAACTATTGGTGTCTGCTGCTAGATACATCA | 365 |
| Db | 407 | GTGTGGGGTCAAGGGCACTACAGAAACCATCGGTGTAAGTGCAGCCGCCGCTACAAATCA | 466 |
| QY | 366 | ATGTAATACTACTAGAGGTAAAGAACTTACTTCTGTTAATTAAGAGCTAAGAGCGTGG | 425 |
| Db | 467 | GTGCAACACAGACACGTGGGAATGAGGTCACGTCTGTGATCAACCGGGCCAAGAAAGCAGG | 526 |
| QY | 426 | TAAGGCTGTGTGTGTGTAATACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA | 485 |
| Db | 527 | GAAAGCCCGTGGAGTGTGTGACCAACCACGAGGTGCAGATGCTCCCCAGCCGGGGCTTA | 586 |
| QY | 486 | CGCTCATCTGTTAATAGAAATTTGGTACTCTGATGCTGAATTTGCCAGCTGATGCTCAAAA | 545 |
| Db | 587 | CGCGCACACGGGTGAACCGAATACTGGTACTCAGACGCCGACCTGCTGTGATGCACAGAA | 646 |
| QY | 546 | GAAATGTTGTCAAGATATTGCTGCTCAATTGGTTTACAAATATGATATTGATGTTATTTT | 605 |
| Db | 647 | GAAATGCTGCCAGACATCCCGCACAAGCTGGTCTTACAAATGATATTGACGTGATCTT | 706 |
| QY | 606 | GGGTGGTGTAGAAATGACATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCCAGATGA | 665 |
| Db | 707 | GGGTGGAGGCCGAATGTACATGTTTCTGAGGGAGACCCAGAACCTGAATACCCAGATGA | 766 |
| QY | 666 | TGCTTCTGTTAATGSGTGTAGAAAGATTAAGCAAAATTTGGTTCAAGAAATGGCAAGCTAA | 725 |
| Db | 767 | TGCCAGTGTGAATGAGTCCGGAAGACAGACAGAACTGGTGCAGGAATGGCAGGCCAA | 826 |
| QY | 726 | GCATCAAGGTGCTCAATATGTTTGGAAATAGAACTGCTTTGTTGCAAGCTGCTGATGATTC | 785 |
| Db | 827 | GCACCAGGGAGCCCAGTATGTGTGAACCGCACTGCGCTCTTCAAGCGGCCGATGACTC | 886 |
| QY | 786 | TAGTGTTACTCATTTGATGGGTTTGTTTGAACCAAGCTGATATGAAGTATATGTTTCAACA | 845 |
| Db | 887 | CAGTGTAAACACACCTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTTACGA | 946 |
| QY | 846 | AGATCATACTAAGGATCCAATTGGCTGAAATGACTGAAGCTGCTTTGCCAAGTTTGTTC | 905 |
| Db | 947 | AGACCACACCAAGGACCCTGCACCTGGCGAGATGACGGAAGCGGCCCTGCAAGTGTGAG | 1006 |
| QY | 906 | TAGAAATCCAGAAGGTTTAACTTGTGTGTAAGGTGTGAGAAATGATCATGTCATCA | 965 |
| Db | 1007 | CAGGAACCCCGGGGCTTCTACCTCTTCGTGAGGAGGCGCATTGACCAACGCTACCA | 1066 |
| QY | 966 | TGATGGTAAGCTTATATGGCTTGAAGCTATTAATGTTGATAATGCTATTGCTAA | 1025 |
| Db | 1067 | TGACGGCAAAAGCTTATATGGCACTGACTGAGCGCATCATGTTTGACAATGCCATCGCAAA | 1126 |
| QY | 1026 | GGCTAATGAATTGACTTCTGAATTGGATCTTTGATTTTGGTTACTGCTGATCATAGTCA | 1085 |
| Db | 1127 | GGCTAAACGAGCTCACTAGCGAACTGGAACACGCTGATCTTGTTCACCTGCAGAACCATCCCA | 1186 |
| QY | 1086 | TGTTTTTTCTTTTGGTGGTTACACTTTGAAGAGTACTTTTAATTTTGGTTTGGCTCCAGG | 1145 |
| Db | 1187 | TGTTCTTCTTTTGGTGGCTACACACTGCGTGGGACCTTCATTTTCCGCTGGGCCCCCGG | 1246 |
| QY | 1146 | TAAAGCTTTGGATAGTAAGTCTTACACTTCTATTGTTGATGTAATGGTCCAGGTTATGC | 1205 |
| Db | 1247 | CAAGGCTTGAACAGCAAGTCTTACACTCCATCTCTATGGCAATGGCCAGGCTATGC | 1306 |
| QY | 1206 | TTTGGGTGGTGTCTTAGAACCAAGATGTTAATGGTAGTACTAGTGAAGAACCATCTTACAG | 1265 |
| Db | 1307 | GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGACAGCGAAGAACCTCATACCG | 1366 |
| QY | 1266 | ACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTTGGTGAAGATGTTGCTGTTT | 1325 |
| Db | 1367 | GCAGCAGCGCGCGCTGCTGCTGCTAGCGAAGACCAACGGGGCGAAGACGTGCGGTGTT | 1426 |
| QY | 1326 | TGCTAGAAGTCCACAAGCTCATTTGGTTCATGGTGTTCAGAAGAAACTTTGTGTGCTCA | 1385 |
| Db | 1427 | CGCGCGAGGGCCCGCAGGCGCACTGGTGCACGGCGTGCAGAGAGAACCTTCTGTGGCGCA | 1486 |
| QY | 1386 | TATTTATGCGCTTTTGTGCTGTGTGTGTAACCATACACTGATGTATTTGCCAGCTCCAGC | 1445 |

Db 1487 CATCATGGCCTTGGGGGCTGCGTGAGACCCCTACACGACTGCATCTGGCAGCCCCCGC 1546

QY 1446 TACTGCTACTAGTATTCAGA 1466

Db 1547 CACCGCACCCAGCATCCCCGA 1567

RESULT 2

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US-09-305-681-3
; Sequence 3, Application US/09305681
; Patent No. 6406899
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Highly active alkaline phosphatase
; NUMBER OF SEQUENCES: 54
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/305,681
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2460 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
;
US-09-305-681-3

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Query Match 52.6%; Score 777; DB 4; Length 2460;

Best Local Similarity 71.2%; Pred. No. 3.8e-196;
Matches 1026; Conservative 0; Mismatches 415; Indels 0; Gaps 0;

| | | | | |
|----|--|-----|--|-----|
| OY | | 6 | CTTGATTCCAGCTGAAGAAGAAAATCCAGCTTTTGGAAATGACAAGCTGTCAAACGCTTT | 65 |
| Db | | 122 | CTTCATCCCAGTTGAGGAGGAAGACCCTCCTTCTGGAACCGCCAGGCAGCCAGGCCCT | 181 |
| OY | | 66 | GGATGTTGCTAAGAGCTTGCAACCAATTCAAACCTGCTAAGAATGTTATTTGTTTTT | 125 |
| Db | | 182 | TGATGTGGCTAAGAACGTGCAGCCCATCCAGAAAGCCCAAGATGTCATCCTCTCTT | 241 |
| OY | | 126 | GGGTGATGGTATGGGCTGTTCCAACCTGTTACTGCTACTAGAATTTGAAGGCTCAAATGAA | 185 |
| Db | | 242 | GGGAGATGGGATGGGGGTGCTTAACGGTGACAGCCACTCGGATACTGAAGGGGCAGATGAA | 301 |
| OY | | 186 | TGGTAAGTTGGGTCAGAAAACTCCATTGGCTATGATCAATTTCCATAAGTTGCTTTGTC | 245 |
| Db | | 302 | TGACAAGCTGGGACCTGAGACACCCCTGGCCATGACCAAGTTCATACGTGGCTCTGTC | 361 |
| OY | | 246 | TAAGACTTACAATGTTGATAGACAAGTTCAGATCTGCTGCTACTGCTACTGCTTACTT | 305 |
| Db | | 362 | CAAGACATACAACGTGGACAGACAGGTGCAGACAGCGCACACTGCACCTGCCTTACTT | 421 |
| OY | | 306 | GTCGTGTTAAGGGTAATTACAGAACTATTGGTCTCTGCTGCTGCTAGATACATCA | 365 |
| Db | | 422 | GTGTGGGGTCAAGGGCAACTACAGAACCATCGGTGTAACTGACAGCCCCGCTACATCA | 481 |
| OY | | 366 | ATGTAATACTACTAGAGSTAATGAAGTTACTTCTGTATTAATAGAGCTAAGAAGGCTGG | 425 |
| Db | | 482 | GTGCAACACGACACGTGGGAATGAGTCAACGTCCTGTATGAAGAACCGGCCAAGAAAGCAGG | 541 |
| OY | | 426 | TAAAGCTGTTGGTGTGTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA | 485 |
| Db | | 542 | GAAATCAGTGGGAGTGTGACCAACCAAGGCTGACAGCAGCTCCCAAGCCGGTGTTA | 601 |
| OY | | 486 | CGCTCATCTGTTAATAGAATTTGCTACTCTGATGCTGATTTGCCAGCTGATGCTCAAA | 545 |
| Db | | 602 | TGCACACACGGGTGAACCGTGACTGTACTCAAGACGCGCACTGCTGCGGATGCACAGAC | 661 |

| | | | |
|----|------|---|------|
| QY | 546 | GAATGGTTGTCAAGATATTGCTGCTCAATTGGTTTACAAATATGGATATTGATGTTATTTT | 605 |
| Db | 662 | GTATGGCTGCCAGACATCGCCACACAACCTGGTCAACAAATGATATTGACGTGATCT | 721 |
| QY | 606 | GGGTGGTGTAGAAATGTACATGTTCCAGAAAGTACTCCAGATCCAGAATACCCAGATGA | 665 |
| Db | 722 | GGGTGAGGCGCGAAAGTACATGTTTCTGAGGGGACCCCGAACCTGATATACCAACAG | 781 |
| QY | 666 | TCCTTCTGTTAATGSGTTGAAGAAGATTAAGCAAAATTTGGTTCAAGAATGGCAAGCTAA | 725 |
| Db | 782 | TCCCAGTGTGAATGGAATCGCGAAGAACCAAGCGGAATCTGTGTGACAGGAGTGGCAGGCCAA | 841 |
| QY | 726 | GCATCAAGGTGCTCAATATGTTTGGAAATGAACCTGCTTTGTTGCAAGCTGCTGATGATTC | 785 |
| Db | 842 | GCAACGAGGAGCCAGATATGTGTGAACCGCACGAGCTCCTTCAGGCAGCCAAATGACTC | 901 |
| QY | 786 | TAGTGTACTCATTTGATGGGTTTGTGGAACCAAGCTGATATGAAGTATATGTTCAACA | 845 |
| Db | 902 | CAGTGTACACATCTCATGGGCTCTTTGAGCCGCGACATGAAGTATATGTTCAAGCA | 961 |
| QY | 846 | AGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCCAAGTTTGTTC | 905 |
| Db | 962 | AGACCCCAACCAAGACCCGACCTTGAGAGATGACGAGGCGGCCCTGCAAGTGTGAG | 1021 |
| QY | 906 | TAGAAATCCAAAGGTTTTCATCTGTTGTTGTAAGGTGTGAATTGATCATGTCATCA | 965 |
| Db | 1022 | CAGGAACCCCAAGGCTTCTACTCTTGTGTGAGGAGGCGCATTTGACCAACGCTACCA | 1081 |
| QY | 966 | TGATGTAAGCTTATATGGCTTTGAAGCTATATGTTGATAATGCTATTTGCTAA | 1025 |
| Db | 1082 | TGATAGCAAAAGTTATATGGCGCTGACTGAGGCGGTCACTGTTGACAATGCCATCGCCAA | 1141 |
| QY | 1026 | GGCTAATGAATTGACTTCTGAATTGGATTACTTTGATTTTGGTTACTGTCATCATAGTCA | 1085 |
| Db | 1142 | GGCTAAACGAGCTCACTAGCGAATGGAACACGCTGATCTTGTCTCACTGCAGACCACTCCA | 1201 |
| QY | 1086 | TGTTTTTTCTTTGGGTGTACACTTTGAGAGGTACTTCTAATTTTGGTTTGGCTCCAGG | 1145 |
| Db | 1202 | TGTTCTTCTTTTGGGTGTACACTGCGTGGAGCTTCATTTTGGTCTGGCCCCCAG | 1261 |
| QY | 1146 | TAAAGCTTTGATAGTAACTCTTCACTTCTAATTTGTAATGTAATGCTCCAGGTTATGC | 1205 |
| Db | 1262 | CAAGGCTCAGACAAAGATCTTACACTCTCATCTCTATGGCAATGGCCCTGGCTACGT | 1321 |
| QY | 1206 | TTTGGGTGTGTTCTAGACCAAGATGTTAATGTAAGTACTAGTGAAGAACCATTATACG | 1265 |
| Db | 1322 | GCTTGGTGGGGCTCAAGGCCGATGTTAATGACAGCATTAACGAGGACCCCTCATACCG | 1381 |
| QY | 1266 | ACAACAAGCTGCTGTTCCATTTGCTAGTGAACCTCATGTGTGAAGATGTTGCTGTTT | 1325 |
| Db | 1382 | GCAAGCAGGCGGCGTGCCTGTCTAGCGAGACCCACGCGGCGAAGACGTGGCGGTGTT | 1441 |
| QY | 1326 | TGCTAGAGGTCCACAAAGCTCAATTGGTTCATGTGTTCAGAAAGAACTTTTGTGTCTCA | 1385 |
| Db | 1442 | CGCGCAGGCGCGCAGCGCACTGTGTGACGCGGTGACAGAGAACCTTCTGTGGCGCA | 1501 |
| QY | 1386 | TATTAATGCTTTTGTGCTGTGTGTGAACCATACACTGAATTGAATTTGCCAGCTCCAGC | 1445 |
| Db | 1502 | CGTCATGGCCTTTGCGGGCTGTGAGACCCCTACACCGACTGCAATCTGCCGCGCCCTTC | 1561 |
| QY | 1446 | T 1446 | |
| Db | 1562 | T 1562 | |

RESULT 3
 US-09-305-681-5
 ; Sequence 5, Application US/09305681
 ; Patent No. 6406899
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Highly active alkaline phosphatase

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; NUMBER OF SEQUENCES: 54
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/305,681
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2542 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
;
US-09-305-681-5

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|----------------------------|--------|---------------------|-----------|--------------|
| Query Match | 52.3% | Score 772.2; | DB 4; | length 2542; |
| Best Local Similarity | 71.0%; | Pred. No. 7.3e-195; | | |
| Matches 1023; Conservative | 0; | Mismatches 418; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| QY | 6 | CTTGATTCACGCTGAAGAAATAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTTT | 65 |
| Db | 121 | CTTCATCCACGCTGAGAGAGAACCCCGCCTTCTGGAAACCGCCAGGCAGCCAGGCCCT | 180 |
| QY | 66 | GGATGTTGCTAAGAAGTTCACAACCAATTCAAACCTGCTGCTAAGAAATGTAATTTGTTTTT | 125 |
| Db | 181 | TGATGTAGCCAAAGAAGTTGCAGCCGATCCAGACAGCTGCCAAGAATGTATCTTCTTT | 240 |
| QY | 126 | GGGTGATGTTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGTCAAAATGAA | 185 |
| Db | 241 | GGGGGATGGGATGGGGGTGCTTAACGGTGAACAGCCACTCGATCTTAAGGGGAGATGAA | 300 |
| QY | 186 | TGCTAAGTTGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTGCTTGTGTC | 245 |
| Db | 301 | TGCTAAGCTGGGACCTGAGACACCCCTGGCCATGAGACAGTTCCCATACGTGCTGTGTC | 360 |
| QY | 246 | TAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTAAGTCTGTAAGTCTTACTT | 305 |
| Db | 361 | CAAGACATTACAACGTGACACAGACAGTGCACAGACAGGACAGGACATGCTCCACTGCTTACT | 420 |
| QY | 306 | GTTGTGTTTAAAGGTAATTACAGAACTATTGGTGTCTCTGCTGCTGCTAGATCAATCA | 365 |
| Db | 421 | GTTGTGGGTCAAGGGCAACTACAAACCAATTGGTGTAAAGTGACAGCCGCCGCTACAACCA | 480 |
| QY | 366 | ATGTAATTAAGTACTAGAGGTAATGAAGTACTTCTGTTATTAATAGAGCTAAGAAAGGCTGG | 425 |
| Db | 481 | GTGCAACACACAAGAGTGCCAAATGAGGTCAAGTCTGTGATGAACGGGCCAAGAAAGCAGG | 540 |
| QY | 426 | TAAGGCTGTTGTTGTTGTTACTACTAGAGTTCAACATGCTTCCAGCTGGTGCTTA | 485 |
| Db | 541 | AAAGTCAAGTGGAGTGTGACCACTCCAGGGTGACATGCTCCCGCAGCGGTGCTTA | 600 |
| QY | 486 | CGCTCATACTGTTAATAGAAATTGTACTCTGATGCTGATTTGCGACGTGATGCTCAAAA | 545 |
| Db | 601 | TGCACACACCGGTGAACCGAACTGTAATCTCAGATGCGGACCTGCTGCCGATGCACAGAC | 660 |
| QY | 546 | GAATGCTGTCAAGATATTGCTGCTCAATTTGTTTACAATAATGATATGATGTTATTTT | 605 |
| Db | 661 | GTAATGCTGCCAGACATGCGCACACAACCTGTTCAACACATGATATTTGACGTGATCTT | 720 |
| QY | 606 | GGGTGCTGTAGAAATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGA | 665 |
| Db | 721 | GGGTGAGGCCGAATGTACATGTTTCTGAGGGGACCCCGGATCTGAATACCCATACGA | 780 |
| QY | 666 | TGCTTCTGTTAATGTTGTAGAAAGGATTAAGCAAAATTTGTTCAAGATGGCAAGCTAA | 725 |
| Db | 781 | TGTCAATCAGACTGGAATCCGGAAGGACAAAGCGGAATCTGTGACGAGTGGCAGGCCAA | 840 |
| QY | 726 | GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGATGATTC | 785 |

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QY 786 TAGTGTACTCATTTGATGGTTTGTGAACAGCTGATATGAATGTTCAACA 845
Db 901 CAGTGTAAACACCTCATGGGCTTTGAGCCGGCAGACATGATATATGTTGACA 960
QY 846 AGATCACTACTAAGATCCACTTTGGCTGAATGACTGAAGCTGCTTGCAAGTTTGTG 905
Db 961 AGACCCCAACCAAGGACCCGACCTGGAGAGATGACGAGGCGGCTGCAAGTGTGAG 1020
QY 906 TAGAAATCCAAGAGTTTACTTGTGTTGTTGAAGGTGTTGAATGATCATGTCATCA 965
Db 1021 CAGGAACCCCAAGGCTTCTACTCTTCTGTTGAGGAGGAGCGCATTTGACCAAGTCA 1080
QY 966 TGATGTGAAGGCTTATATGCTTGAAGTGAAGCTATATGTTGATTAATGCTATTGCTAA 1025
Db 1081 TGAAGCAAAAGCTTATATGCACTGATACATGATGTTGCAATGCCATCGCCAA 1140
QY 1026 GGCTAATGAATTGACTTCTGAATTGATCTTGAATTTGGTTAAGTCTGATCATAGTCA 1085
Db 1141 GGCTAAGAGCTCAGTACGAACTGACAGCTGATCTTGCCACTGACAGACCACTCCA 1200
QY 1086 TGTCTTCTTTTGGTGTGTTACACTTGAAGAGTACTTCTATTTTGGTTGGCTCCAG 1145
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QY 1146 TAAGCTTTGGATAGTACTTACACTTCTATTTTGTATGTTAATGTTCCAGGTTATGC 1205
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QY 1326 TGCTAGAGGTCCACAAGCTCATTTGTTGTTGTTCAAGAGAACTTTGTTGTTCA 1385
Db 1441 CGCGCAGGCGCGCAGCGCACCTGGTGACGCGTGACAGAGAGACCTTGTGCGCA 1500
QY 1386 TATTAAGCTTTTGTGTTGTTGTTGAACATACACTGATTTGTAATTTGCCAGCTCCAGC 1445
Db 1501 CGTCAAGCTTTTGGGCTGCGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCGGCCCCCTC 1560
QY 1446 T 1446
Db 1561 T 1561

RESULT 4
US-08-867-352-20
; Sequence 20, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multicistronic expression units and their use
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,352
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,847
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:

LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: pS2-SEAP (Berger et al., 1988)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1560
OTHER INFORMATION: /note= "human SEAP gene; flanked
OTHER INFORMATION: by 5'-BcoRI and 3'-HindIII restriction cleavage
OTHER INFORMATION: sites"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 94..1560
OTHER INFORMATION: /product= "mature protein"
PUBLICATION INFORMATION:
AUTHORS: Berger, J.
AUTHORS: Hauber, J.
AUTHORS: Geiger, R.
AUTHORS: Cullen, B. R.
JOURNAL: Gene
VOLUME: 66
PAGES: 1-10
DATE: 1988
PUBLICATION INFORMATION:
AUTHORS: Millan, J. L.
JOURNAL: J. Biol. Chem.
VOLUME: 261
PAGES: 3112-3115
DATE: 1986
US-08-867-352-20

Query Match 38.8%; Score 572.8; DB 3; Length 1956;
Best Local Similarity 62.4%; Pred. No. 4.7e-142;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
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QY 66 GGATGTGCTAAGAGTTCGAACCAATTCAAACTGCTGCTAAGAAATGTTATTTGTTT 125
Db 153 GGGTCCCGCAAGAAAGCTGCAGCTGCACAGACAGACCGCCAAAGAACTCATCTTCT 212
QY 126 GGGTATGATGATGGTGTTCCTCAACTGTTACTGCTACTAGAAATTTGAAGGTCAAATGA 185
Db 213 GGGGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCTAAAGGCGAGAGAA 272
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Db 273 GGACAAACTGGGGCTGAGATACCCCTGGCCATGAGCCGCTTCCATATGTGGCTGTC 332
QY 246 TAAGACTTCAATGTTGATAGCAAGTTCAGATTCTGCTGTTACTGCTACTGCTTACTT 305
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Db 393 GTGGGGGTCAAGGGCAACTTCCAGACCATTTGGCTTGAATGACGCGCGCTTAAACA 452
QY 366 ATGTAATACTACTAGAGGTAATGAAGTACTTCTGTTAATTAAGAGCTAAGAGGCTGG 425
Db 453 GTGCAACAGACAGCGGCAAGAGTATCTCGGTGATGAATCGGGCAAGAAAGCAGG 512
QY 426 TAAGCTGTGTTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGCTGCTTA 485
Db 513 GAAGTCAGTGGAGTGTGTAACCAACAGAGTGCAGACGCTCGCAAGCGGCACTTA 572


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Db 573 CGCCACACCGGTGAACCGCAACTGGTACTCGGACGCCGACGCTGCTGCGCCGCCCA 632
QY 546 GAATGGTGTCAAGATATATGCTGCTCAATGGTTTACAATATGATATGATATGTTATTT 605
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Db 633 GGAGGGTGCAGACATCGCTACGACGCTCATCTCAACATGACATGACATGACGATGATCCT 692
QY 606 GGGTGGTGTAGATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCCAGATGA 665
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Db 753 CTACAGCCAAAGGTGGACCAAGGCTGACCGGAGAAATCTGTCAGGAATGGCTGGCGAA 812
QY 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTCGAAGCTGCTGATGATTC 785
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Db 813 GCGCAGGGTGCCGGGTATGTGTGAACCGCACTGAGCTCATGCAAGGCTTCCCTGACCC 872
QY 786 TAGTGTACTCATTTGATGGGTTGTTGAACCACTGATATGAAGTATTAATGTTCAACA 845
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Db 873 GTCTGTACCCATCTCATGGGTCTCTTGAAGCTGAGACATGAATAGAGATCCACCG 932
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Db 933 AGACTCCACACTGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGGCCTGTGAG 992
QY 906 TAGAATCCAAAGGTTTTTACTGTTGTTGTAAGGTGTTAGATTGATGATGTCATCA 965
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QY 1086 TGTCTTTCTTTGGTGTGTTACACTTTGAGAGTACTTCTATTTTGGTTGGCTCCAGG 1145
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QY 1386 TATTATGCTTTTGTGCTGTGTGTGAACCATACACTGATTGTAATTTGCGACGCTCCAGC 1445
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RESULT 5
US-09-263-933-1

; Sequence 1, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.

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; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
; FILE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/09/263,933  
; EARLIER FILING DATE: 1999-03-08  
; EARLIER APPLICATION NUMBER: 09/129,611  
; EARLIER FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 13910  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 1  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (497)..(772)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1425)..(6500)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (8579)..(9034)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10191)..(10445)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (11877)..(12734)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(774)  
; OTHER INFORMATION: Vaccinia Virus thymidine Kinase gene recombination  
; OTHER INFORMATION: site  
; FEATURE:  
; NAME/KEY: Promoter  
; LOCATION: (794)..(816)  
; OTHER INFORMATION: T7 promoter  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (846)..(1424)  
; OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1426)..(1437)  
; OTHER INFORMATION: MCS (Multiple Cloning Site)  
; FEATURE:  
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; LOCATION: (1446)..(2318)  
; OTHER INFORMATION: HCV E2/ NS2 domain  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2315)..(4231)  
; OTHER INFORMATION: HCV NS3 Domain containing the serine protease and  
; OTHER INFORMATION: helicase enzymes  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4203)..(4260)  
; OTHER INFORMATION: HCV NS3-NS4A cleavage site  
; FEATURE:  
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; LOCATION: (4375)..(4424)  
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; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4233)..(4394)  
; OTHER INFORMATION: HCV NS4A domain  
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; NAME/KEY: misc feature
; LOCATION: (4920)..(4991)
; OTHER INFORMATION: HCV NS5A-NS5B cleavage site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4992)..(6501)
; OTHER INFORMATION: SEAP Protein
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7915)..(7945)
; OTHER INFORMATION: MCS (Multiple Cloning Site)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (7938)..(8078)
; OTHER INFORMATION: term T7
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (8080)..(8365)
; OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8560)..(11317)
; OTHER INFORMATION: E. coli gpt; for selection of recombinants
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11318)..(13909)
; OTHER INFORMATION: remaining DNA from 3' end of Tropicx PCMV/SEAP
; OTHER INFORMATION: plasmid
US-09-263-933-1
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Query Match          38.8%; Score 572.8; DB 3; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
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QY      6 CTTGATCCAGCTGAAGAAGAAATCCAGCTTTTGAATAGACAAGCTGCTCAAGCTTT 65
Db      5033 CATATCCCAAGTTGAGAGAGAAACCGGACTTCTGGAACCGGAGGCGAGGCCCT 5092

QY      66 GGATGTTGCTAAGAAGTTGCAACCAATTCAACTGCTGCTAAGATGTTATTTGTTTT 125
Db      5093 GGGTGGCCCAAGAAGCTGCAGCTGCACAGACGCCCAAGAACTCATCTTCTCT 5152

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QY      186 TGGTAAGTTGGGTCAGAAACTCCATTGGCTATGGATCAATTTCCATACGTTGCTTGTTC 245
Db      5213 GGACAACTGGGGCTGAGATACCCCTGGCCATGGAACCGCTTCCATATGTGGCTGTTC 5272

QY      246 TAAAGCTTACAATGTTGATAGACAAGTTCAGATTCTGCTGGTACTGCTACTGCTTACTT 305
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QY      306 GTGTGTTGTTAAGGTAATTACAGAATAATTGTTGTTCTGCTGCTGCTAGATACAATCA 365
Db      5333 GTGCGGGGTCAAGGGCACTTCCAGACCAATTGGCTTGAAGTGCAGCCGCCGCTTAAACA 5392

QY      366 ATGTAATACTACTAGAGTAATGAAGTTACTTCTGTATTAATAGACTAAGAAGGCTGG 425
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QY      426 TAAAGCTGTTGTTGTTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGTGCTTA 485
Db      5453 GAAGTCAAGTGGAGGTGTTAACCAACCAAGAGTGCAGCACGCTTGCACAGCCGGCACTTA 5512

QY      486 CGCTCACTGTTAATAGAAATTGTAAGTCTGATGCTGATTGGCAGCTGATGCTCAAAA 545
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QY      546 GAATGTTGTCAAGATATTGCTGCTCAATTGTTTACAAATATGATATTGATGTTATTTT 605
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Db      5633 AGGTGAGGCGCGAAAGTACATGTTTCCCATGTGGAAACCCCAAGACCTGAGTACCCAGATGA 5692

QY      666 TGCTTCTGTTAATGTTGTTAGAAAGATAGCAAAATTTGGTTCAAGAAATGGCAAGCTAA 725
Db      5693 CTACAGCCAAGGTGGAGACCAAGCTGACCGGAAGAACTGTGTGAGAAATGGCTGGCGAA 5752

QY      726 GCATCAAGGTGCTCAATATGTTGGAATAGAACTGCTTGTGCAAGCTGCTGATGATTC 785
Db      5753 GCGCCAGGGTGCCCGGTATGTGTGAACCGCACTGAGCTGATGCAGCTTCCCTGGAACC 5812

QY      786 TAGTGTACTCATTTGATGGGTTGTTGGAACCAAGCTGATATGAAGTATATGTTCAACA 845
Db      5813 GTCTGTGAACCATCTCATGGGTCTCTTGAAGCTGAGACATGAATACGAGATCCACCG 5872

QY      846 AGATCATACTAAGGATCCAATTGGCTGAATGACTGAAGCTGCTTGCAAGTTTGTTC 905
Db      5873 AGACTCCACACTGGAACCCCTCTCTGATGAGATGACAGAGGCTGCCCTGCGCTGTAG 5932

QY      906 TAGAAATCCAAAGGTTTAACTGTTGTTGTAAGGTGTGAATGATCATGTGTCATCA 965
Db      5933 CAGGAACCCCGCGGCTTCTCTCTCTGTTGAGGGGTGTCGATGACCATGTGTCATCA 5992

QY      966 TGATGTAAAGCTTATATGGCTTTGACTGAAGCTAATATGTTGATATGCTAATTGCTAA 1025
Db      5993 TGAAGCAGAGGCTTACCGGGCACTGACTGAGACGATCATGTTCGACGACCATTGAGAG 6052

QY      1026 GGCTAATGAATTGACTTCTGAAATGGATACTTGTATTTGGTTAGTCTGATCATAGTCA 1085
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QY      1086 TGTTTTCTTTTGGTGTGTTACACTTTGAGAGGTACTTCTATTTTGGTTGGCTCCAGG 1145
Db      6113 CGTCTTCTCTTCCGAGGCTAACCCCTGCGAGGAGCTGCATCTTCCGGCTGGCCCTGG 6172

QY      1146 TAAAGCTTTGATAGTAGTACTTACACTTCTATTTGTTGTTAGTTAGTTAGTCCAGTTATGC 1205
Db      6173 CAAGGCCCGGACAGGAAGGCTTACACGGTCTCTTATACGGAACGGTCCAGGCTATGT 6232

QY      1206 TTTGGGTGTTGTTCTAGACAGATGTTAATGTTAGTACTAGTGAAGAACCATCTTACAG 1265
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QY      1266 ACAACAAGCTGCTGTTCATGCTAGTGAACCTCATGCTGAGATGTTGCTGTTT 1325
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QY      1326 TGCTAGAGGTCACAAAGCTCATTTGGTTTCATGTTGTTCAAGAAGAACTTTGTGCTCA 1385
Db      6353 CGCGCGCGCGCCGACAGCGCACTGTTCAAGCGCGTGCAGAGACACCTTCATAGCGCA 6412

QY      1386 TATTATGCTTTTGTGTTGTTGTTGAACCATACATGATTTGTAATTGGCAGCTCCAGC 1445
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RESULT 6
US-09-263-933-8
; Sequence 8, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potcs, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263, 933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129, 611
; EARLIER FILING DATE: 1998-08-05
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; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13910
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497)..(772)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1425)..(6500)
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; LOCATION: (8579)..(9034)
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; LOCATION: (10191)..(10445)
; FEATURE:
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; LOCATION: (11877)..(12734)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(774)
; OTHER INFORMATION: Vaccinia Virus thymidine Kinase gene recombination
; OTHER INFORMATION: site
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (794)..(816)
; OTHER INFORMATION: T7 promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (846)..(1424)
; OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1426)..(1437)
; OTHER INFORMATION: MCS (Multiple Cloning Site)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1446)..(2318)
; OTHER INFORMATION: HCV E2/ NS2 domain
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2315)..(4231)
; OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
; OTHER INFORMATION: helicase enzymes
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4203)..(4260)
; OTHER INFORMATION: HCV NS3-NS4A cleavage site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4375)..(4424)
; OTHER INFORMATION: HCV NS4A-4B cleavage site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4233)..(4394)
; OTHER INFORMATION: HCV NS4A domain
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4395)..(4919)
; OTHER INFORMATION: HCV NS4B Domain
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4920)..(4991)
; OTHER INFORMATION: HCV NS5A-NS5B cleavage site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4992)..(6501)
; OTHER INFORMATION: SEAP Protein
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7915)..(7945)
; OTHER INFORMATION: MCS (Multiple Cloning Site)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (7938)..(8078)
; OTHER INFORMATION: term T7
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (8080)..(8365)
; OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8560)..(11317)
; OTHER INFORMATION: E. coli gpt; for selection of recombinants
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11318)..(13909)
; OTHER INFORMATION: remaining DNA from 3' end of Tropicx PCMV/SEAP
; OTHER INFORMATION: plasmid
; US-09-263-933-8

Query Match      38.8%; Score 572.8; DB 3; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

QY      6 CTGATTCAGCTGAGAAGAAATTCAGCTTTTGGATAGACAGCTGCTCAGCTTT 65
DB      5033 CATCATCCCGATTGAGAGAGAACCCGGAATTCTGGAACCGCGAGGCGAGGCCCT 5092
QY      66 GGATGTGCTAAGAAGTTGCAACCAATTCAACTGCTGTAAGATGTTATTTGTTT 125
DB      5093 GGGTCCCGCAAGAAGCTGCAGCCTGCACAGACGCCGCAAGAACTCATCTTCT 5152
QY      126 GGGTGAATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGTCGAATGAA 185
DB      5153 GGGCGATGGATGGGGGTGTTCTACGGTGACAGCTGCCAGGATCTTAAGGGCAGAGAA 5212
QY      186 TGGTAAGTTGGGTCCAGAACTCCATTGGCTATGATCAATTTCATAGCTTGTCTGTC 245
DB      5213 GGACAACTGGGGCTGAGATACCCCTGGCCATGAGACCGCTTCCATATGTGCTGTGTC 5272
QY      246 TAAGACTTCAATGTGTATAGACAGATTCTGCTGTTGTTGCTACTGCTTACTT 305
DB      5273 CAAGACATACATGTAGACAAACATGTGCCAGACAGTGAAGCCACAGCCGCTACCT 5332
QY      306 GTGTGCTGTTAAGGTAATTACAGAACTATTGTTGTTCTGCTGCTAGATACAATCA 365
DB      5333 GTCCGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAGTGCAGCCGCCCTTAACCA 5392
QY      366 ATGTAACTACTAGAGCTAATAGTAATTACTTCTGTTATTAATAGACTAAGAGGCTGG 425
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QY      426 TAAGGCTGTGTTGTTTACTACTAGAGTTCAACATGCTTCTCCAGCTGTGCTTA 485
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QY      486 CGCTCACTGTTAATAGAAATGCTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAA 545
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QY      546 GAATGCTGTCAAGATATGCTGCTCAATTGTTTACAATATGATATTTGATGTTATTT 605
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QY      606 GGGTGGTGTAGATGTATCATGTTTCCAGAAAGTACTCCAGATCCAGATACCCAGATGA 665
DB      5633 AGGTGAGGCCGAAAGTACATGTTTCCCATGGAAACCCAGACCTTGAGTACCCAGATGA 5692
QY      666 TGCCTTCTGTTAATGCTGTAGAAAGATTAAGCAAAATTTGGTTCAAGATGGCAAGCTAA 725
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| QY | 726 | GCATCAAGGTGCTCAATATGTTTGGAAATAGAACTGCTTTGTTGCAAGCTGCTGATGATTC | 785 |
| Db | 5753 | GCGCCAGGGTGCCCCGGTATGTTGGAAACCGCACTGAGCTGATGACAGGCTTCCCTGGACCC | 5812 |
| QY | 786 | TAGTGTACTCATTTGATGGGTTTGTGTAACCACTGATGATGAAGTATATGTTCAACA | 845 |
| Db | 5813 | GTTCTGTAACCATCTCATGGGTCTCTTTGAGCCTGGAAGCATGAATAACGAGATCCACCG | 5872 |
| QY | 846 | AGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCAAGTTTGTTC | 905 |
| Db | 5873 | AGACTCCACACTGGAACCCCTCCCTGATGGAGATGACAGAGGCTGCCCTGCGCTGTAG | 5932 |
| QY | 906 | TAGAAATCCAAAGAGTTTAACTTGTCTTTGTTGTAAGGTGGTAAATTTGATCATGCTATCA | 965 |
| Db | 5933 | CAGGAACCCCCCGGCTTCTTCTCTTCTGTTGAGGGGTGTTCATCGAACCATGGTCAATCA | 5992 |
| QY | 966 | TGATGCTAAGGCTTATATGGCTTTGACTGGAAGCTATATGTTGTAATGCTATTTGCTAA | 1025 |
| Db | 5993 | TGAAGCAGGGCTTACCGGGCACTGAGACGATCATGTTTGCACGACGCCATTGGAGAG | 6052 |
| QY | 1026 | GGCTAATGAATTGACTTCTGAATTGGATACCTTTGATTTGGTTACTGCTGATCATAGTCA | 1085 |
| Db | 6053 | GCGGGGCCAGCTCACCGAGGAGAGACACGCTGAGCCTGTCTCACTGCCAGCACCTCCA | 6112 |
| QY | 1086 | TGTTTTTCTTTTGGTGTTACACTTTGAGAGGTACTTTATTTTGGTTGGCTCCAGG | 1145 |
| Db | 6113 | CGTCTTCTCTTGGAGCTACCCCTGCGAGGAGCTCATCTTGGGCTGGCCCCCTGG | 6172 |
| QY | 1146 | TAAAGCTTTGATAGTAAGTCTTACACTTCTATTTTGTAATGTAATGTCACAGTTATGC | 1205 |
| Db | 6173 | CAAGGCCCGGACAGGAAGGCTTACACGCTCTCTTAACGAAACGCTCAGGCTATGT | 6232 |
| QY | 1206 | TTTGGGTGGTGTCTAGACCAAGATGTTAATGTAAGTACTAGTGAAGAACCATCTTACAG | 1265 |
| Db | 6233 | GCTCAAGGACGGCGCCCGCGGATGTTACCGAGAGCGAGAGCGGGAGCCCCGAGTATCG | 6292 |
| QY | 1266 | ACAACAAGCTGCTGTTCATTGGCTAGTGAACCTCATGGTGGTGAAGATGTTGCTGTTT | 1325 |
| Db | 6293 | GCAAGCAGTCAAGAGTGCCCTTGACGAAGAGACCCACGACGCGGAGGACGTGGCGGTGT | 6352 |
| QY | 1326 | TGCTAGAGGTCCACAAGCTCATTTGGTTCATGGTGTTCAAAGAAACTTTTGTGCTCA | 1385 |
| Db | 6353 | CGCGCGCGCCCCGACGGCGCACTGTGTTACGGCGGTGACGAGACGACACTTCAATAGCGCA | 6412 |
| QY | 1386 | TATTATGGCTTTTGGTGTGTGTTGAACCATACATGATTTGTAATTTGCCAGCTCCAGC | 1445 |
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RESULT 7
US-09-263-933-15
; Sequence 15, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Polts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 13910
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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? LOCATION: (497)..(772)
? FEATURE:
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? LOCATION: (1425)..(6500)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (8579)..(9034)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (10191)..(10445)
? FEATURE:
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? LOCATION: (11877)..(12734)
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)..(774)
? OTHER INFORMATION: Vaccinia Virus thymidine Kinase gene recombination
? OTHER INFORMATION: site
? FEATURE:
? NAME/KEY: promoter
? LOCATION: (794)..(816)
? OTHER INFORMATION: T7 promoter
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (846)..(1424)
? OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1426)..(1437)
? OTHER INFORMATION: MCS (Multiple Cloning Site)
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1446)..(2318)
? OTHER INFORMATION: HCV E2/ NS2 domain
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (2319)..(4231)
? OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
? OTHER INFORMATION: helicase enzymes
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (4203)..(4260)
? OTHER INFORMATION: HCV NS3-NS4A cleavage site
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (4375)..(4424)
? OTHER INFORMATION: HCV NS4A-4B cleavage site
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (4233)..(4394)
? OTHER INFORMATION: HCV NS4A domain
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (4395)..(4919)
? OTHER INFORMATION: HCV NS4B Domain
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (4920)..(4991)
? OTHER INFORMATION: HCV NS5A-NS5B cleavage site
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (4992)..(6501)
? OTHER INFORMATION: SEAP Protein
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (7915)..(7945)
? OTHER INFORMATION: MCS (Multiple Cloning Site)
? FEATURE:
? NAME/KEY: terminator
? LOCATION: (7938)..(8078)

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; OTHER INFORMATION: term T7
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (8080)..(8365)
; OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8560)..(11317)
; OTHER INFORMATION: E. coli gpt; for selection of recombinants
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11318)..(13909)
; OTHER INFORMATION: remaining DNA from 3' end of Tropicx PCMV/SEAP
; OTHER INFORMATION: plasmid
US-09-263-933-15
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Query Match      38.8%; Score 572.8; DB 3; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
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DB      5033 CATCATCCAGTTGAGAGAGAACCCGAGCTTCTGGAACCGGAGCGAGCGAGCCCT 5092
OY      66 GGATGTTGCTAAGACTTGCAACCAATTCAACTGCTGCTAAGATGTTATTGTTT 125
DB      5093 GGGTGCCGCCAAGAACTGCAAGCTGCAACAGACCCGCCAAGAACTTCATCTTCT 5152
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DB      5153 GGGCGATGGATGGGGGTGTCTACGGTGACAGCTGCCAGATCTTAAAGGCGAAGAA 5212
OY      186 TGGTAAGTTGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGT 245
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DB      5273 CAAGACATACAATGTAGACAACATGTGCCAGACAGTGAGCCACAGCCGCTTACT 5332
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DB      5333 GTGCGGGGTCAAGGCACTTCCAGACCATTTGGCTTGAAGTGCAAGCCGCCCTT 5392
OY      366 ATGTAATACTACTAGAGCTAATGAAGTACTTCTGTTATTATAGAGCTAAGAGGCT 425
DB      5393 GTGCAACACGACACGGGCAACGAGGTCTATCTCGTATGAATCGGGCCAGAAAGCAG 5452
OY      426 TAAGGCTGTTGGTGTGTTACTACTACTAGATTCACATGCTTCTCCAGCTGCTGCT 485
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DB      5513 CGCCACACGCTGAACCGCAACTGTACTCGGACGCCGAGCTGCTGCTGCGCCGCCA 5572
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OY      606 GGGTGTGTTAGATGATCATGTTTCCAGAAAGGTACTCCAGATCCAGAAATCCAGATGA 665
DB      5633 AGGTGAGGCGGAAAGTACATGTTTCCCATGGGAACCCAGACCTGAGTACCCAGATGA 5692
OY      666 TGCTTCTGTTAATGTTGTAGAAAGATTAAGCAAAATTTGTTCAAGATGCAAGCTAA 725
DB      5693 CTACAGCCAAGGTGGACCAAGCTGACCGGGAAGAAATCTGTGACAGAAATGCTGGCGAA 5752
OY      726 GCATCAAGGTGCTCATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGATGATTC 785
DB      5753 GCGCAGGTTGCCGGTATGTGTGAACCGCACTGAGCTGATGCAAGGCTTCCCTGAGCCC 5812
OY      786 TAGTGTACTCATTTGATGGTTTGTGTAACCAAGCTGATATGAAGTATATGTTCAACA 845
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OY      846 AGATCATACTTAAGGATCCCACTTTGGCTGAATGACTGAAGCTGCTTTGCAAGTTTGTG 905
DB      5873 AGACTCCACACTGGAACCCCTCCCTGATGGAGATGAACAGAGGCTGCCCTGCTGAG 5932
OY      906 TAGAATCCAGAGGTTTCTTACTGTTGTTGTTGAAGGTGTAGAAATTCATGCTCATCA 965
DB      5933 CAGGAACCCCGGCTTCTTCTCTTGTGAGGGGTGTGCAATGCAATGCTCATCA 5992
OY      966 TGATGTTAAGCTTATATGCTTTGACTGAAGCTATTATGTTGATAATGCTATTGCTTAA 1025
DB      5993 TGAAGCAGGGCTTACCGGCACTGACATGACATCATGTTGACGACGCAATTTGAGAG 6052
OY      1026 GGCTAATGAATGACTTCTGAAATGGAATGTAATTTGGTTACTGCTGATCATAGTCA 1085
DB      6053 GGGGGCCAGCTCACACGAGGAGACACGCTGAGCCTGCTCATGCTGCCAATCCCA 6112
OY      1086 TGTTTTTCTTTTGGTGTGCTTACACTTTGAGAGTACTTCTATTTTTGGCTTGCCTCAGG 1145
DB      6113 GCTTCTCTCTTGGAGGCTACCCCTGCGAGGAGCTGATCTTGGGCTGCCCCCTGG 6172
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DB      6173 CAAGGCCCGGACAGGAAGGCTTACACGGTCTCTATACGAAACGGTCCAGGCTATGT 6232
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OY      1266 ACACAGAGCTGCTGTTCCATTGGCTAGTGAATCTCATGTGTGTAAGATGTTGCTGTTT 1325
DB      6293 GCAGCAGTCAAGAGTGCCTCCCTGACGAGAGACCAACGAGCGAGCGTGGCTGTT 6352
OY      1326 TGCTAGAGTTCACAAAGCTCATTTGTTGATGCTGTTCAGAGAAACCTTTGTTGCTCA 1385
DB      6353 CGCGCGCGCGGCAAGCGCACTGTTTCAAGCGGCTGACAGGACAGACTTCATAGCGCA 6412
OY      1386 TATTATGGCTTTTGTGCTGTTGTGTTGAACATACACTGATTTGTAATTTGCCAGCTCAGC 1445
DB      6413 CGTCATGGCTTGCCTGCGGCTGCTGAGGCTTACACCGCTGCGACTGGCGCCCCCGC 6472

RESULT 8
US-09-919-901-1
; Sequence 1, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 13910
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 1
; NAME/KEY: CDS
; LOCATION: (497)..(772)
; FEATURE:
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/ LOCATION: (11877)..(12734)
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/ OTHER INFORMATION: site
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/ OTHER INFORMATION: T7 promoter
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/ LOCATION: (1426)..(1437)
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/ OTHER INFORMATION: HCV E2/ NS2 domain
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/ OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
/ OTHER INFORMATION: helicase enzymes
/ FEATURE:
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/ OTHER INFORMATION: HCV NS4A-4B cleavage site
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/ OTHER INFORMATION: HCV NS4A domain
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/ OTHER INFORMATION: HCV NS4B Domain
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/ OTHER INFORMATION: HCV NS5A-NS5B cleavage site
/ FEATURE:
/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: SEAP Protein
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/ NAME/KEY: misc_feature
/ LOCATION: (7915)..(7945)
/ OTHER INFORMATION: MCS (Multiple Cloning Site)
/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (7938)..(8078)
/ OTHER INFORMATION: term T7
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (8080)..(8365)
/ OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (8560)..(11317)
/ OTHER INFORMATION: E. coli gpc; for selection of recombinants
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (11318)..(13909)
/ OTHER INFORMATION: remaining DNA from 3' end of Tropicx PCMV/SEAP
/ OTHER INFORMATION: plasmid
/ US-09-919-901-1

Query Match      38.8%; Score 572.8; DB 4; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

QY      6 CTTCATTCACGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAGCTTT 65
DB      503 CATCATCCCAAGTTGAGAGAGAAACCCGACTTCTGGAACCGGAGCAGCGGCCCT 5092
QY      66 GGATGTTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGAATGTTATTTT 125
DB      5093 GGGTGCCGCCAAGAAAGCTGCAAGCTTGACACAGACAGCCGCAAGAACCTCATCTTCT 5152
QY      126 GGGTGATGTTATGGGTGTTCCAACTGTTACTGCTTACTAGAAATTTGAAGGCTCAATGAA 185
DB      5153 GGGCGATGGATGGGGGTGTTCTACGGTGACAGCTGCCAGGATCTTAAAGGGCAGAGAA 5212
QY      186 TGGTAAGTTGGGTCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGTG 245
DB      5213 GGACAAACTGGGCGCTGAGATACCCCTGGCCATGGAACGCTTCCATATGTGCTGTG 5272
QY      246 TAAGACTTACAATGTTGATAGACAAGTTCCAGATTCTGCTGTTACTGTTACTGTTACTT 305
DB      5273 CAAGACATACAATGTAGACAACATGTGCCAGACAGTGAAGCCACAGCCAGGCTTACT 5332
QY      306 GTGTGTTGTTAAGGTAATTACAGAATATGTTGTTTCTGCTGCTGCTAGATACAATCA 365
DB      5333 GTGGGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAAGTGCAAGCCGCCCTTAAACA 5392
QY      366 ATGTAATTAATACTAGAGTAATGAAGTTACTTCTGTTAATTAAGAGCTAAGAGGCTGG 425
DB      5393 GTGCAACACGACACGCGGCAACGAGTCAATCTCCGTGATGAATCGGGCCAAAGAACGAG 5452
QY      426 TAAGCTGTTGTTGTTTACTACTACTAGAGTTCAATGCTTCTCCAGCTGGTGTCTTA 485
DB      5453 GAAGTCAGTGGAGTGTAAACCAACACAGAGTGCACGCGCTCGCCAGCGGCACTTA 5512
QY      486 CGCTCATCTGTTAATGAATAATGTTGTTACTCTGATGCTGATTTGCCAGCTGATCTCAAAA 545
DB      5513 CGCCACACGCGTGAACCGCACTGTTACTCGAGCGCGAGCTGCTGCTGCGCGCCCA 5572
QY      546 GAATGTTGTCAGAATAATGCTGCTCAATTGGTTTACAATATGATATGATGTTATTTT 605
DB      5573 GAGGGGTGCCAGACATGCTTACGAGCTCATCTCAACATGACATGACATGACGATGATCT 5632
QY      606 GGGTGGTGTAGATGATGATGTTTCCAGAGGTAATCCAGATCCAGATACCCAGATGA 665
DB      5633 AGGTGAGGCGGAAAGTACATGTTTCCCATGGGAACCCAGACCTGAGTACCCAGATGA 5692
QY      666 TGCTTCTGTTAATGTTGTTGAAGATGAAGATAATTTGTTCAAGATGGCAAGCTAA 725
DB      5693 CTACAGCCCAAGGTGGGACCAAGGCTGACCGGAAGAACTGTGTCAGGAATGGCTGGCGAA 5752
QY      726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGTTGTTGCAAGCTGCTGATGATTC 785
DB      5753 GCGCCAGGGTGCCCGGTATGTGTGAACCGCACGTGATGACAGGCTTCCCTGGAACCC 5812
QY      786 TAGTGTACTCATTTGATGGGTTTGTGGAACGACGCTGATATGAAGTATTAATGTTCAACA 845
DB      5813 GTCTGTGACCATCTCATGGGCTCTTTGAGGCTGGAGACATGAATAACGAGATCCACCG 5872
QY      846 AGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGCAGTTTGTTC 905
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Db 6233 GCTCAAGGACGCGCGCCCGCGGATGTTACCGAGAGCGAGCGGAGCCCGAGTATCG 6292
Qy 1266 ACAACAAGCTGCTGTTCCATTGGCTAGTGAACATCATGTGTTGAAGATGTTGCTGTTT 1325
Db 6293 GCAGCAGTCAGAGTGCCTCCCTGAGCAGGAAGACCCACGAGGCGAGGACGTGGCGTGT 6352
Qy 1326 TGCTAGAGTCCAGAGCTCATTTGTTGTTGAACCATACATGATTGTAATTGCCAGCTCCAGC 1385
Db 6353 CGCGCGCGCGCGCAGCGCGCAGCTGTTACGCGCTGCAGAGCAGACCTTCATAGCGCA 6412
Qy 1386 TATTATGCTTTGCTGTTGTTGTTGAACCATACATGATTGTAATTGCCAGCTCCAGC 1445
Db 6413 CGTCATGCTCTTCCGCCCTGCTGAGCCCTACACCGCCTGCGACCTGCGCGCCCGCCGC 6472
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RESULT 9

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US-09-919-901-8
; Sequence 8, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13910
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (497)..(772)
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8579)..(9034)
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10191)..(10445)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11877)..(12734)
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; NAME/KEY: misc feature
; LOCATION: (1)..(774)
; OTHER INFORMATION: Vaccinia Virus thymidine Kinase gene recombination
; OTHER INFORMATION: site
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (794)..(816)
; OTHER INFORMATION: T7 promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (846)..(1424)
; OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1426)..(1437)
; OTHER INFORMATION: MCS (Multiple Cloning Site)
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; NAME/KEY: misc feature
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; OTHER INFORMATION: HCV E2/ NS2 domain
; FEATURE:
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; LOCATION: (2319)..(4231)
; OTHER INFORMATION: HCV NS3 Domain, containing the serine protease and
; OTHER INFORMATION: helicase enzymes
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; LOCATION: (4203)..(4260)
; OTHER INFORMATION: HCV NS3-NS4A cleavage site
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; OTHER INFORMATION: HCV NS4A-4B cleavage site
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; OTHER INFORMATION: HCV NS4A domain
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; OTHER INFORMATION: HCV NS4B Domain
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; NAME/KEY: misc feature
; LOCATION: (4920)..(4991)
; OTHER INFORMATION: HCV NS5A-NS5B cleavage site
; FEATURE:
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; LOCATION: (4992)..(6501)
; OTHER INFORMATION: SEAP Protein
; FEATURE:
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; LOCATION: (7915)..(7945)
; OTHER INFORMATION: MCS (Multiple Cloning Site)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (7938)..(8078)
; OTHER INFORMATION: term T7
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (8080)..(8365)
; OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8560)..(11317)
; OTHER INFORMATION: E. coli gpt; for selection of recombinants
; FEATURE:
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; NAME/KEY: misc.feature
; LOCATION: (11318)..(13909)
; OTHER INFORMATION: remaining DNA from 3' end of Tropicx pcmv/SEAP
; OTHER INFORMATION: plasmid
US-09-919-901-8
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Query Match      38.8%; Score 572.8; DB 4; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
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QY      6 CTTGATCCAGCTGAAGAAGAAATCCAGCTTTTGAATAGACAAGCTGCTCAAGCTTT 65
Db      5033 CATCATCCCAAGTTGAGAGAGAACCCGGAATTCTGGAACCGGAGGAGAGCCCT 5092
QY      66 GGATGTTGCTAAGAAGTTCACCAATTCAAACTGCTGCTAAGAAATGTTATTTT 125
Db      5093 GGGTGGCCCAAGAAGCTGCAGCCTGCACAGACGCCCAAGAACTCATCTTCT 5152
QY      126 GGGTATGTTATGGGTGTTCCAACTGTTACTGCTACTAGAATTTGAAGGGTCAATGAA 185
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QY      186 TGGTAAGTTGGGTCCAGAAACTCCATGGCTATGATCAATTCATACGTTGCTTGT 245
Db      5213 GGACAACTGGGGCTGAGATACCCCTGGCCATGACCGCTTCCATATGTGCTGTG 5272
QY      246 TAAAGCTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTTACTGCTACTT 305
Db      5273 CAAGACATACAATGTAGACAACAATGTGCCAGACAGTGGAGCCACAGCCAGCTTACCT 5332
QY      306 GTGTGTTGTTAAGGTAATTAACAATAATTGTTCTGCTGCTGCTAGATACAATCA 365
Db      5333 GTGGGGGTCAGAGGCACTTCAGACCATTTGGCTTGAGTGCAGCCGCCCTTAAACA 5392
QY      366 ATGTAATACTACTAGAGTAATGAAGTTACTTCTGTTATTAATAGACTAAGAGGCTG 425
Db      5393 GTGCAACACGACACGCGGCAACGAGTCATCTCCGTGATGAATCGGGCCAAAGAACGAG 5452
QY      426 TAAGCTGTGTTGTTTACTACTACTAGAGTTCACACATGCTTCTCCAGCTGCTT 485
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QY      486 CGCTCATCTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAA 545
Db      5513 CGCCACACGCGTGAACCGCAACTGTACTCGGACCGCAGCTGCTCGGCCGCCA 5572
QY      546 GAAATGTTGTCAAGATATTGCTCAATTGTTTACAAATAGGATATTGATGTTATTT 605
Db      5573 GGAAGGGTGCAGGACATCGTACGACCTCATCTCCAACATGGAATTTGACGTGATCT 5632
QY      606 GGGTGGTGTAGAAATGATCATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCAGATGA 665
Db      5633 AGGTGAGAGGCCGAAGTACATGTTTCCCATGGGAACCCCAACCTGAGTACCCAGATGA 5692
QY      666 TGCTTCTGTTAATGTTAGAAAGATAAGCAAAATTTGTTCAAGATGGCAAGCTTA 725
Db      5693 CTACAGCCCAAGGTGGGACCAAGGCTGGAACGGGAAGATCTGTTGCAAGATGGCTGGCAA 5752
QY      726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGTCAGAGCTGCTGATGATTC 785
Db      5753 GCGCCAGGGTGCCCGGTATGTGGAACCGCACTGAGCTGATGCAAGGCTTCCCTGAGCCC 5812
QY      786 TAGTGTACTCATTTGATGGGTTTGTGAACCAAGCTGATATGAAGTATATGTTCAACA 845
Db      5813 GTCTGTGACCATCTCATGGGTCTTTTGAAGCCTGGAACATGAATATCAGATCCACCG 5872
QY      846 AGATCATACTAAGATCCAACTTTGGCTGAATGACTGAGCTGCTTGAAGTTTGTTC 905
Db      5873 AGACTCACAACCTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGAG 5932
QY      906 TAGAAATCCAAGAGTTTAACTTGTGTTGTTGAAGGTGTTAGATGATCATGCTCATCA 965
Db      5933 CAGGAACCCCCCGGCTTCTTCTCTTCTGAGAGGTGTTGCAATGCAATGCTCATCA 5992
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QY      966 TGATGTAAGCTTATATGCGTTTGACTGAAGCTATATGTTGATATGCTATTTGCTAA 1025
Db      5993 TGAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGACGCCATTGAGAG 6052
QY      1026 GGCTAATGAATTGACTTCTGAAATTTGATACTTTGATTTTGTACTGCTGATCATAGTCA 1085
Db      6053 GGGGGGCCAGCTCACCGACGAGAGAGACACGCTGAGCCTGCTCACTGCCGACCACTGCCA 6112
QY      1086 TGTTTTCTTTTGGTGTGTTACACTTTGAGAGGTACTTCTATTTTGGTTGGCTCCAGC 1145
Db      6113 GTCTTCTCTTCTGAGGCTAACCCCTCGAGGAGCTGATCTTGGGCTGGCCCTGG 6172
QY      1146 TAAGCTTTGATAGTAAGTCTTACACTTCTAATTTGTATGTATGTATGCTCAGCTTATGC 1205
Db      6173 CAAGGCCCGGACAGAGAGGCTTACACGCTCCTCTATACGAAACGGTCCAGGCTATGT 6232
QY      1206 TTTGGGTGTTGTTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCTTACAG 1265
Db      6233 GCTCAAGGACGGCGCCCGCGGATGTTACCGAGAGCAGAGCGGAGCCCGAGTATCG 6292
QY      1266 ACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGCTGATGTTGCTTTT 1325
Db      6293 GCAACGATCAGCAGTGCCTTGAACGAGAGACCCACGACGAGGAGACGTGGCGGT 6352
QY      1326 TGCTAGAGGTCCACAAGCTCATTTGTTTCAATGTTGTTCAAGAAGAACTTTGTTGCTCA 1385
Db      6353 CGCGCGCGCGCCGACAGGCGCACCTGTTTCAACGCGCTGCAAGAGACGACCTTCAATAGCGCA 6412
QY      1386 TATTATGCTTTTGTGTTGTTGTTGAACCATACCTGATTTGTAATTTGCCAGCTCCAGC 1445
Db      6413 CGTATGCGCTTGCCTGCGCCTGCTGAGCCCTTACACCGCTGCGAGCCTGGCGCCCGCCG 6472
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RESULT 10
US-09-919-901-15
; Sequence 15, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 13910
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 4
; NAME/KEY: CDS
; LOCATION: (497)..(772)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1425)..(6500)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8579)..(9034)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10191)..(10445)
; FEATURE:
; NAME/KEY: CDS
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LOCATION: (11877)..(12734)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(774)
OTHER INFORMATION: Vaccinia Virus thymidine Kinase gene recombination
OTHER INFORMATION: site
FEATURE:
NAME/KEY: promoter
LOCATION: (794)..(816)
OTHER INFORMATION: T7 promoter
FEATURE:
NAME/KEY: misc_feature
LOCATION: (846)..(1424)
OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1426)..(1437)
OTHER INFORMATION: MCS (Multiple Cloning Site)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV E2/ NS2 domain
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
OTHER INFORMATION: helicase enzymes
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4203)..(4260)
OTHER INFORMATION: HCV NS3-NS4A cleavage site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4375)..(4424)
OTHER INFORMATION: HCV NS4A-4B cleavage site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4233)..(4394)
OTHER INFORMATION: HCV NS4A domain
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4395)..(4919)
OTHER INFORMATION: HCV NS4B Domain
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4920)..(4991)
OTHER INFORMATION: HCV NS5A-NS5B cleavage site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP Protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (Multiple Cloning Site)
FEATURE:
NAME/KEY: terminator
LOCATION: (7938)..(8078)
OTHER INFORMATION: term T7
FEATURE:
NAME/KEY: promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
FEATURE:
NAME/KEY: misc_feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for selection of recombinants
FEATURE:
NAME/KEY: misc_feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining DNA from 3' end of Tropicx pCMV/SEAP
OTHER INFORMATION: plasmid
US-09-919-901-15

Query Match 38.8%; Score 572.8; DB 4; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 1898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
QY 6 CTTGATTCACCTGAGAGAGAAAATCCAGCTTTTGGAAATAGACAGCTGCTCAAGCTTT 65
DB 5033 CATCATCCCGAGTTGAGAGAGAGAACCCGCACTTCTGGAACCGCGAGCGAGGCCCT 5092
QY 66 GGATGTTGCTAAGAAAGTTGCAACCAATTCAACTGCTGCTAAGAAATGTTATTTT 125
DB 5093 GGGTGCCCGCAAGAAAGCTGCAGCCTTGACAGACAGCCGCAAGAACTCATCTTCT 5152
QY 126 GGGTGAATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGGTCAATGAA 185
DB 5153 GGGCGATGGATGGGGGTGTTCTACGGTGAACAGCTGCCAGATCCTAAAGGGCAGAAAGAA 5212
QY 186 TGGTAAGTTGGGTCAGAAACTCCATGCTATGATCAATTTCCATGCTTGTGTC 245
DB 5213 GGACAAACTGGGGCTGAGATACCCCTGGCCATGAGACCGCTTCCCATATGTGCTGTC 5272
QY 246 TAAGACTTACAATGTGATAGACAAGTTCAGATTCTGCTGCTACTGCTACTT 305
DB 5273 CAAGACATACATGTAGACAAACATGTGCCAGACAGTGAAGCCACAGCCACTACT 5332
QY 306 GTGTGTTGAAGGGTAATTACAGAACTATTGTTGTTCTGCTGCTGCTAGATACATCA 365
DB 5333 GTGCGGGTCAAGGGCAACTTCCAGACATTGGCTTGAAGTGACGCGCCGCTTTAACCA 5392
QY 366 ATGTAATACCTAGAGGTAAATGAAGTTACTTCTGTTATTAATAGACTAAGAGGCTG 425
DB 5393 GTGCAACACGACACGCGGCAACGAGTCACTCCGTGATGAATCGGCGCAAGAAAGCAG 5452
QY 426 TAAGCTGTGTTGTTGTTACTACTAGAGTTCAACATGCTTCCAGCTGCTGCTTA 485
DB 5453 GAAGTCAGTGGAGTGTGTAACCAACAGAGTGACAGACGCTGCGCAGCCGACCTA 5512
QY 486 CGCTCACTGTTAATAGAAATTTGTTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAA 545
DB 5513 CGCCACACCGGTGAACCGCACTGTTACTCGGACGCGCAGCTGCTGCTGCGCCGCCA 5572
QY 546 GAATGTTTCAAGATATTGCTGCTCAATTTGTTTACAATATGATATGATGTTATTT 605
DB 5573 GGAGGGTGCCAGACATCGTACGCACTCATCTCAACATGACATTGAAGTGATCCT 5632
QY 606 GGGTGTGTGAATGTACATGTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGA 665
DB 5633 AGGTGAGGCGGAAAGTACATGTTTCCATGGGAACCCAGACCTTGAGTACCAGATGA 5692
QY 666 TGCTTCTGTTAATGCTGTAGAAAGATTAAGCAAAATTTGTTCAAGATGGCAAGCTAA 725
DB 5693 CTACAGCCAGAGTGGAGACCAAGCTGACGGGAAGAAATCTGGTGACGAATGGCTGGCAA 5752
QY 726 GCATCAAGTGTCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGATGATTC 785
DB 5753 GCGCCAGGTGCGCGGTATGTGTGAACCGCACTGAGCTGATGACAGCTTCCCTGGAACC 5812
QY 786 TAGTGTACTATTGATGGGTTGTTTGAACCAAGCTGATATGAAGTATATGTTCAACA 845
DB 5813 GTCTGTGACCATCTCATGGGTCTCTTGAAGCTTGAGACATGAATAACAGATCCACCG 5872
QY 846 AGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTTTGTGTC 905
DB 5873 AGACTCCACACTGGAACCCCTCCCTGATGAGATGACAGAGGCTGCGCTGCTGAG 5932
QY 906 TAGAATCCAGAGGTTTACTTGTGTTGTAAGGTGCTAGAAATGATCATGTCATCA 965
DB 5933 CAGGAACCCCGCGGCTTCTCTCTGTTGAGAGGTGTCGATGACCATGTCATCA 5992
QY 966 TGATGTTAAGCTTATATGCTTGAAGCTGAAGCTATATGTTGTAATGCTATTGCTAA 1025
DB 5993 TGAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTTCAGCAGCAGCATTTGAGAG 6052

| | | | |
|----|------|---|------|
| QY | 1026 | GGCTAATGAATTGACTTCTGAATTGGATACCTTTGATTTTGGTTACTGCTGATCATATGCA | 1085 |
| Db | 6053 | GGCGGGCCAGCTCACCGAGGAGGACACGCTGAGCCTGTGCTGACCTGCCAGCACTCCCA | 6112 |
| QY | 1086 | TGTTTTTCTTTTGGTGTTACACTTTGAGAGGTACTTCTATTTTGGTTGGCTCCAGG | 1145 |
| Db | 6113 | CGTCTTCTCTTGGAGGTACCCCTGCGAGGAGCTGCATCTTGGGCTGGCCCTTGG | 6172 |
| QY | 1146 | TAAAGCTTTGATAGTAAGTCTTACACTTCTATTTTGTATGTATGTGCCAGTTATGC | 1205 |
| Db | 6173 | CAAGGCCCGGACAGAAAGCCTTACACGCTCCTCTATACGAAACGCTCAGGCTATGT | 6232 |
| QY | 1206 | TTTGGTGTTGTTCTAGACCAAGTGTTAATGTAGTACTAGTGAAGAACCATTCTACAG | 1265 |
| Db | 6233 | GCTCAAGACGCGCGCCCGCCGATGTTACCGAGAGCGAGCGGGAGCCCGAGTATCG | 6292 |
| QY | 1266 | ACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTGTGTGAAGATGTTGCTGTTT | 1325 |
| Db | 6293 | GCAGCAGTCAAGTAGTCCCTTGGACGAAGAAGACCCACGACGCGGAGCAGTGGCGGT | 6352 |
| QY | 1326 | TGCTAGAGGTCCACAAGCTCATTTGGTTTCATGTTGTTCAAGAAACTTTTGTGTTCA | 1385 |
| Db | 6353 | CGCGCGCGGCCCGCAGGCGCACCTGTGTTACGCGCGTGCAGAGACGACCTTCATAGCGCA | 6412 |
| QY | 1386 | TATTAATGCTTTTGTCTGTGTGTGAACCATACACTGATTTGTAATTTGCCAGCTCCAGC | 1445 |
| Db | 6413 | CGTCATGGCCTTCGCGCGCTTCTGTGAAGCCCTACACCGCTGCGACCTTGCGCCCCCGC | 6472 |

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RESULT 11
US-10-191-966-1
; Sequence 1, Application US/10191966
; Patent No. 6790612
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 13910
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid phcap 1
; NAME/KEY: CDS
; LOCATION: (497)..(772)
; NAME/KEY: CDS
; LOCATION: (1425)..(6500)
; NAME/KEY: CDS
; LOCATION: (1425)..(6500)
; NAME/KEY: CDS
; LOCATION: (8579)..(9034)
; NAME/KEY: CDS
; LOCATION: (10191)..(10445)
; NAME/KEY: CDS
; LOCATION: (11877)..(12734)
; NAME/KEY: misc feature
; LOCATION: (1)..(774)
; OTHER INFORMATION: Vaccinia Virus thymidine Kinase gene recombination
; OTHER INFORMATION: site
; NAME/KEY: promoter
; LOCATION: (794)..(816)
; OTHER INFORMATION: T7 promoter
; NAME/KEY: misc feature
; LOCATION: (846)..(1424)

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; OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
; NAME/KEY: misc feature
; LOCATION: (1426)..(1437)
; OTHER INFORMATION: MCS (Multiple Cloning Site)
; NAME/KEY: misc feature
; LOCATION: (1446)..(2318)
; OTHER INFORMATION: HCV E2/ NS2 domain
; NAME/KEY: misc feature
; LOCATION: (2319)..(4231)
; OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
; OTHER INFORMATION: helicase enzymes
; NAME/KEY: misc feature
; LOCATION: (4203)..(4260)
; OTHER INFORMATION: HCV NS3-NS4A cleavage site
; NAME/KEY: misc feature
; LOCATION: (4375)..(4424)
; OTHER INFORMATION: HCV NS4A-4B cleavage site
; NAME/KEY: misc feature
; LOCATION: (4233)..(4394)
; OTHER INFORMATION: HCV NS4A domain
; NAME/KEY: misc feature
; LOCATION: (4395)..(4919)
; OTHER INFORMATION: HCV NS4B Domain
; NAME/KEY: misc feature
; LOCATION: (4920)..(4991)
; OTHER INFORMATION: HCV NS5A-NS5B cleavage site
; NAME/KEY: misc feature
; LOCATION: (4992)..(6501)
; OTHER INFORMATION: SEAP Protein
; NAME/KEY: misc feature
; LOCATION: (7915)..(7945)
; OTHER INFORMATION: MCS (Multiple Cloning Site)
; NAME/KEY: terminator
; LOCATION: (7938)..(8078)
; OTHER INFORMATION: term T7
; NAME/KEY: promoter
; LOCATION: (8080)..(8365)
; OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
; NAME/KEY: misc feature
; LOCATION: (8560)..(11317)
; OTHER INFORMATION: E. coli gpt; for selection of recombinants
; NAME/KEY: misc_feature
; LOCATION: (11318)..(13909)
; OTHER INFORMATION: remaining DNA from 3' end of Tropicx PCMV/SEAP
; OTHER INFORMATION: plasmid
;
US-10-191-966-1

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| | Query Match | 38.8%; | Score 572.8; | DB 4; | Length 13910; | |
|----|-----------------------|---|---------------------|-----------|---------------|--|
| | Best Local Similarity | 62.4%; | Pred. No. 1.2e-141; | | | |
| | Matches 898; | Conservative 0; | Mismatches 542; | Indels 0; | Gaps 0; | |
| QY | 6 | CTTGATTCAGCTGAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTTT | 65 | | | |
| Db | 5033 | CATCATCCCACTGAGAGAGAAACCCGACTTCTGGAAACCGAGGACCGAGGCCCT | 50922 | | | |
| QY | 66 | GGATGTTGCTAAGAGTTGCCAACCAATTCCAACCTGCTGCTAAGATGTTATTTGTTTT | 125 | | | |
| Db | 5093 | GGGTGCCGCAAGAAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACTCATCTTTCT | 51522 | | | |
| QY | 126 | GGGTGATGTTATGGGTGTTCCAACTGTTACTGCTACTAGAATTTGAAAGGCTCAATGAA | 185 | | | |
| Db | 5153 | GGCGATGGATGGGGTGTCTACGTTGACAGCTGCCAGGATCCTAAAAGGGCAGAGAA | 52122 | | | |
| QY | 186 | TGTTAAGTTGGTCCAGAAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGT | 245 | | | |
| Db | 5213 | GGACAAACTGGGGCTGAGATACCCCTGGCCATGACCGCTTCCCATATGTGGCTCTGT | 52722 | | | |
| QY | 246 | TAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTACTGCTACTGCTTACTT | 305 | | | |
| Db | 5273 | CAAACATACAATGTAGACAACAATGTGTCAGACAGTGGAGCCACAGCCAAGGCTTACT | 53322 | | | |
| QY | 306 | GTGTGTGTTAAGGTAATTACAGAACTATTGGTGTCTGCTGCTGTAGATACAATCA | 365 | | | |

Db 5333 GTGCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCGCTTTAACCA 5392

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Qy 486 CGCTCATCTGTTAATAGAAATGGTACTCTGATGCTGATTTGGCAGCTGATGCTCAAA 545

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Qy 606 GGGTGTGTGAATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGA 665

Db 5633 AGGTGAGGCGGAAGTACATGTTTCCATGGGAACCCAGACCCTGAGTACCCAGATGA 5692

Qy 666 TGCTTCTGTTAATGGTGTGAAGAGATAAGCAAAATTTGTTCAAGATGGCAAGCTAA 725

Db 5693 CTACAGCCCAAGGTGGAGACCAAGCTGACGGGAAGAATCTGTGCAAGAAATGCGCTGGCGAA 5752

Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGATGATTC 785

Db 5753 GCGCCAGGGTGCCGGTATGTGTGAACCGCACTGAGCTGATGCAAGGCTTCCCTGAGCCC 5812

Qy 786 TAGTGTACTCATTTGATGGGTTGTTGAACAGCTGATATGAAGTATTAATGTTCAACA 845

Db 5813 GTCTGTGACCCATCTCATGGGTCTCTTGAGCTGGAAGACATGAATAGAGATCCACCG 5872

Qy 846 AGATCATACTAAGATCCAACTTTGGCTGAAATGAAGCTGCTTTCAGAGTTTGTTC 905

Db 5873 AGACTCCACACTGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCTGCTGAG 5932

Qy 906 TAGAATCCAAAGGTTTTTACTTGTGTTGAGAGGTGAGATGAATGATGATGTCATCA 965

Db 5933 CAGGAACCCCGCGGCTTCTCTCTGTTGAGGGGTGTCGCATCGACCATGTCATCA 5992

Qy 966 TGATGTAAGCTTATATGCGCTTGACTGAAGCTATATGTTGATTAATGCTATTGCTAA 1025

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Db 6113 CGTCTTCTCTCGAGGCTACCCCTGCGAGGAGCTGCATCTTGGGCTGGCCCCCTGG 6172

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Qy 1206 TTTGGGTGGTGTCTAGACCAAGATGTTAATGTAAGTACTAGTGAAGAACCATCTTACAG 1265

Db 6233 GCTCAAGGACGGCGCCCGCGGCGGATGTTACCGAGAGCGAGAGCGGAGCCCGAGTATCG 6292

Qy 1266 ACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTTGTTGTAAGATGTTGCTGTTT 1325

Db 6293 GCAGCAGTACAGTGCCTCTGAGCAGAAAGACCCACGAGGCGAGAGCTGGCGGTGT 6352

Qy 1326 TGCTAGAGTCCACAAGCTCATTTGTTGTTCAAGAGAACTTTTGTGCTCA 1385

Db 6353 CGCGCGCGCGCGCAGCGCACCTGTTTCAAGGCGTGAGAGCAGACCTTCATAGCGCA 6412

Qy 1386 TATTATGCTTTTGTGCTGTGTGTGAACCATACATGATTTGATTTGCCAGCTCCAGC 1445

Db 6413 CGTCATGCGCTTGGCGCCCTGCGCTGAGAGCCCTTACACCGCCCTGCGACCTGGCGCCCCCGCG 6472

RESULT 12

US-10-191-966-8

; Sequence 8, Application US/10191966

; Patent No. 6790612

; GENERAL INFORMATION:

; APPLICANT: Potts, Karen E.

; APPLICANT: Jackson, Roberta L.

; APPLICANT: Patrick, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

; FILE REFERENCE: 0125-0005A

; CURRENT APPLICATION NUMBER: US/10/191,966

; CURRENT FILING DATE: 2002-07-10

; PRIOR APPLICATION NUMBER: US/09/263,933

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/129,611

; PRIOR FILING DATE: 1998-08-05

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 13910

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 3

; NAME/KEY: CDS

; LOCATION: (497)..(772)

; NAME/KEY: CDS

; LOCATION: (1425)..(6500)

; NAME/KEY: CDS

; LOCATION: (8579)..(9034)

; NAME/KEY: CDS

; LOCATION: (10191)..(10445)

; NAME/KEY: CDS

; LOCATION: (11877)..(12734)

; NAME/KEY: misc_feature

; LOCATION: (1)..(774)

; OTHER INFORMATION: Vaccinia virus thymidine kinase gene recombination

; OTHER INFORMATION: site

; NAME/KEY: Promoter

; LOCATION: (794)..(816)

; OTHER INFORMATION: T7 promoter

; NAME/KEY: misc_feature

; LOCATION: (846)..(1424)

; OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)

; NAME/KEY: misc_feature

; LOCATION: (1426)..(1437)

; OTHER INFORMATION: MCS (Multiple Cloning Site)

; NAME/KEY: misc_feature

; LOCATION: (1446)..(2318)

; OTHER INFORMATION: HCV E2/ NS2 domain

; NAME/KEY: misc_feature

; LOCATION: (2315)..(4231)

; OTHER INFORMATION: HCV NS3 Domain containing the serine protease and

; OTHER INFORMATION: helicase enzymes

; NAME/KEY: misc_feature

; LOCATION: (4203)..(4260)

; OTHER INFORMATION: HCV NS3-NS4A cleavage site

; NAME/KEY: misc_feature

; LOCATION: (4375)..(4424)

; OTHER INFORMATION: HCV NS4A-4B cleavage site

; NAME/KEY: misc_feature

; LOCATION: (4233)..(4394)

; OTHER INFORMATION: HCV NS4A domain

; NAME/KEY: misc_feature

; LOCATION: (4395)..(4919)

; OTHER INFORMATION: HCV NS4B Domain

; NAME/KEY: misc_feature

; LOCATION: (4920)..(4991)

; OTHER INFORMATION: HCV NS5A-NS5B cleavage site

; NAME/KEY: misc_feature

LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP Protein
NAME/KEY: misc feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (Multiple Cloning Site)
NAME/KEY: terminator
LOCATION: (7938)..(8078)
OTHER INFORMATION: term T7
NAME/KEY: promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
NAME/KEY: misc feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for selection of recombinants
NAME/KEY: misc feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining DNA from 3' end of Tropicx pCMV/SEAP
OTHER INFORMATION: plasmid
US-10-191-966-8

Query Match 38.8%; Score 572.8; DB 4; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

QY 6 CTTGATCCAGCTGAGAGAAATCCAGCTTTTGAATAGACAAGCTGCTCAAGCTTT 65
Db 5033 CATCATCCCAAGTTGAGAGAGAACCCGGAAGCTTCTGAAACCGGAGGCGAGGCCCT 5092
QY 66 GGAATGTTCTAAGAAGTTCACCAATTCAACTGCTGCTAAGAAATGTTATTTT 125
Db 5093 GGGTGGCCCAAGAAGCTGCAGCTGCACAGACAGCCGCCAAGAAGCTCATCTTCT 5152
QY 126 GGGTGAATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGGTCAAAATGAA 185
Db 5153 GGGCATGGGATGGGGTGTCTACGGTGACAGCTGCCAGATCTTAAAGGGCAGAAAGAA 5212
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QY 366 ATGTAATACTACTAGAGTAATGAAGTACTTCTGTTATTAATAGACTAAGAAAGGCTGG 425
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QY 426 TAAAGCTGTTGTTGTTTACTACTAGAGTTCACACATGCTTCTCCAGCTGCTGCTTA 485
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Db 5633 AGGTGAGGCGCGAAAGTACATGTTTCCCATGGGAACCCCAAGACCTGAGTACCCAGATGA 5692
QY 666 TGCCTTCTGTTAATGTTTGAAGAGTAAGCAAAATTTGTTTCAAGAATGGCAAGCTTA 725
Db 5693 CTACAGCCCAAGGTGGAGCCAGGCTGACGCGAAGAAATCTGTGCAAGAAATGGCTGGCAA 5752
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QY 1386 TATTATGCTTTGCTGTTGTTGTTGTTGAACCATACACTGATTTGTTGTTGTTGTTGTT 1445
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RESULT 13
US-10-191-966-15
Sequence 15, Application US/10191966
Patent No. 6790612
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 13910
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 4

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LOCATION: (497)..(772)
NAME/KEY: CDS
LOCATION: (1425)..(6500)
NAME/KEY: CDS
LOCATION: (8579)..(9034)
NAME/KEY: CDS
LOCATION: (10191)..(10445)
NAME/KEY: CDS
LOCATION: (11877)..(12734)
NAME/KEY: misc_feature
LOCATION: (1)..(774)
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NAME/KEY: promoter
LOCATION: (794)..(816)
OTHER INFORMATION: T7 promoter
NAME/KEY: misc_feature
LOCATION: (846)..(1424)
OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
NAME/KEY: misc_feature
LOCATION: (1426)..(1437)
OTHER INFORMATION: MCS (Multiple Cloning Site)
NAME/KEY: misc_feature
LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV E2/ NS2 domain
NAME/KEY: misc_feature
LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
OTHER INFORMATION: helicase enzymes
NAME/KEY: misc_feature
LOCATION: (4203)..(4260)
OTHER INFORMATION: HCV NS3-NS4A cleavage site
NAME/KEY: misc_feature
LOCATION: (4375)..(4424)
OTHER INFORMATION: HCV NS4A-4B cleavage site
NAME/KEY: misc_feature
LOCATION: (4233)..(4394)
OTHER INFORMATION: HCV NS4A domain
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LOCATION: (4395)..(4919)
OTHER INFORMATION: HCV NS4B Domain
NAME/KEY: misc_feature
LOCATION: (4920)..(4991)
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OTHER INFORMATION: SEAP Protein
NAME/KEY: misc_feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (Multiple Cloning Site)
NAME/KEY: terminator
LOCATION: (7938)..(8078)
OTHER INFORMATION: term T7
NAME/KEY: promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
NAME/KEY: misc_feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for selection of recombinants
NAME/KEY: misc_feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining DNA from 3' end of Tropicx PCMV/SEAP
OTHER INFORMATION: plasmid
US-10-191-966-15

Query Match 38.8%; Score 572.8; DB 4; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
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QY 66 GGATGTTGCTAAGAAGTTGCAACCAATTCAAACTGCTGCTAAGATGTATTTGTTTTT 125
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DB 5153 GGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCTTAAAGGGCAGAGAA 5212
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DB 5213 GGACAACTGGGGCTGAGATACCCCTGGCCATGAGACCGCTTCCATATGTGCTGTGTC 5272
QY 246 TAAGACTTAATGTTGATAGACAAGTTCCAGATTCTGCTGGTACTGCTACTGCTTACTT 305
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DB 5393 GTCAACACGACACCGCGCAACGAGTCAATCTCCGTATGAAATCGGGCCAAAGAACAGG 5452
QY 426 TAAGCTGTGTGTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGTGCTTA 485
DB 5453 GAAGTCACTGGAGTGTAAACACACACAGAGTGCAGACGCTGCGCAAGCCGACCTTA 5512
QY 486 CGCTCACTGTTAATAGAAATGTAATCTGATGCTGATTTGCCAGCTGATGCTCAAAA 545
DB 5513 CGCCACACGGTGAACCGCAACTGTAATCGGACGCGAGCTGCTGCTGCGCCGCCA 5572
QY 546 GAATGTTGCTCAAGATATTTGCTGCTCAATGCTTACAAATATGATATGATGTTATTT 605
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QY 606 GGGTGTGTTGAATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGA 665
DB 5633 AGGTGAGGCCGAAGTACATGTTTCCATGGGAACCCCAAGCCTGAGTACCAGATGA 5692
QY 666 TGCTTCTGTTAATGTTGTTAGAAAGATAAGCAAAATTTGTTCAAGATGGCAAGCTAA 725
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QY 786 TAGTGTACTCATTTGATGGGTTGTTGAACCAAGCTGATATGAAGTATATATGTTCAACA 845
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QY 846 AGATCATACTAAGGATCCAACTTTGCTGAATGACTGAAGCTGCTTGCAGATTGTC 905
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US-09-693-011-11
; Sequence 11, Application US/09693011
; Patent No. 6632978
; GENERAL INFORMATION:
; APPLICANT: Kaslin, Edgar
; APPLICANT: Luyten, Marcel
; APPLICANT: Zermes, Hans-Gunter
; TITLE OF INVENTION: Transgenic Animals For
; FILE REFERENCE: 4-31176A
; CURRENT APPLICATION NUMBER: US/09/693,011
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 5083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA CONSTRUCT
US-09-693-011-11

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| Best Local Similarity | 62.3%; | Pred. No. 2e-141; | | |
| Matches 897; | Conservative | 0; | Mismatches 543; | Indels 0; |
| | | | | Gaps 0; |

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| Db | 1194 | GGGTGCCGCCAAGAAGCTGCAGCTGCACAGACAGCCGCCAAGAACCTCATCTTCCCT | 1253 |
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| QY | 366 | ATGTAATACTACTAGAGTAATGAAGTTACTTCTGTTATTAATAGAGCTAAGAAGGCTGG | 425 |
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| Db | 1674 | GGAAGGGGTGCAGACATCGCTACGCAAGCTCATCTCCAACATGACATTGACGTGATCCT | 1733 |
| QY | 606 | GGGTGCTGTAGATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACCAAGATGA | 665 |
| Db | 1734 | AGGTGGAAGGCCGAAAGTACATGTTTCCCATGCGGAACCCCAAGACCTGAGTACCAGATGA | 1793 |
| QY | 666 | TGCTTCTGTTAATGTTGTAGAAAAGATTAAGCAAAATTGGTTCAAGAAATGGCAAGCTTA | 725 |
| Db | 1794 | CTACAGCCAAAGGTGGAGCCAGCGCTGGAACGGGAAGAAATCTGGTGCAGGAATGGCTGGCGAA | 1853 |

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| QY | 846 | AGATCATACTAAGATCCAACTTTGCGTGAATGACTGAAGCTGCTTTGCAAGTTTGTGTC | 905 |
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| QY | 906 | TAGAATCCAGAAGTTTCTTACTTGTGTTGAAGTGTGAGATTGATTCATGTCATCA | 965 |
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| QY | 966 | TGATGTAAGGCTTATATGCTTTGACTGAACTATTATGTTGATATGCTATTGCTAA | 1025 |
| Db | 2094 | TGAAGCAGGGCTTACCGGCACTGACTGAGACGATCATGTTGACGACGCATTGAGAG | 2153 |
| QY | 1026 | GGCTAATGAATTGACTTCTGAATTGATACCTTGATTTTGGTTACTGCTGATCATAGTCA | 1085 |
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| QY | 1086 | TGTTTTTCTTTGCTGCTTACACTTTGAGAGTACTTCTATTTTGGTTGGCTCCAGG | 1145 |
| Db | 2214 | CGTCTTCTCTCGAGGCTACCCCTCGGAGGAGCTCCATCTTCGGGCTGGCCCTGG | 2273 |
| QY | 1146 | TAAAGCTTGGATAGTAAGTCTTACACTTTCTATTTTGTATGTTATGTTAGTCCAGTTATGC | 1205 |
| Db | 2274 | CAAGCCCCGGACAGGAAGGCTTACACGCTCTCTATACGAAACGGTCCAGGCTATGT | 2333 |
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| Db | 2334 | GCTCAAGACGGCGCCCGCGATGTTACCGAGAGCAGAGCGGAGCCCGAGTATCG | 2393 |
| QY | 1266 | ACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTGTGTGAAGATGTGCTGTTT | 1325 |
| Db | 2394 | GCAGCAGTCAGCAGTGCCTTGACGAAGAGACCCACGACAGGCGAGAGCGTGGCGTGT | 2453 |
| QY | 1326 | TGCTAGAGTCCACAAGCTCATTTGGTTCAATGCTTCAAGAAGAACTTTGTGCTCA | 1385 |
| Db | 2454 | CGCGCGCGCGCCGACAGCGCACCTGTTTACGCGCGTGCAGGACGACCTTCATAGCGCA | 2513 |
| QY | 1386 | TATTATGGCTTTGCTGTGTGTGTTGAACCATACCTGATTGTAATTTGCCAGCTCCAGC | 1445 |
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Job time : 144.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: October 19, 2004, 14:44:42 ; Search time 753.5 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3403857 seqs, 2557783690 residues

Total number of hits satisfying chosen parameters: 6807714

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1476 | 100.0 | 1476 | 16 US-10-395-790A-3 | Sequence 3, Appli |
| 3 | 1474.4 | 99.9 | 1476 | 16 US-10-395-790A-8 | Sequence 8, Appli |
| 4 | 1472.8 | 99.8 | 1476 | 16 US-10-395-790A-9 | Sequence 9, Appli |
| 5 | 1471.2 | 99.7 | 1476 | 16 US-10-395-790A-10 | Sequence 10, Appli |
| 6 | 1469.6 | 99.6 | 1476 | 16 US-10-395-790A-11 | Sequence 11, Appli |
| 7 | 845.6 | 57.3 | 1476 | 10 US-09-911-132A-1 | Sequence 1, Appli |
| 8 | 834.8 | 56.6 | 1464 | 16 US-10-053-790A-1 | Sequence 1, Appli |
| 9 | 572.8 | 38.8 | 1597 | 15 US-10-053-637-9 | Sequence 9, Appli |
| 10 | 572.8 | 38.8 | 1634 | 9 US-09-006-298-22 | Sequence 22, Appli |
| 11 | 572.8 | 38.8 | 1675 | 15 US-10-053-637-11 | Sequence 11, Appli |
| 12 | 572.8 | 38.8 | 1728 | 10 US-09-908-943A-127 | Sequence 127, Appli |
| 13 | 572.8 | 38.8 | 1748 | 15 US-10-053-637-19 | Sequence 19, Appli |

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| 17 | 572.8 | 38.8 | 1975 | 15 US-10-053-637-27 | Sequence 27, Appli |
| 18 | 572.8 | 38.8 | 2239 | 9 US-09-747-419-18 | Sequence 18, Appli |
| 19 | 572.8 | 38.8 | 2239 | 15 US-10-259-275-18 | Sequence 18, Appli |
| 20 | 572.8 | 38.8 | 7469 | 9 US-09-776-167A-6 | Sequence 6, Appli |
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| 23 | 572.8 | 38.8 | 13910 | 10 US-09-919-901-15 | Sequence 15, Appli |
| 24 | 572.8 | 38.8 | 13910 | 15 US-10-191-966-1 | Sequence 1, Appli |
| 25 | 572.8 | 38.8 | 13910 | 15 US-10-191-966-8 | Sequence 8, Appli |
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| 27 | 572.4 | 38.8 | 1779 | 15 US-10-071-645-4 | Sequence 4, Appli |
| 28 | 572.4 | 38.8 | 2051 | 16 US-10-182-094-7 | Sequence 7, Appli |
| 29 | 572.4 | 38.8 | 2121 | 16 US-10-182-094-9 | Sequence 9, Appli |
| 30 | 571.2 | 38.7 | 1558 | 17 US-10-332-733-26 | Sequence 26, Appli |
| 31 | 571.2 | 38.7 | 1560 | 9 US-09-965-697-10 | Sequence 10, Appli |
| 32 | 571.2 | 38.7 | 2645 | 17 US-10-645-794-3 | Sequence 3, Appli |
| 33 | 571.2 | 38.7 | 2662 | 17 US-10-645-883A-5 | Sequence 5, Appli |
| 34 | 571.2 | 38.7 | 2662 | 18 US-10-645-187-5 | Sequence 5, Appli |
| 35 | 571.2 | 38.7 | 4260 | 16 US-10-395-709-16 | Sequence 16, Appli |
| 36 | 571.2 | 38.7 | 4260 | 16 US-10-315-907A-16 | Sequence 16, Appli |
| 37 | 571.2 | 38.7 | 4260 | 17 US-10-281-067B-16 | Sequence 16, Appli |
| 38 | 571.2 | 38.7 | 4356 | 17 US-10-655-702-2 | Sequence 2, Appli |
| 39 | 571.2 | 38.7 | 4677 | 15 US-10-237-146-7 | Sequence 7, Appli |
| 40 | 571.2 | 38.7 | 4989 | 16 US-10-620-627-12 | Sequence 12, Appli |
| 41 | 571.2 | 38.7 | 5083 | 16 US-10-620-627-11 | Sequence 11, Appli |
| 42 | 571.2 | 38.7 | 5115 | 15 US-10-237-146-8 | Sequence 8, Appli |
| 43 | 571.2 | 38.7 | 5928 | 10 US-09-932-581-25 | Sequence 25, Appli |
| 44 | 571.2 | 38.7 | 5928 | 15 US-10-338-294-25 | Sequence 25, Appli |
| 45 | 571.2 | 38.7 | 6314 | 16 US-10-620-627-10 | Sequence 10, Appli |

ALIGNMENTS

RESULT 1
US-09-911-132A-5
; Sequence 5, Application US/09911132A
; Publication No. US20030096341A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Expression of Alkaline Phosphatase in Yeast
; FILE REFERENCE: RDID 0073US
; CURRENT APPLICATION NUMBER: US/09/911,132A
; CURRENT FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon-optimized DNA sequence
US-09-911-132A-5

| | | | | |
|-----------------------|-----------------|---|-----------|--------------|
| Query Match | 100.0%; | Score 1476; | DB 10; | Length 1476; |
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 1476; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | GAATTCCTGATCCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA | 60 | |
| DB | 1 | GAATTCCTGATCCAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA | 60 | |
| QY | 61 | GCTTTGATGTTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGATGTTATTG | 120 | |
| DB | 61 | GCTTTGATGTTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGATGTTATTG | 120 | |
| QY | 121 | TTTTGGGATGATGGTATGGGTGTTCCAACTGTACTGCTACTAGAAATTTGAAGGCTCAA | 180 | |
| DB | 121 | TTTTGGGATGATGGTATGGGTGTTCCAACTGTACTGCTACTAGAAATTTGAAGGCTCAA | 180 | |

OY 181 ATGAATGGTAAGTTGGGTCAGAACTCCATTGGCTATGGATCAATTCCATACGTTGCT 240
DB 181 ATGAATGGTAAGTTGGGTCAGAACTCCATTGGCTATGGATCAATTCCATACGTTGCT 240
OY 241 TTGCTAAGCTTACAATGTTGATAGACAAGTCCAGATTCTGCTGTACTGCTACTGCT 300
DB 241 TTGCTAAGCTTACAATGTTGATAGACAAGTCCAGATTCTGCTGTACTGCTACTGCT 300
OY 301 TACTTGTGTGGTGTAAAGGTAATTACAGAACTATTGGTGTCTGCTGCTAGATAC 360
DB 301 TACTTGTGTGGTGTAAAGGTAATTACAGAACTATTGGTGTCTGCTGCTAGATAC 360
OY 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTATTATAGAGCTAAGAAG 420
DB 361 AATCAATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTATTATAGAGCTAAGAAG 420
OY 421 GCTGTAAGGCTGTTGGTGTGTTACTACTACTAGAGTCAACATGCTTCTCCAGCTGCT 480
DB 421 GCTGTAAGGCTGTTGGTGTGTTACTACTACTAGAGTCAACATGCTTCTCCAGCTGCT 480
OY 481 GCTTACGCTCATACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540
DB 481 GCTTACGCTCATACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540
OY 541 CAAAAGAAATGTTGTCAAGATATGCTGCTCAATTGTTTACAATATGATATTGATGTT 600
DB 541 CAAAAGAAATGTTGTCAAGATATGCTGCTCAATTGTTTACAATATGATATTGATGTT 600
OY 601 ATTTGGGTGGTGTAGATGTACATGTTCCAGAAGGTACTCCAGATCCAGATACCACCA 660
DB 601 ATTTGGGTGGTGTAGATGTACATGTTCCAGAAGGTACTCCAGATCCAGATACCACCA 660
OY 661 GATGATGCTTCTGTTAATGTTGTAGAAAGATAAGCAAAATTTGGTTCAAGATGGCAA 720
DB 661 GATGATGCTTCTGTTAATGTTGTAGAAAGATAAGCAAAATTTGGTTCAAGATGGCAA 720
OY 721 GCTAAGCATCAAGGCTCTCAATATGTTGGAAATAGAACTGCTTGTGCAAGCTGCTGAT 780
DB 721 GCTAAGCATCAAGGCTCTCAATATGTTGGAAATAGAACTGCTTGTGCAAGCTGCTGAT 780
OY 781 GATTCTAAGTGTACTCATTTGATGGGTTGTTGTAACCAAGCTGATATGAAGTATATGTT 840
DB 781 GATTCTAAGTGTACTCATTTGATGGGTTGTTGTAACCAAGCTGATATGAAGTATATGTT 840
OY 901 TTGCTAAGAAATCCAAGAGGTTTACTTGTGTTGTAAGGTGTAGAATTGATCATGCT 960
DB 901 TTGCTAAGAAATCCAAGAGGTTTACTTGTGTTGTAAGGTGTAGAATTGATCATGCT 960
OY 961 CATCATGATGTTAAGGCTTATATGGCTTTGACTGAAGCTATATGTTGTAATGCTATT 1020
DB 961 CATCATGATGTTAAGGCTTATATGGCTTTGACTGAAGCTATATGTTGTAATGCTATT 1020
OY 1021 GCTAAGGCTAATGAATTGACTTCTGAATTGGATACCTTGAATTTGGTTACTGCTGATCAT 1080
DB 1021 GCTAAGGCTAATGAATTGACTTCTGAATTGGATACCTTGAATTTGGTTACTGCTGATCAT 1080
OY 1081 AGTCATGTTTTCTTTGGTGTGTTCACTTTGAGAGGTAATTTTGGTTGGCT 1140
DB 1081 AGTCATGTTTTCTTTGGTGTGTTCACTTTGAGAGGTAATTTTGGTTGGCT 1140
OY 1141 CCAGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTGTATGTTAATGTCAGAGT 1200
DB 1141 CCAGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTGTATGTTAATGTCAGAGT 1200
OY 1201 TATGCTTTGGGTGGTGTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCT 1260
DB 1201 TATGCTTTGGGTGGTGTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCT 1260
OY 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAAACTCATGTTGGTGAAGATGTTGCT 1320

DB 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAAACTCATGCTGTGAAGATGTTGCT 1320
OY 1321 GTTTTGTCTAGAGGTCCACAAGCTCATTTGGTTCATGGTGTCAAGAGAAGAACTTTTGT 1380
DB 1321 GTTTTGTCTAGAGGTCCACAAGCTCATTTGGTTCATGGTGTCAAGAGAAGAACTTTGT 1380
OY 1381 GCTCATATTATGGCTTTTGTGCTGTTGTGTGAACCATACATGATTGTAATTTGCCAGCT 1440
DB 1381 GCTCATATTATGGCTTTTGTGCTGTTGTGTGAACCATACATGATTGTAATTTGCCAGCT 1440
OY 1441 CCAGCTACTGCTACTAGTAATTCAGATTAAAGTACC 1476
DB 1441 CCAGCTACTGCTACTAGTAATTCAGATTAAAGTACC 1476

RESULT 2
US-10-395-790A-3
; Sequence 3, Application US/10395790A
; Publication No. US20040072316A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase
; TITLE OF INVENTION: and their expression in yeast
; FILE REFERENCE: RDID 0202805
; CURRENT APPLICATION NUMBER: US/10/395,790A
; CURRENT FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: codon-optimized alkaline phosphatase sequence
US-10-395-790A-3

Query Match 100.0%; Score 1476; DB 16; Length 1476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GAATCTTGATTCAGCTGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
DB 1 GAATCTTGATTCAGCTGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
OY 61 GCTTTGATGTTGCTAAGAGTGTCAACCAATTCAAAGCTGCTAAGAAATGTTATTTTG 120
DB 61 GCTTTGATGTTGCTAAGAGTGTCAACCAATTCAAAGCTGCTAAGAAATGTTATTTTG 120
OY 121 TTTTGGGTGATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
DB 121 TTTTGGGTGATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAA 180
OY 181 ATGAATGTAAGTTGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCT 240
DB 181 ATGAATGTAAGTTGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCT 240
OY 241 TTGCTAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTAATGCTGCTGCT 300
DB 241 TTGCTAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTAATGCTGCTGCT 300
OY 301 TACTTGTGTGGTGTAAAGGTAATTACAGAACTATTTGCTGCTGCTGCTAGATAC 360
DB 301 TACTTGTGTGGTGTAAAGGTAATTACAGAACTATTTGCTGCTGCTGCTAGATAC 360
OY 361 AATCAATGTATATACTACTAGAGGTAATGAAGTTACTTCTGTATTATATAGAGCTAAGAAG 420
DB 361 AATCAATGTATATACTACTAGAGGTAATGAAGTTACTTCTGTATTATATAGAGCTAAGAAG 420
OY 421 GCTGTAAGGCTGTTGGTGTGTTACTACTACTAGAGTCAACATGCTTCTCCAGCTGCT 480
DB 421 GCTGTAAGGCTGTTGGTGTGTTACTACTACTAGAGTCAACATGCTTCTCCAGCTGCT 480

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OY 481 GCTTACGCTCATACTGTTAATAGAAATTGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540
DB 481 GCTTACGCTCATACTGTTAATAGAAATTGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540
OY 541 CAAAAGATGGTGTCAAGATATTGCTGCTCAATTGGTTACAAATATGATATTGATGTT 600
DB 541 CAAAAGATGGTGTCAAGATATTGCTGCTCAATTGGTTACAAATATGATATTGATGTT 600
OY 601 ATTTGGGTGGTGTAGATGTACATGTTTCCAGAAGGTACTCCAGATCCAGATATACCA 660
DB 601 ATTTGGGTGGTGTAGATGTACATGTTTCCAGAAGGTACTCCAGATCCAGATATACCA 660
OY 661 GATGATGCTTCTGTTAATGCTGTAGAAAGATAAGCAAAATTTGGTTCAAGAATGGCAA 720
DB 661 GATGATGCTTCTGTTAATGCTGTAGAAAGATAAGCAAAATTTGGTTCAAGAATGGCAA 720
OY 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780
DB 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780
OY 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGTAACCAAGCTGATATGATATATGTT 840
DB 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGTAACCAAGCTGATATGATATATGTT 840
OY 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCAAGTT 900
DB 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCAAGTT 900
OY 901 TTGCTAGAAATCCAAAGGTTTTCCTGTTTGTGTAAGGTGGTGAATTCATCATGCT 960
DB 901 TTGCTAGAAATCCAAAGGTTTTCCTGTTTGTGTAAGGTGGTGAATTCATCATGCT 960
OY 961 CATCATGATGTGAAGGCTTATATGCTTGAAGCTATTAATGTTGATTAATGCTATT 1020
DB 961 CATCATGATGTGAAGGCTTATATGCTTGAAGCTATTAATGTTGATTAATGCTATT 1020
OY 1021 GCTAAGGCTAATGAATGACTTCTGAATGATCTTGAATGTTGTTGTTGTTGCTGATCAT 1080
DB 1021 GCTAAGGCTAATGAATGACTTCTGAATGATCTTGAATGTTGTTGTTGTTGCTGATCAT 1080
OY 1081 AGTCATGTTTTTTCTTTGGTGTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
DB 1081 AGTCATGTTTTTTCTTTGGTGTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
OY 1141 CCAGGTAAGGCTTTGGATAGTAACTTCTTACCTTCTATTTGTATGTTAATGGTCCAGGT 1200
DB 1141 CCAGGTAAGGCTTTGGATAGTAACTTCTTACCTTCTATTTGTATGTTAATGGTCCAGGT 1200
OY 1201 TATGCTTTGGGTGGTGTCTAGACCAAGTGTAAATGTTAGTACTAGTGAAGAACCATCT 1260
DB 1201 TATGCTTTGGGTGGTGTCTAGACCAAGTGTAAATGTTAGTACTAGTGAAGAACCATCT 1260
OY 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGTGTAAGATGTTGCT 1320
DB 1261 TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGTGTAAGATGTTGCT 1320
OY 1321 GTTTTGTCTAGAGTCCACAAGCTCATTTGGTTCAATGCTGTGTTCAAGAGAACTTTTGT 1380
DB 1321 GTTTTGTCTAGAGTCCACAAGCTCATTTGGTTCAATGCTGTGTTCAAGAGAACTTTTGT 1380
OY 1381 GCTCATATTAATGGCTTTGCTGCTGTGTTGAACCATACACTGATTTGTTGCTGAGCT 1440
DB 1381 GCTCATATTAATGGCTTTGCTGCTGTGTTGAACCATACACTGATTTGTTGCTGAGCT 1440
OY 1441 CCAGCTACTGCTACTAGTATTCAGATTAAGGTACC 1476
DB 1441 CCAGCTACTGCTACTAGTATTCAGATTAAGGTACC 1476
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RESULT 3
US-10-395-790A-8
; Sequence 8, Application US/10395790A
; Publication No. US20040072316A1

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; GENERAL INFORMATION:  
; APPLICANT: Roche Diagnostics Corp.  
; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase  
; TITLE OF INVENTION: and their expression in yeast  
; FILE REFERENCE: RDID 02028US  
; CURRENT APPLICATION NUMBER: US/10/395,790A  
; CURRENT FILING DATE: 2003-03-24  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 1476  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: coding sequence for Ser92Ala mutant  
US-10-395-790A-8  
  
Query Match 99.9%; Score 1474.4; DB 16; Length 1476;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
OY 1 GAATTCCTGATTCACAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60  
DB 1 GAATTCCTGATTCACAGCTGAAGAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60  
OY 61 GCTTTGGATGTTGCTTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGAATGTTATTG 120  
DB 61 GCTTTGGATGTTGCTTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGAATGTTATTG 120  
OY 121 TTTTGGGTGATGATGGGTGTTTCCAACTGTTACTGCTACTAGAAATTTGAAGGGTCAA 180  
DB 121 TTTTGGGTGATGATGGGTGTTTCCAACTGTTACTGCTACTAGAAATTTGAAGGGTCAA 180  
OY 181 ATGAATGTAAAGTTGGTCCAGAAATCCATTGGCTATGATCAATTCATACGTTGCT 240  
DB 181 ATGAATGTAAAGTTGGTCCAGAAATCCATTGGCTATGATCAATTCATACGTTGCT 240  
OY 241 TTGTTGAAGACTTACAATGTTGATAGACAAGTTCCAGATTTCTGCTGTAATGCTACTGCT 300  
DB 241 TTGTTGAAGACTTACAATGTTGATAGACAAGTTCCAGATTTCTGCTGTAATGCTACTGCT 300  
OY 301 TACTTGTGTGTTAAGGGTAAATTAAGAACTATTGTTGTTCTGCTGCTAGATAC 360  
DB 301 TACTTGTGTGTTAAGGGTAAATTAAGAACTATTGTTGTTCTGCTGCTAGATAC 360  
OY 361 AATCAATGTAACTACTAGAGTAAAGTAACTTCTGTTAATAAGCTAAGAAG 420  
DB 361 AATCAATGTAACTACTAGAGTAAAGTAACTTCTGTTAATAAGCTAAGAAG 420  
OY 421 GCTGTGAAGGCTGTTGGTGTGTTACTACTAGATTCACATGCTTCTCCAGCTGCT 480  
DB 421 GCTGTGAAGGCTGTTGGTGTGTTACTACTAGATTCACATGCTTCTCCAGCTGCT 480  
OY 481 GCTTACGCTCATCTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540  
DB 481 GCTTACGCTCATCTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540  
OY 541 CAAAAGATGGTGTCAAGATATTGCTGCTCAATTTGTTTACAAATATGATATTGATGTT 600  
DB 541 CAAAAGATGGTGTCAAGATATTGCTGCTCAATTTGTTTACAAATATGATATTGATGTT 600  
OY 601 ATTTGGGTGGTGTAGATGTACATGTTTCCAGAAGGTACTCCAGATCCAGATATACCA 660  
DB 601 ATTTGGGTGGTGTAGATGTACATGTTTCCAGAAGGTACTCCAGATCCAGATATACCA 660  
OY 661 GATGATGCTTCTGTTAATGCTGTAGAAAGATAAGCAAAATTTGGTTCAAGAATGGCAA 720  
DB 661 GATGATGCTTCTGTTAATGCTGTAGAAAGATAAGCAAAATTTGGTTCAAGAATGGCAA 720  
OY 721 GCTAAGCATCAAGGTGCTCAATATGTTTGGAAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780  
DB 721 GCTAAGCATCAAGGTGCTCAATATGTTTGGAAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780
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[illegible]

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RESULT 4
US-10-395-790A-9
; Sequence 9, Application US/10395790A
; Publication No. US20040072316A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase
; TITLE OF INVENTION: and their expression in yeast
; FILE REFERENCE: RDID 02028US
; CURRENT APPLICATION NUMBER: US/10/395,790A
; CURRENT FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: coding sequence for Gly322Phe mutant
US-10-395-790A-9

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| | | | | |
|----------------------------|--------|---------------|-----------|--------------|
| Query Match | 99.8% | Score 1472.8; | DB 16; | Length 1476; |
| Best Local Similarity | 99.9%; | Pred. No. 0; | | |
| Matches 1474; Conservative | 0; | Mismatches 2; | Indels 0; | Gaps 0; |

✓

[illegible]

Db 1021 GCTAAGCCTAATGACTTCTGAAATGACATCTTGGTTACTGCTGATCAT 1080

✓

| | | | |
|----|------|---|------|
| QY | 1081 | AGTCATGTTTTTCTTTTGGTGGTTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT | 1140 |
| Db | 1081 | AGTCATGTTTTTCTTTTGGTGGTTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT | 1140 |
| QY | 1141 | CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGGTAATGGTCCAGGT | 1200 |
| Db | 1141 | CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCTATTTTGTATGGTAATGGTCCAGGT | 1200 |
| QY | 1201 | TATGCTTTGGGTGGTGTTCTAGACCAGATGTTAATGTAAGTACTAGTGAAGAACCATCT | 1260 |
| Db | 1201 | TATGCTTTGGGTGGTGTTCTAGACCAGATGTTAATGTAAGTACTAGTGAAGAACCATCT | 1260 |
| QY | 1261 | TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTGGTGAAGATGTTGCT | 1320 |
| Db | 1261 | TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTGGTGAAGATGTTGCT | 1320 |
| QY | 1321 | GTTTTTGTAGAGGTCCACAAGCTCATTTGGTTCATGGTGTTCAAGAAGAACTTTGTT | 1380 |
| Db | 1321 | GTTTTTGTAGAGGTCCACAAGCTCATTTGGTTCATGGTGTTCAAGAAGAACTTTGTT | 1380 |
| QY | 1381 | GCTCATATTATGCGCTTTTGGCTGTGTGTTGAACCATACACTGATTTGTAATTTGCCAGCT | 1440 |
| Db | 1381 | GCTCATATTATGCGCTTTTGGCTGTGTGTTGAACCATACACTGATTTGTAATTTGCCAGCT | 1440 |
| QY | 1441 | CCAGCTACTGCTACTAGTAATTTCCAGATTTAAGGTACC | 1476 |
| Db | 1441 | CCAGCTACTGCTACTAGTAATTTCCAGATTTAAGGTACC | 1476 |

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RESULT 5
US-10-395-790A-10
; Sequence 10, Application US/10395790A
; Publication No. US20040072316A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase
; TITLE OF INVENTION: and their expression in yeast
; FILE REFERENCE: RDID 02028US
; CURRENT APPLICATION NUMBER: US/10/395,790A
; CURRENT FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: coding sequence for His320Asn/Gly322Phe mutant
US-10-395-790A-10

```

[illegible]

| | | | |
|----|------|--|------|
| QY | 301 | TACTGTGTGTGTTAAGGTAATTACAGAACTATTGGTGTTCCTGCTGCTAGATAC | 360 |
| Db | 301 | TACTGTGTGTGTTAAGGTAATTACAGAACTATTGGTGTTCCTGCTGCTAGATAC | 360 |
| QY | 361 | AATCAATGTATACTACTAGAGTAATGAAGTTACTCTGTATTATAGAGCTAAGAG | 420 |
| Db | 361 | AATCAATGTATACTACTAGAGTAATGAAGTTACTCTGTATTATAGAGCTAAGAG | 420 |
| QY | 421 | GCTGTAAGGCTGTGGTGTGTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGT | 480 |
| Db | 421 | GCTGTAAGGCTGTGGTGTGTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGT | 480 |
| QY | 481 | GCTTACGCTCATCTGTGTTAATAGAAATTGGTACTCTGATGCTGATTTTGGCAGCTGATGCT | 540 |
| Db | 481 | GCTTACGCTCATCTGTGTTAATAGAAATTGGTACTCTGATGCTGATTTTGGCAGCTGATGCT | 540 |
| QY | 541 | CAAAAGAATGTTGTCAGAGATATTGCTGCTCAATTGGTTTACAATATGATATTGATGTT | 600 |
| Db | 541 | CAAAAGAATGTTGTCAGAGATATTGCTGCTCAATTGGTTTACAATATGATATTGATGTT | 600 |
| QY | 601 | ATTTTGGGTGGTGGTAGAATGTACATGTTTCCAGAAGTACTCCAGATCCAGAATACCA | 660 |
| Db | 601 | ATTTTGGGTGGTGGTAGAATGTACATGTTTCCAGAAGTACTCCAGATCCAGAATACCA | 660 |
| QY | 661 | GATGATGCTTCTGTTAATGCTGTAGAAAGATTAAGCAAAATTGGTTCAGAATGGCAA | 720 |
| Db | 661 | GATGATGCTTCTGTTAATGCTGTAGAAAGATTAAGCAAAATTGGTTCAGAATGGCAA | 720 |
| QY | 721 | GCTAAGCATCAAGTGCTCAATATGTTTGGAAATAGAACTGCTTGTGCAAGCTGCTGAT | 780 |
| Db | 721 | GCTAAGCATCAAGTGCTCAATATGTTTGGAAATAGAACTGCTTGTGCAAGCTGCTGAT | 780 |
| QY | 781 | GATTCTAGTGTACTCATTTGATGGGTTGTTGAAACAGCTGATATGAAGTATATATGTT | 840 |
| Db | 781 | GATTCTAGTGTACTCATTTGATGGGTTGTTGAAACAGCTGATATGAAGTATATATGTT | 840 |
| QY | 841 | CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTT | 900 |
| Db | 841 | CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTT | 900 |
| QY | 901 | TTGCTAGAAATCCAAGAGTTTCTACTTGTGTTGTAAGGTGTTAGATTCATGCT | 960 |
| Db | 901 | TTGCTAGAAATCCAAGAGTTTCTACTTGTGTTGTAAGGTGTTAGATTCATGCT | 960 |
| QY | 961 | CATCATGATGTTAAGGCTTATATGCTTTGACTGAAGCTATTATGTTGATAATGCTATT | 1020 |
| Db | 961 | CATCATGATGTTAAGGCTTATATGCTTTGACTGAAGCTATTATGTTGATAATGCTATT | 1020 |
| QY | 1021 | GCTAAGGCTAATGAATTGACTTCTGAATTGATACTTGAATTTGGTTACTGCTGATCAT | 1080 |
| Db | 1021 | GCTAAGGCTAATGAATTGACTTCTGAATTGATACTTGAATTTGGTTACTGCTGATCAT | 1080 |
| QY | 1081 | AGTCATGTTTTTCTTTTGGTGTACACTTTGAGAGTACTTCTATTTTTTGGTTGGCT | 1140 |
| Db | 1081 | AGTCATGTTTTTCTTTTGGTGTACACTTTGAGAGTACTTCTATTTTTTGGTTGGCT | 1140 |
| QY | 1141 | CCAGGTAAGGCTTTGGAATGTAAGTCTTACACTTCTAATTTTGTATGTTAATGCTCCAGGT | 1200 |
| Db | 1141 | CCAGGTAAGGCTTTGGAATGTAAGTCTTACACTTCTAATTTTGTATGTTAATGCTCCAGGT | 1200 |
| QY | 1201 | TATGCTTTGGGTGGTGTCTAGACCAGATGTTAATGTAAGTACTAGTGAAGAACCATCT | 1260 |
| Db | 1201 | TATGCTTTGGGTGGTGTCTAGACCAGATGTTAATGTAAGTACTAGTGAAGAACCATCT | 1260 |
| QY | 1261 | TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGTGTAAGATGTTGCT | 1320 |
| Db | 1261 | TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGTGTAAGATGTTGCT | 1320 |
| QY | 1321 | GTTTTTGTAGAGTCCACAAGCTCATTTGGTTCATGGTGTCAAGAAGAACTTTGTT | 1380 |
| Db | 1321 | GTTTTTGTAGAGTCCACAAGCTCATTTGGTTCATGGTGTCAAGAAGAACTTTGTT | 1380 |

QY 1381 GCTCATATATGCGCTTTTGCTGCTGTGTGTTGAACCATACACTGATTGTAAATTGCCAGCT 1440
Db 1381 GCTCATATATGCGCTTTTGCTGCTGTGTGTTGAACCATACACTGATTGTAAATTGCCAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTATTTCCAGATTAAAGGTACC 1476
Db 1441 CCAGCTACTGCTACTAGTATTTCCAGATTAAAGGTACC 1476

RESULT 6

US-10-395-790A-11
; Sequence 11, Application US/10395790A
; Publication No. US20040072316A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase
; TITLE OF INVENTION: and their expression in yeast
; FILE REFERENCE: RDID 02028US
; CURRENT APPLICATION NUMBER: US/10/395,790A
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: coding sequence for Ser92Ala/His320Asn/Gly322Phe mutant
US-10-395-790A-11

Query Match 99.6%; Score 1469.6; DB 16; Length 1476;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAATTCCTGATTCAGCTGAAGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
Db 1 GAATTCCTGATTCAGCTGAAGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
QY 61 GCTTTGGATGTTGCTAAGAAGTGCACCAATTCCAACTGCTGCTAAGAATGTTATTTTG 120
Db 61 GCTTTGGATGTTGCTAAGAAGTGCACCAATTCCAACTGCTGCTAAGAATGTTATTTTG 120
QY 121 TTTTGGGATGATGATGATGGGTGTTCCAAGTCTTACTGCTACTAGAAATTTGGAAGGGTCAA 180
Db 121 TTTTGGGATGATGATGATGGGTGTTCCAAGTCTTACTGCTACTAGAAATTTGGAAGGGTCAA 180
QY 181 ATGAATGTAAGTTGGGTCAGAAACTCCATTGGCTATGATCAATTTCCATACGTGCT 240
Db 181 ATGAATGTAAGTTGGGTCAGAAACTCCATTGGCTATGATCAATTTCCATACGTGCT 240
QY 241 TTGCTTAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGCTACTGCTACTGCT 300
Db 241 TTGCTTAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGCTACTGCTACTGCT 300
QY 301 TACTGTGTGCTGTTAAGGGTAATTAACAAGTATTTCTGCTGCTGCTAGATAC 360
Db 301 TACTGTGTGCTGTTAAGGGTAATTAACAAGTATTTCTGCTGCTGCTAGATAC 360
QY 361 AATCAATGTAATTAATACTAGAGGTAATGAAGTTACTTCTGTTAATTAAGAGCTAAGAG 420
Db 361 AATCAATGTAATTAATACTAGAGGTAATGAAGTTACTTCTGTTAATTAAGAGCTAAGAG 420
QY 421 GCTGTAAGGCTGTGCTGTTGTTAATACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
Db 421 GCTGTAAGGCTGTGCTGTTGTTAATACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
QY 481 GCTTAAGCTCATACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540
Db 481 GCTTAAGCTCATACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540
QY 541 CAAAGAATGTTGTCAAGATATGCTGCTCAATTGTTTACAATATGATATGATGTT 600
Db 541 CAAAGAATGTTGTCAAGATATGCTGCTCAATTGTTTACAATATGATATGATGTT 600

QY 601 ATTTGGGTGCTGTAGATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACCCA 660
Db 601 ATTTGGGTGCTGTAGATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACCCA 660
QY 661 GATGATGCTTCTGTTAATGGTGTAGAAAGGATAAGCAAAATTTGGTTCAGAATGGCAA 720
Db 661 GATGATGCTTCTGTTAATGGTGTAGAAAGGATAAGCAAAATTTGGTTCAGAATGGCAA 720

QY 721 GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGAT 780
Db 721 GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGAT 780

QY 781 GATTCTAGTGTACTCATTTGATGGCTTTGTTGAACCACTGATATGAAGTAAATGTT 840
Db 781 GATTCTAGTGTACTCATTTGATGGCTTTGTTGAACCACTGATATGAAGTAAATGTT 840

QY 841 CAAGAATCATATAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGCAGTT 900
Db 841 CAAGAATCATATAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGCAGTT 900

QY 901 TTGCTAGAAATCCAGAGGTTTACTTGTGTTGTTGAAGGTGCTGAATGATCATGCT 960
Db 901 TTGCTAGAAATCCAGAGGTTTACTTGTGTTGTTGAAGGTGCTGAATGATCATGCT 960

QY 961 CATCATGATGTTAAGGCTTATATGCTTGTGACTGAAAGCTATATGTTGATATGCTATT 1020
Db 961 CATCATGATGTTAAGGCTTATATGCTTGTGACTGAAAGCTATATGTTGATATGCTATT 1020

QY 1021 GCTAAGGCTAATGAATGACTTCTGAATTGGATACCTTGTGTTGTTACTGCTGATCAT 1080
Db 1021 GCTAAGGCTAATGAATGACTTCTGAATTGGATACCTTGTGTTGTTACTGCTGATCAT 1080

QY 1081 AGTCATGTTTTTTCTTTGGTGGTTACACCTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
Db 1081 AGTCATGTTTTTTCTTTGGTGGTTACACCTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140

QY 1141 CCAGTAAAGCTTTGGATAGTAAGCTTACACTTCTAATTTTGTATGTAATGCTCCAGGT 1200
Db 1141 CCAGTAAAGCTTTGGATAGTAAGCTTACACTTCTAATTTTGTATGTAATGCTCCAGGT 1200

QY 1201 TATGCTTTGGGTGCTGTTCTAGACCAAGTGTAAATGTTAGTACTAGTGAAGAACCATCT 1260
Db 1201 TATGCTTTGGGTGCTGTTCTAGACCAAGTGTAAATGTTAGTACTAGTGAAGAACCATCT 1260

QY 1261 TACAGACACAAAGCTGCTGTTCCATTGGCTAGTGAAACTCATGTGCTGAAGATGTTGCT 1320
Db 1261 TACAGACACAAAGCTGCTGTTCCATTGGCTAGTGAAACTCATGTGCTGAAGATGTTGCT 1320

QY 1321 GTTTTGTAGAGGTCACAAGCTCATTTGGTTCATAGTGTTCAGAAGAACTTTTGT 1380
Db 1321 GTTTTGTAGAGGTCACAAGCTCATTTGGTTCATAGTGTTCAGAAGAACTTTTGT 1380

QY 1381 GCTCATATATGCGCTTTTGCTGCTGTGTTGAACCATACACTGATTGTAAATTGCCAGCT 1440
Db 1381 GCTCATATATGCGCTTTTGCTGCTGTGTTGAACCATACACTGATTGTAAATTGCCAGCT 1440

QY 1441 CCAGCTACTGCTACTAGTATTTCCAGATTAAAGGTACC 1476
Db 1441 CCAGCTACTGCTACTAGTATTTCCAGATTAAAGGTACC 1476

RESULT 7

US-09-911-132A-1
; Sequence 1, Application US/09911132A
; Publication No. US20030096341A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Expression of Alkaline Phosphatase in Yeast
; FILE REFERENCE: RDID 0073US
; CURRENT APPLICATION NUMBER: US/09/911,132A
; NUMBER OF SEQ ID NOS: 38

SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1476
TYPE: DNA
ORGANISM: Bovine
US-09-911-132A-1

Query Match 57.3%; Score 845.6; DB 10; Length 1476;
Best Local Similarity 73.3%; Pred. No. 1.1e-182;
Matches 1082; Conservative 0; Mismatches 394; Indels 0; Gaps 0;

QY 1 GAATTCCTGATCCAGCTGAAGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA 60
DB 1 GAATTCCTCATCCAGCTGAGAGAGAAACCCTGCTTCTGGAACCGCAGGCGCCAG 60
QY 61 GCTTTGATGTTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGAATGTTAATTTG 120
DB 61 GCCCTTGATGTAGCCAGAAGAGTTGCAGCCGATCCAGACAGCTGCCAGAATGTCTC 120
QY 121 TTTTGGGTGATGTTAGTGGGTGTTCCAACTGTTACTGCTACTAGAATTTGAAGGCTCAA 180
DB 121 TTCTTGGGGATGGGATGGGGGTGCTTACCGGTGACAGCCACTCGGATCCTAAAGGGGCGAG 180
QY 181 ATGAATGTAAGTTGGGTCCAGAACTCCATTGGCTATGATCAATTTCCATAGCTTGTCT 240
DB 181 ATGAATGGCAAACTGGGACTGAGACACCCCTGGCCATGGAACCAATTCCATACGTGGCT 240
QY 241 TTGTTAAGACTTACAATGTGATAGACAAAGTTCAGATTCTGCTGTAAGTCTGCTACTGCT 300
DB 241 CTGTCCAAGACATCAACGTGACAGACAGAGTGCAGACAGCGCAGCAGCTGCCACTGCC 300
QY 301 TACTGTGTGTTAGGAGGTAATTACAGAACTATTGTTTCTGCTGCTGCTAGATAC 360
DB 301 TACCTGTGTGGGTCAAGGGCACTACAGAACCAATCGGTGTAAGTGCAGCCGCCGCTAC 360
QY 361 AATCAATGTAATACTAGAGTAATGAAGTACTTCTGTATTATAGAGCTAAGAAG 420
DB 361 AATCAGTGCAACAGCACAGTGGGAATGAGGTCACTGTGATCAACCGGGCCAAAGAA 420
QY 421 GCTGTAGGCTGTGTTGTTGTTACTACTACTAGAGTTCAACATGCTTCTCAGCTGCT 480
DB 421 GCAGGGAAGGCCGTGGAGTGTGTACCAACCAAGGTTGAGCATGCTTCCCAAGCCGGG 480
QY 481 GCTTACGCTCATACTGTTAATAGAAATTTGTAATGCTGATGCTGATTTGCCAGCTGATGCT 540
DB 481 GCCTACGCGCACACGGTGAACCGAACTGTACTCAGACGCCGACCTGCTGCTGATGCA 540
QY 541 CAAAAGAAATGTTGTCAAGATATTGCTGCTCAATTGTTTACAATATGATATGATGTT 600
DB 541 CAGAAGAATGGCTGCAGAGCATCGCCGACAGCTGTTCTACAACATGATATGACGTG 600
QY 601 ATTTGGGTGTTAGATGTATGATGTTTCCAGAGGTAAGTCTCAGATCCAGAAATACCA 660
DB 601 ATCCTGGGTGAGGCCGAATGTATCATGTTTCTGAGGGGACCCCAAGACCTGAAATACCA 660
QY 661 GATGATGCTTCTGTTAATGTTGTTAGAAAGGATTAAGCAAAATTTGGTTCAAGATGGCAA 720
DB 661 GATGATGCCAGTGTGAATGAGTCCGGAAGGACAAGCAAACTGTTGCAAGAAATGGCAG 720
QY 721 GCTAAGCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGAT 780
DB 721 GCCAAGCACAGGAGCCAGTATGTGTGAACCGCACTGCGCTCTTCAAGCGGCGGAT 780
QY 781 GATTTAGTGTACTCATTTGATGAGGTTTGTGTAACCAAGCTGATATGATATGATGTT 840
DB 781 GACTCCAGTGTACACACCTCATGCGCTCTTGTGACCGGACAGACATGAATATATGTT 840
QY 841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCAAGTT 900
DB 841 CAGCAAGACCAACCAAGAACCCGACCTTGGCGAGATGACGAGCGCGCTGCAAGTG 900
QY 901 TTGTCTAGAATCCAGAGGTTTACTTGTGTTGTTGAAAGTGTGATATGATCATGCT 960
DB 901 TTGTCTAGAATCCAGAGGTTTACTTGTGTTGTTGAAAGTGTGATATGATCATGCT 960

DB 901 CTGAGCAGGAACCCCGGGGCTTCTACCTCTTCTGTGAGGAGGCGCCGATTGACACCGCT 960
QY 961 CATCATGATGTTAAGCTTATATGCTTTGACTGAAGCTATATGTTGATTAATGCTATT 1020
DB 961 CACCATGACGGCAAGCTTATATGCACTGACTGAGCGATCATGTTTGACAAATGCCATC 1020
QY 1021 GCTAAGGCTAATGAATGACTTCTGAATGGAATCTTTGATTTTGTACTGCTGATCAT 1080
DB 1021 GCCAAGGCTAAGAGCTCACTAGCGAAGTGAACAGCTGATCCTGTCACTGACAGACCAC 1080
QY 1081 AGTCATGTTTTTTCTTTTGGTGTGTACACTTTGAGAGGTAAGTCTTATTTTGGTTGGCT 1140
DB 1081 TCCCATGTTCTTCTTTTGGTGTGTACACTGCTGAGACCTCCTATGGAATGGCCAGGC 1140
QY 1141 CCAGTAAAGCTTTGATAGTAACTTACACTTTCTATTTGTATGTAATGTTGCTCAGGT 1200
DB 1141 CCGGCAAGGCTTGAACAGCAAGTCTTACACTTCACTCTATGGAATGGCCAGGC 1200
QY 1201 TATGCTTTGGGTGTTGTTCTAGACCAAGTGAATGTTAGTACTAGTAAAGAACCATCT 1260
DB 1201 TATGCGCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGCACAAGCGAGAACCTCA 1260
QY 1261 TACAGACAACAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTTGTTGATGTTGCT 1320
DB 1261 TACCGCAGCAGGCGCGCTGCGCTGCTAGCAGAACCCAGCGGCGAGACGTGGCG 1320
QY 1321 GTTTTGTAGAGGTCCACAAGCTCATTTGGTTTCAATGTTTCAAGAAACTTTTGT 1380
DB 1321 GTGTTGCGCGGAGGCGCCGACAGGCGCACTGTGTGACGCGGTGACAGAGACCTTCTG 1380
QY 1381 GCTCATATTATGCTTTTGTGCTGTTGTGTTGAACCATACACTGATTTGTAATTTGCCAGCT 1440
DB 1381 GCGCATCATAGGCTTTTGGGCTGCTGAGGCTTACACCGACTGCAATCTGCGACGCC 1440
QY 1441 CCAGCTACTGCTACTAGTATTCAGATTAAGTACC 1476
DB 1441 CCGGCAAGGCGCCAGCATCCCGACTAGGTTACC 1476

RESULT 8
US-10-395-790A-1
Sequence 1, Application US/10395790A
Publication No. US20040072316A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics Corp.
TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase
FILE REFERENCE: RDID 02028US
CURRENT APPLICATION NUMBER: US/10/395, 790A
CURRENT FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1464
TYPE: DNA
ORGANISM: Bovine
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1464)
OTHER INFORMATION:
US-10-395-790A-1

Query Match 56.6%; Score 834.8; DB 16; Length 1464;
Best Local Similarity 73.2%; Pred. No. 3.3e-180;
Matches 1070; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

QY 8 TGATTCAGCTGAAGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTTTGG 67
DB 2 TCATCCAGCTGAGAGAGAAACCCGCTTCTGGAACCGCAGGACGCCAGGCCCTTG 61
QY 68 ATGTTGCTAAGAGTTGCAACCAATTCAACTGCTGCTAAGAATGTTAATTTGTTTGG 127
DB 62 ATGTAGCAAGAAGTTGCAAGCCGATCCAGACAGCTGCCAAGAATGTCAATCTTCTTG 121

Db 361 GTGCGGGGTCAAGGGCAACTTCCAGACCATTTGGCTTGAGTGCAGCCCGCCCTTTAACCA 420
Qy 366 ATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTATAGAGCTAAGAGGCTGG 425
Db 421 GTGCAACACGACACGCGGCAACGAGTCACTCTCGTGATGAATCGGGCCAAGAAAGCAGG 480
Qy 426 TAAGGCTGTGGTGTGTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTGCTTA 485
Db 481 GAAGTCAGTGGAGTGGTAACCAACCAACAGACGACGAGCCTCGCCAGCGGCAACCTA 540
Qy 486 CGCTCATACTGTAAATAGAAATTTGACTCTGATGCTGATTTGCCAGCTGATGCTCAAA 545
Db 541 CGCCACACGCTGAACCGCAACTGTACTCGACGCCGACGCTGCTGCGGCCGCCCA 600
Qy 546 GAATGCTGTCAAGATATTTGCTGCTCAATGGTTTACAATATGATATGATGTTATTTT 605
Db 601 GGAAGGGTCCAGACATCGCTACGACGCTCATCTCCAACATGACATGACGTGATCCT 660
Qy 606 GGGTGGGTAGAAATGATCATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGA 665
Db 661 AGGTGAGGCGGAAAGTACATGTTTCCATGGGAAACCCAGACCTGAGTACCCAGATGA 720
Qy 666 TGCTTCTGTTAATGCTGTAGAAAGATTAAGAAATTTGTTCAAGATGGCAAGCTAA 725
Db 721 CTACAGCCAAAGTGGGACACAGGCTGACGCGGAAGATCTGTGACAGAAATGGCTGGCGAA 780
Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTTCAAGCTGCTGATGATTC 785
Db 781 GCGCCAGGGTGCCCGGATATGTGGAACCGCATGAGCTCATGACAGGCTTCCCTGAGCCC 840
Qy 786 TAGTGTACTCATTTGATGGGTTGTTGAACCAAGCTGATATGAAGTATATGTTCAACA 845
Db 841 GTCTGTGACCCCATCTCATGGGCTCTTTGAGCCTGGAACATGAATATGACGATCCACCG 900
Qy 846 AGATCATACTTAAGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTGGCAAGTTTGTG 905
Db 901 AGACTCCACACTGGAACCTCTCTGATGAGATGACAGAGGCTGCTGCTGCTGCTGAG 960
Qy 906 TAGAAATCCAAGAGTTTCTTACTGTTGTTGAAGGTGAGAAATGATCATGCTCATCA 965
Db 961 CAGGAACCCCGCGGCTTCTTCTCTGTTGAGAGGTTGTCGATCGACCATGTCATCA 1020
Qy 966 TGATGTAAGCTTATATGCTTTGACTGAGCTATATGTTGATAATGCTATTGCTAA 1025
Db 1021 TGAAGCAGGGCTTACCGGGCACTGATGAGACGATCATGTTGACGACGCCATTGAGAG 1080
Qy 1026 GGCTAATGAATGACTTCTGAATTTGATTTGATTTTGGTTACTGCTGATCATAGTCA 1085
Db 1081 GGGCGGCCAGCTCAACGAGGAGGACGCTGAGCCTGTCACACTGCCGACCACTCCA 1140
Qy 1086 TGTCTTTCTTTGGTGTTACACTTTGAGAGGTACTTCTATTTTGGTTTGGCTCCAGG 1145
Db 1141 CGTCTTCTCTTGGAGGCTACCCCTGCGAGGAGCTCCATCTTGGGCTGGCCCTGG 1200
Qy 1146 TAAGGCTTTGATAGTAACTTACACTTCTATTTGATGTAATGTCAGGTTATGC 1205
Db 1201 CAAGGCCCGGACAGAAAGGCTACACGCTCTCTATACGAAACGCTCCAGGCTATGT 1260
Qy 1206 TTTGGGTGGTCTTAGACAGATGTTAATGTAAGTACTAGTGAAGAACATCTTACAG 1265
Db 1261 GCTCAAGAGCGGGCGCCCGGATGTTACGAGAGCAGAGCGGGAGCCCGAGTATCG 1320
Qy 1266 ACAACAAGCTGCTGTTCCATTGGCTAGTAACTCATGTGTTGAAGTGTGCTGTTT 1325
Db 1321 GCAGCAGTCAAGTCCCTCCCTGACGAAGAGACCCACGACGCGAGAGCTGGCGGTGT 1380
Qy 1326 TGCTAGAGGTCCAAAGCTCATTTGGTTCATGGTGTTCAGAGAGAACTTTTGTGCTCA 1385
Db 1381 CGCGCGCGCGCGCAGGCGCACTGTGTTACGGCGTGCAGAGACAGACTTCATAGCGCA 1440
Qy 1386 TATTATGGCTTTTGGTGTGTGTTGAACCATCACTGATGTAATTTGCCAGCTCCAGC 1445
Db 1441 CGTCATGGCTTTCGCGCGCTGCGCTGAGCCCTTACACCGCCTGCGACCTGGCGCCCGCCG 1500

RESULT 10
US-09-006-298-22
; Sequence 22, Application US/09006298
; Patent No. US20020082224A1
; GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Moore, Margaret D.
; APPLICANT: Chada, Sunil
; TITLE OF INVENTION: NON-IMMUNOGENIC PRODRUGS AND SELECTABLE
; TITLE OF INVENTION: MARKERS FOR USE IN GENE THERAPY
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,298
; FILING DATE: 13-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.459
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..1617
; US-09-006-298-22
Query Match 38.8%; Score 572.8; DB 9; Length 1634;
Best Local Similarity 62.4%; Pred. No. 2.2e-120;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
Qy 6 CTTGATTCAGCTGAAGAGAAATCCAGCTTTTGGATAGACAAAGCTGCTCAAGCTTT 65
Db 78 CATCATCCAGTTGAGAGGAGAAACCCGACTTCTGGAACCGGACGAGCGAGGCCCT 137
Qy 66 GGATGTTGCTAAGAGTTCACCAATTCAAACTGCTGCTAAGAAATGTTATTTGTTT 125
Db 138 GGGTGGCCCAAGAGCTGACGCTGCAACAGACGCGCCAAAGAACTCATCTTCT 197
Qy 126 GGGTATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGTCAAATGAA 185
Db 198 GGGGATGGGATGGGGGTGTTACGTTGACAGCTGCGCAGATCTTAAAGGCGAGAA 257
Qy 186 TGGTAAGTTGGCTCCAGAACTCCATGGCTATGATCAATTTCCATACGTTGCTTGTG 245
Db 258 GGACAACTGGGGCTGAGATACCCCTGGCCATGACCGCTTCCATATGTGCTGTGTC 317
Qy 246 TAAGACTTCAATGTTGATAGCAAGTTCAGATTTGCTGCTGTAAGTCTGCTTACTT 305
Db 318 CAAGACATACATGTAGACAAACATGTGCCAGACAGTGAAGCCACAGCCGCTTACCT 377
Qy 306 GTGTGGTTAAGGTAATTACAGAACTATTGTTGTTTCTGCTGCTGATACATCA 365


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Db 661 AGGTGAGGCGGAAAGTACATGTTTCCCATGGGAACCCAGACCCTGAGTACCCAGATGA 720
Qy 666 TGCTTCTGTTAATGGTGTAGAAAGATAAGCAAAATTGGTCAAGAATGGCAAGCTAA 725
Db 721 CTACAGCCCAAGGTGGGACCAAGGCTGGACGGGAAGAAATCTGGTCAGGAATGGCTGGCGAA 780
Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGTTTGTGCAAGCTGCTGATGATTC 785
Db 781 GCGCCAGGGTGCCGGTATGTGTGGAACCGCACTGAGCTCATGCAAGGCTTCCTGGACCC 840
Qy 786 TAGTGTACTCATTTGATGGGTTTGTGGAACCAAGCTGATATGAAGTATAATGTTCAACA 845
Db 841 GTCTGTACCCATCTCATGGGTCTCTTGGAGCCTGGAGACATGAATACGATCCACCG 900
Qy 846 AGATCATACTAAGGATCCAACTTTGGCTGAAATGACTGAACTGCTTGCAGTTTGTTC 905
Db 901 AGACTCCACACTGGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCCCTGCTGAG 960
Qy 906 TAGAATCCAAAGGTTTTTACTTGTGTGTAAGGTGTGTAATGATGATGTCATCA 965
Db 961 CAGGAACCCCGCGGCTTCTTCTCTTGTGAGGGGTGTCGCATGCACTGATGTCATCA 1020
Qy 966 TGATGTAAGGCTTATATGCTTGTGACTGAACTATTATGTTGTAATATGCTATTGCTAA 1025
Db 1021 TGAAGCAGGGCTTACCGGGCACTGACTGAGATCATGTTGACAGACGCAATTGAGAG 1080
Qy 1026 GGCTAATGAATGACTTCTGAATGATGATCTTGTGTTGTTACTGCTGATCATAGTCA 1085
Db 1081 GGGGCGCAGCTACCAAGAGAGAGACAGCTGAGCTGCTCACTGCCACCACTCCCA 1140
Qy 1086 TGTTTTCTTTGGTGTGTACACTTTGAGAGTACTTCTATTTTTGGTTGGCTCCAGG 1145
Db 1141 CGTCTTCTCTTGGAGGCTACCCCTGCGAGGAGCTCCATCTTGGGCTGGCCCCCTGG 1200
Qy 1146 TAAGGCTTGTAGTACTTACACTTCTAATTTGTATGTAATGTTCCAGGTTATGC 1205
Db 1201 CAAGGCCCCGGGACAGGAAGGCTTACACGGTCTCTTATACGAAAAGGTTCCAGGCTATGT 1260
Qy 1206 TTTGGGTGGTGTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCTTACAG 1265
Db 1261 GCTCAAGGACGGGCGCGCGCGGCGGATGTATACAGAGCGAGCGGGAGCCCGAGTATCG 1320
Qy 1266 ACAACAAGCTGCTGTTCATTGGCTAGTGAACCTCATGTGTGTAAGATGTGCTGTTT 1325
Db 1321 GCAGCAGTCAAGTGCCTCTGAGCAAGAGAACCCACGACGAGAGAGTGGCGGT 1380
Qy 1326 TGCTAGAGTCCACAAGCTCATTTGGTTCATGTTGTTCAAGAAGAACTTTTGTGCTCA 1385
Db 1381 CGCGCGCGGCGCGCAGGCGCACCTGTTTCAAGCGGTGACAGAGACACTTTCATAGCGCA 1440
Qy 1386 TATTATGGCTTTTGTGCTGTGTGTGAACCATACACTGATTTGTAATTTGCCAGCTCCAGC 1445
Db 1441 CGTCATGGCTTCGCGCGCTGCTGAGCCCTACACCGCCTGCGACTGGCGGCCCGCGC 1500
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RESULT 12

US-09-908-943A-127

; Sequence 127, Application US/09908943A

; Publication No. US20030017991A1

; GENERAL INFORMATION:

; APPLICANT: Yan, Riqiang

; APPLICANT: Tomasselli, Alfredo G.

; APPLICANT: Gurney, Mark E.

; APPLICANT: Emmons, Thomas L.

; APPLICANT: Bienkowski, Mike J.

; APPLICANT: Heinrichson, Robert L.

; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY

; FILE REFERENCE: 29915/00281A.US1

; CURRENT APPLICATION NUMBER: US/09/908,943A

; PRIOR FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: 60/219,795

; PRIOR FILING DATE: 2000-07-19

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; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 127
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleic acid
; US-09-908-943A-127
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Query Match 38.8%; Score 572.8; DB 10; Length 1728;
Best Local Similarity 62.4%; Pred. No. 2.3e-120;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
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Qy 6 CTTGATCCAGCTGAAGAAGAAATCCAGCTTTTGGATAGACAAAGCTGCTCAAGCTT 65
Db 51 CATCATCCCGATTGAGAGAGAGAACCCGACTTCTGGAACCGGAGCGACCGAGCCCT 110
Qy 66 GGATGTTGCTAAGAAAGTTGCAACCAATTCAAACTGCTGCTAAGAATGTTATTTGTTT 125
Db 111 GGGTGCCGCAAGAAAGCTGCAAGCTTGACAGACAGACGCCCAAGAACTTCATCTTCT 170
Qy 126 GGGTATGTTAGTGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGTCAAATGAA 185
Db 171 GGGCGATGGATGGGGGTGTCTACGGTGACAGCTGCCAGATCTTAAAGGGCAGAGAA 230
Qy 186 TGTAAGTGGGTCCAGAACTCCATGGCTATGATCAATTTCCATACGTTGCTTGTGC 245
Db 231 GGACAAACTGGGGCTGAGATACCCCTGGCCATGAGACCGCTTCCATATGTGCTGTGC 290
Qy 246 TAAGACTTCAATGTTGATAGACAAGTTCCAGATTCTGCTGTACTGCTACTTACTT 305
Db 291 CAAGACATACATGTAGACAACATGTGCCAGACAGTGAAGCCACAGCCAGCTTACCT 350
Qy 306 GTGTGTTTAAAGGTAATTACAGAACTATTGCTGTTCTGCTGCTGCTAGATACAATCA 365
Db 351 GTGCGGGGTCAAGGGCAACTTCCAGACCAATTGGCTTGAAGTGCAGCGGCCCTTTAACCA 410
Qy 366 ATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAAATAGACTAAGAGGCTGG 425
Db 411 GTCAACACAGACACGCGGCAAGAGTCAATCTCGTATGAATGGGCAAGAAAGCAGG 470
Qy 426 TAAGGCTGTGTTGTTTACTACTACTAGAGTTCAACATGCTTCCAGCTGCTGCTTA 485
Db 471 GAAGTCAAGTGGAGTGTAAACCAACACAGAGTGACAGCGCTGCCACGCGCACCTA 530
Qy 486 CGCTCATCTGTTAATAGAAATTTGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAA 545
Db 531 CGCCCAACCGGTGAACCGCAACTGTGTACTGGACGCGGACGTGCTGCGGCCGCA 590
Qy 546 GAATGTTGTCAAGATATTGCTGCTCAATTGTTTACAATATGATATGATATGTTATTT 605
Db 591 GGAGGGGTGCCAGACATCGTACGAGCTCATCTCAACATGACATTGACGTGATCCT 650
Qy 606 GGGTGTGTTAGATGTATCATGTTTCCAGAAAGTACTCCAGATCCAGATACCCAGATGA 665
Db 651 AGGTGAGCGCGAAAGTACATGTTTCCATGGGAACCCAGACCTGAGTACCAGATGA 710
Qy 666 TGCTTCTGTTAATGTTAGAAAGGATTAAGCAAAATTTGTTTCAAGATGGCAAGCTAA 725
Db 711 CTACAGCCCAAGGTGGACCAAGCTGACCGGAAGAATCTGTGACGAATGGCTGGCGAA 770
Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAAGACTGCTTGTGCAAGCTGCTGATGATTC 785
Db 771 GCGCCAGGTGCGCGGTATGTGTGAACCGCACTGAGCTCATGCAAGCTTCCCTGACCC 830
Qy 786 TAGTGTACTCATTTGATGGGTTTGTGAAACCAAGCTGATATGAAGTATAATGTTCAACA 845
Db 831 GTCTGTGACCATCTCATGGGTCTCTTTGAGCCTGGAGACATGAATAACGAGATCCACCG 890
Qy 846 AGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTTTGTTC 905
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Db 891 AGACTCCACACTGGACCCCTCCGTGATGAGATGACAGAGGCTGCCCTGCGCTGCTGAG 950
Qy 906 TAGAAATCCAGAGGCTTTTACTGTTGTTGTAAGGTGTAAGATTGATCATGTGTCATCA 965
Db 951 CAGGAACCCCGCGGCTTCTTCTCTTCGTGAGGGGTGTCGCATCGAACCATGGTCATCA 1010
Qy 966 TGATGTGAAGGCTTATATGGCTTTGACTGAAGCTATTATGTTGATTAATGCTATTGCTAA 1025
Db 1011 TGAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGACGCCATTGAGAG 1070
Qy 1026 GGCTAATGAATTGACTTCTGAATTGGATTACTTTGATTGTTACTGCTGATCATAGTCA 1085
Db 1071 GCGGGCCAGCTCACCGAGAGAGACAGCTGAGCCTCGTCACTGCGGACCACTCCCA 1130
Qy 1086 TGTCTTTCTTTTGGTGTGTTACACTTTGAGAGTACTTCTATTGTTTGGTTGGCTCCAGG 1145
Db 1131 CGTCTTCCTTCGGAGGCTACCCCGCGAGGAGCTCCATCTTCGGGCTGCGCCCTGG 1190
Qy 1146 TAAGGCTTGGATAGTAAGTCTTACACTTCTATTGTTATGTTAGTCCAGGTTATGC 1205
Db 1191 CAAGGCCCCGACAGGAAGGCTTACCGCTCTCTATACGGAACGCTCCAGGCTATGT 1250
Qy 1206 TTTGGGTGGTCTTAGACCAAGATTAAATGTTAGTACTAGTGAAGAACCATCTTACAG 1265
Db 1251 GCTCAAGGACGGCGCCCGCGGATGTTAACGAGAGCGAGAGCGGGAGCCCCGAGTATCG 1310
Qy 1266 ACAACAAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGTTGTTGAAGATTGTTGCTGTTT 1325
Db 1311 GCAGAGTCAGCAGTGCCCTTGACGAAGAGACCCACGAGGCGAGGACGTGGCGGTGTT 1370
Qy 1326 TGCTAGAGTCCACAAGCTCATTTGGTTCAATGTTGTTCAAGAGAACTTTGTTGCTCA 1385
Db 1371 CGCGCGCGCGCCGACGCGCACCTGGTTCAAGCGGTGACAGAGACACCTTCATAGCGCA 1430
Qy 1386 TATTATGGCTTTTGTGTTGTTGTTGAACCATACACTGATTGTAATTGACCAGCTCCAGC 1445
Db 1431 CGTCATGGCCTTCGCGCCTGCTGAGCCCTTACACCGCCTGCGACTGGCGCCCCCGC 1490

RESULT 13
US-10-053-637-19
; Sequence 19, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEAP/MK fusion
; NAME/KEY: CDS
; LOCATION: (11)..(1735)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (1538)..(1732)
; OTHER INFORMATION: MK domain
US-10-053-637-19

Query Match 38.8%; Score 572.8; DB 15; Length 1748;
Best Local Similarity 62.4%; Pred. No. 2.3e-120;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
Qy 6 CTTGATTCACAGTGAAGAAATCCAGCTTTTGGATAGACAAAGCTGCTCAAGCTTT 65
Db 61 CATCATCCAGTTGAGAGAGAGAACCCGGAAGCTTCTGGAACCGGAGGCGAGCCGAGGCCCT 120

Qy 66 GGATGTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGAAATGTTATTGTTT 125
Db 121 GGGTGGCCGCAAGAGCTGCAGCTGCACAGACAGCCGCCAAGAACCTCATCATCTTCT 180
Qy 126 GGGTATGTATGGGTGTTCCAAGTGTACTGTCTAAGAAATTTGAAGGTCAAATGAA 185
Db 181 GGGGATGGGATGGGGGTGTCTACGGTGACAGCTGCAGGATCCTAAAGGGCAGAGAA 240
Qy 186 TGTTAAGTTGGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGTG 245
Db 241 GGAACAAGTGGGGCTTGAGATACCCCTGGCCATGAGACCGCTTCCATATGTGGCTGTG 300
Qy 246 TAAGACTTACAATGTTGATAGACCAAGTCCAGATTCTGCTGTGTTACTGCTTACTT 305
Db 301 CAAGACATACAAATGATGACAAACATGTGCCAGACAGTGAAGCCACAGCCGCTTACCT 360
Qy 306 GTGTGTGTTAAGGTTAATTACAGAACTATTGGTTCTGCTGCTGCTAGATACAAATCA 365
Db 361 GTGGGGGTCAAGGGCAACTTCCAGACCATTTGGCTTGAAGTGACGCCCGCTTTAAACA 420
Qy 366 ATGTAATACTACTAGAGGTAATGAAGTACTTCTGTTATTATAGAGCTAAGAGGCTGG 425
Db 421 GTGCAACACGACACGCGGCAACGAGTCACTCCGTGATGAATCGGCCAAGAAACGAG 480
Qy 426 TAAGCTGTGTTGTTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGTGCTTA 485
Db 481 GAACTCAGTGGAGTGTGTAACCAACACACAGAGTGCAGACGCCCTCGCAGCGGCACTA 540
Qy 486 CGCTCATACTGTTAATAGAAATTGGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAA 545
Db 541 CGCCCAACGGTGAACCGCAACTGTTACTCGGACGCCGACGTGCTCGGCCGCCCA 600
Qy 546 GAATGTTGTCAGATATTGCTGCTCAATTGGTTTACAATAATGATATTGATGTTATT 605
Db 601 GAGGGGTGCCAGACATGCTTACGAGCTCATCTCCAACATGACATTGACGTTATCT 660
Qy 606 GGGTGTGTAGAAATGATGATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCAATGA 665
Db 661 AGGTGAGGCGCGAAAGTACATGTTCCCATGGGAACCCAGACCCTGAGTACCAATGA 720
Qy 666 TGCTTCTGTTAATGTTGTTAGAAAGATTAAGCAAAATTTGTTCAAGAAATGCAAGCTAA 725
Db 721 CTACAGCCAAGGTGGACACGAGCTGACGGAAGAACTGGTGACGAATGGCTGGGAA 780
Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGATGATTC 785
Db 781 GCGCCAGGGTCCCGGTATGTGTGAACCGCACTGAGCTCATGCAAGCTTCCCTGAGCCC 840
Qy 786 TAGTGTACTCATTTGATGGGTTTGTGAACCAAGCTGATATGAAGTATATGTTCAACA 845
Db 841 GTCTGTGACCATCTCATGGGTCTCTTTGAGCCTGGAGACATGAATACGAGATCCACCG 900
Qy 846 AGATCATACTAAGGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGCAGATTGTTGC 905
Db 901 AGACTCCACACTGGAACCTCTCCTGATGAGATGACAGAGGCTGCCCTGCGCTGTGAG 960
Qy 906 TAGAAATCCAGAGGTTTCTTACTGTTGTTGAAGGTGTAAGATTGATCATGTGTCATCA 965
Db 961 CAGGAACCCCGCGGCTTCTTCTCTTCTGTGAGGGGTGTCATGACCATGTGTCATCA 1020
Qy 966 TGATGTGAAGCTTATATGGCTTGAAGCTGAGCTATTATGTTGATTAATGCTATTGCTAA 1025
Db 1021 TGAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGACGCATTGAGAG 1080
Qy 1026 GGCTAATGAATTGACTTCTGAATTGGATCTTTGATTGTTACTGCTGATCATAGTCA 1085
Db 1081 GCGGGCCAGCTCACCGAGAGAGACACGCTGAGCCTGCTCACTGCCGACCACTCCCA 1140
Qy 1086 TGTCTTTCTTTTGGTGTGTTACACTTTGAGAGGTAATTCTAATTTTGGTTGGCTCCAG 1145
Db 1141 CGTCTTCCTTCGGAGGCTACCCCTGCGAGGAGCTCATCTTGGGCTGGCCCCCTGG 1200
Qy 1146 TAAGCTTTGGATAGTAAGTCTTACACTTCTATTGTTGATGTTAATGTTCCAGGTTATGC 1205


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Db 1201 CAAGGCCGGACAGAGAGCCCTACACGGTCCCTCTATACGGAACGGTCCAGGCTATGT 1260
Qy 1206 TTGGGTGGTGTCTTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCTTACAG 1265
Db 1261 GCTCAAGGACGGCCCGCCCGCGGATGTTACCGAGAGCGAGAGCGGGAGCCCGCAGTATCG 1320
Qy 1266 ACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGGTGTGAAGATGTTGCTGTTT 1325
Db 1321 GCAGCAGTACAGATGCCCCCTGGACGAGAGACCCAGCGGAGAGCGTGGCGGT 1380
Qy 1326 TGCTAGAGTCCACAGCTCATTTGGTTCATGGTGTCAAGAGAACTTTGTTGCTCA 1385
Db 1381 CGCGCGCGCCCGCAGCGCACCTGTTACGGCGGTGACAGAGCAGACCTTCATAGCGCA 1440
Qy 1386 TATTATGCTTTTGTGTTGTGTGAACCATACATGATTGTAATTTGCCAGCTCCAGC 1445
Db 1441 CGTCATGGCCTTCGCGCGCTGCTGAGCCCTACACCGCCTGCGACCTGGCGCCCCCGC 1500
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RESULT 14

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US-10-053-637-15
; Sequence 15, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1777
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEAP HBNF fusion
; NAME/KEY: CDS
; LOCATION: (11)..(1765)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1538)..(1762)
; OTHER INFORMATION: HBNF domain
US-10-053-637-15
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Query Match 38.8%; Score 572.8; DB 15; Length 1777;
Best Local Similarity 62.4%; Pred. No. 2,3e-120;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
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Qy 6 CTTGATTCAGCTGAAGAAGAAATCCAGCTTTTGAATAGACAAAGCTGCTCAAGCTTT 65
Db 61 CATCATCCAGTTGAGAGAGAGAAACCCGACTTCTGAAACCGGAGCGAGCGAGGCCCT 120
Qy 66 GGATGTTGTAAGAGTTCACCAACCAATTCAAACTGCTGCTAAGAAATGTTATTTGTTT 125
Db 121 GGGTCCGCCAAGAGCTGCAGCTGCACAGACAGCCGCCAAGAACCTCATCTTCT 180
Qy 126 GGGTATGATGATGGGTGTTCCAACTGTTACTGCTACTAGAATTTGAAGGTCAAATGAA 185
Db 181 GGGGATGGGATGGGGGTGTTACGGTGACAGCTGCCAGATCTAAAGGGCAGAGAA 240
Qy 186 TGGTAAGTTGGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGTG 245
Db 241 GGACAAACTGGGGCTGAGATACCCCTGGCCATGGACCGCTTCCATATGTGGCTGTG 300
Qy 246 TAAGACTTACAATGTTGATAGACAAGTTCCAGATTCTGCTGTACTGCTACTTACTT 305
Db 301 CAAGACATACATGTAGACAACATGTGCCAGACAGTGAGCCACAGCCAGCCCTACCT 360
Qy 306 GTGTGTTGTTAAGGTAATTACAGAACTATTGTTGTTCTGCTGCTGCTAGATACAATCA 365
Db 361 GTGCGGGGTCAAGGCAACTTCAGACCATGCTTGAAGTGCAGCCGCCGCTTTAAACA 420
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Qy 366 ATGTATACTACTAGAGTATATGAGTTACTTCTGTATTATATAGACTAAGAGCTGG 425
Db 421 GTGCAACACGACACCGCGCAACGAGGTCTATCTCCGTGATGAATCGGGCCAAAGAACGAG 480
Qy 426 TAAGGCTGTTGGTGTGTTACTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGTGCTTA 485
Db 481 GAAGTCAGTGGAGTGGTAAACCAACACAGAGTGCACAGCCCTCGCCAGCGGCACCTA 540
Qy 486 CGCTCATACTGTTAATAGAAATGGTACTGTAGTGTGATTTGCCAGCTGATGCTCAAAA 545
Db 541 CGCCACACAGGTGAACCGCAACTGTACTGGAACGCCGACGTGCTGCTGCGCCGCCA 600
Qy 546 GAATGTTGTCAAGATATTGCTGCTCAATTGTTTACATATAGATATGATGTTATTTT 605
Db 601 GGAGGGGTGCAGGACATCGCTACGACGCTCATCTCCACATGACATTGACGTGATCCT 660
Qy 606 GGGTGTGTAGAAATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCAGATGA 665
Db 661 AGGTGAGGCGCGAAGATACATGTTTCCCATGGGAACCCAGAACCCCTGAGTACCAGATGA 720
Qy 666 TGCTTCTGTTAATGCTGTTAGAAAGATTAACAAATTTGTTCAAGATGGCAAGCTAA 725
Db 721 CTACAGCCAAAGTGGGACCAAGGCTGAGCGGGAAGAAATCTGTTGACGAAATGGCTGGCAA 780
Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGTCAAAGCTGCTGATGATTC 785
Db 781 GCGCCAGGTGCGCGGTATGTGTGAACCGCACTGAGCTCATGACGCTTCCCTGGAACC 840
Qy 786 TAGTGTACTCATTTGATGGTGTGTTGTAACCAAGCTGATATGAGTAAATGTTCAACA 845
Db 841 GTCTGTACCATCTCATGGGTCTCTTGAGCCTGAGACATGAATAAGATCCACCG 900
Qy 846 AGATCATACTAAGATCCAACTTGGCTGAATGACTGAAGCTGCTTGCAGATTGTC 905
Db 901 AGACTCCACACTGGAACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCTGAG 960
Qy 906 TAGAAATCCAGAGGTTTCTACTGTTGTTGTAAGGTGTTAGAAATGATCATGTCATCA 965
Db 961 CAGGAACCCCGCGGCTTCTTCTCTGTGAGGGGTGTCGATCAGCAATGTCATCA 1020
Qy 966 TGATGTAAAGCTTATATGCTTGAAGCTATATGTTGTTAATGCTATTGCTAA 1025
Db 1021 TGAAGCAGGCTTACCGGCACTGACGACGATCATGTTGACGACGCCATTGAGAG 1080
Qy 1026 GGCTAATGAATTGACTTCTGAATTGATTTGATTTGTTACTGCTGATCATAGTCA 1085
Db 1081 GGGCGGCGCACTACCAAGAGAGACAGCTGAGCCTGCTACAGCCGACCACTCCA 1140
Qy 1086 TGTTTTCTTTTGTGTTGTTACACTTTGAGAGGTACTTCTATTTTTGGTTGGCTCCAGG 1145
Db 1141 CGTCTTCTCTTCGAGGCTACCCCTCGGAGGAGGAGCTCCATCTTCGGGCTGGCCCTGG 1200
Qy 1146 TAAGCTTTGATAGTAACTTACCTTCTATTGTTATGTTATGTTCCAGGTATGC 1205
Db 1201 CAAGGCCCGGACAGAAAGGCTTACAGGTCCTCTATACGAAACGGTCCAGGCTATGT 1260
Qy 1206 TTTGGTGGTGTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATCTTACAG 1265
Db 1261 GCTCAAGAGCGGCGCCCGCGGATGTTAACGAGCGAGAGCGGAGCCCGAGTATCG 1320
Qy 1266 ACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGGTGTGAAGATGTTGCTGTTT 1325
Db 1321 GCAGCAGTACAGATGCCCCCTGGACGAGAGACCCAGCGGAGAGCGTGGCGGT 1380
Qy 1326 TGCTAGAGTCCACAGCTCATTTGTTCAATGTTGTTCAAGAGAACTTTTGTGCTCA 1385
Db 1381 CGCGCGCGCCCGCAGCGCACCTGTTACGGCGGTGACAGAGCAGACCTTCATAGCGCA 1440
Qy 1386 TATTATGCTTTTGTGTTGTGTTGAACCATACATGATTTGTAATTTGCCAGCTCCAGC 1445
Db 1441 CGTCATGGCCTTCGCGCGCTGCTGAGCCCTACACCGCCTGCGACCTGGCGCCCCCGC 1500
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RESULT 15

US-10-053-637-23

; Sequence 23, Application US/10053637

Publication No. US20030158132A1

; GENERAL INFORMATION:

! GENERAL INFORMATION:
! APPLICANT: KOVESDI, IMRE

;; APPLICANT: NOVELSDI, INKE
;; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION

FILE REFERENCE: 206

FILE REFERENCE: 206211
CURRENT APPLICATION NUMBER: US/10/053,637

CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2002-01-22

CURRENT FILING DATE: 20
NUMBER OF CFS TO NOV. 38

NUMBER OF SEQ ID NOS: 28

SOFTWARE: P

SEQ ID NO 23

! SEQ ID NO 2
! LENGTH: 1

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; LENGTH: 1915
; TYPE: DNA

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TYPE: DN
ORGANISM

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: SEA

NAME/KEY: CDS

LOCATION: (11) .. (1903)

OTHER INFORMATION:

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; OTHER INFORMATION:
; NAME/KEY: misc feature
;

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NAME/KEY: M1
LOCATION: (1

OTHER INFORMATION: VEGF121 domain
US-10-053-637-23

| Query Match | 38.8% | Score 572.8 | DB 15 | Length 1915 |
|-----------------------|----------------|--|----------|-------------|
| Best Local Similarity | 62.4% | Pred. No. 2.4e-120 | | |
| Matches 898 | Conservative 0 | Mismatches 542 | Indels 0 | Gaps 0 |
| QY | 6 | CTTGATTCGAGCTGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTTT | 65 | |
| Db | 61 | CATCATCCCAAGTTGAGGAGAGAAACCCGGACTTCTGAAACCGGAGGCGAGGCCCT | 120 | |
| QY | 66 | GGATGTTGCTAAGAAGTTGCAACCAATTCAACTGCTGCTAAGAATGTTATTGTTTT | 125 | |
| Db | 121 | GGGTGCCGCCAAGAAGCTGCAGCTGCACAGACAGCCGCCAAGAACCATCATCTTCT | 180 | |
| QY | 126 | GGGTGATGGTATGGGTGTTCCAACGTGTTACTGCTACTAGAAATTTGAAGGTCAAATGAA | 185 | |
| Db | 181 | GGGGCATGGATGGGGGTGTCTACGGTGACAGCTGCCAGATCCTAAAGGGCAGAAGAA | 240 | |
| QY | 186 | TGGTAAGTTGGGCTCCAGAACTCCATTGGCTATGGATCAATTTCCATAGTTGCTTGTGTC | 245 | |
| Db | 241 | GGACAAACTGGGGCCTGAGATACCCCTGGCCATGGAACCGCTTCCATATGTGGCTGTGC | 300 | |
| QY | 246 | TAAAGCTTACAATGTTGATAGACAAGTTCCAGATTCTGCTGTAAGTCTGCTTACTT | 305 | |
| Db | 301 | CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGAGCCACAGCCAGCCCTTACCT | 360 | |
| QY | 306 | GTGTGTTGTTAAGGTAATTACAGAACTATTGTTCTGCTGCTGCTAGATACAATCA | 365 | |
| Db | 361 | GTGCGGGTCAAGGGCAACTCCAGACCATTGGCTTGAGTGACGCCGCCGCTTTAACCA | 420 | |
| QY | 366 | ATGTAATCTACTAGAGTAATGAAGTTACTTCTGTTATTATAGAGCTAAGAAGGCTGG | 425 | |
| Db | 421 | GTGCAACACGACACGCGGCAACGAGTCACTCCGTGATGAATCGGCCAAGAAACAGG | 480 | |
| QY | 426 | TAAAGCTGTTGGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGTGGTCTTA | 485 | |
| Db | 481 | GAAGTCAGTGGAGTGTGTAACCAACACACGAGTGCACAGCCTCGCCAGCCGGAACCTA | 540 | |
| QY | 486 | CGCTCATCTGTTAATAGAAATTGCTACTCTGATGCTGATTTGGCAGCTGATGCTCAAAA | 545 | |
| Db | 541 | CGCCACACGGTGAAACCGCAACTGTTACTCGGACGCCGACGTGCTCGGCCGCCCA | 600 | |
| QY | 546 | GAATGTTGTCAGATATTGCTGCTCAATTGGTTTACAATATGATATGATGTTATTTT | 605 | |
| Db | 601 | GGAGGGTGCCAGACATGCTACGCAAGCTCATCTCCAACATGACATTGACGTGATCTCT | 660 | |
| QY | 606 | GGGTGTTGTAAGTATCATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCAAGATGA | 665 | |

| | | | |
|----|------|--|------|
| Db | 661 | AGGTGAGGCCGAAAGTACATGTTTCCCATGGAAACCCAGACCCTGAGTACCAGATGA | 720 |
| QY | 666 | TGCTTCTGTTAATGCTGTAGAAAGATAAGCAAAATTTGTTCAAGAAATGGCAAGCTAA | 725 |
| Db | 721 | CTACAGCCAAAGGTGGGACCAAGCTGGACGGGAAGAACTGTGTGACAGAAATGGCTGGCGAA | 780 |
| QY | 726 | GCATCAAGTGCTCATATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGATGATTC | 785 |
| Db | 781 | GCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGAGCTCATGCAAGCTTCCCTGGACCC | 840 |
| QY | 786 | TAGTGTACTCATTTGATGGGTTTGTGAACCAAGCTGATATGAAGTATAATGTTCAACA | 845 |
| Db | 841 | GTCGTGACCATCTCATGGGTCTCTTGAGCCCTGGAGACATGAATATCAGATCCACCG | 900 |
| QY | 846 | AGATCATACTAAGGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTGCAAGTTTGTGTC | 905 |
| Db | 901 | AGACTCCACACTGGAACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGGCTGCTGAG | 960 |
| QY | 906 | TAGAATCCAGAAGTTTCTTACTGTTGTTGTAAGGTGTAGAAATGATCATGCTCATCA | 965 |
| Db | 961 | CAGGAACCCCGCGGCTTCTTCCCTCTCGTGAGGGGTGCGCATGCACCAATGCTCATCA | 1020 |
| QY | 966 | TGATGTAAGCTTATATGCTTGAAGCTATATGTTGATAATGCTATTTGCTTAA | 1025 |
| Db | 1021 | TGAAGCAGGCTTACCGGGCACTGACTGAGACGATCATGTTGACGACGCCATTTGAGAG | 1080 |
| QY | 1026 | GGCTAATGAATTGACTTCTGAATTGGATACTTTGATTTTGGTTACTGCTGATCATAGTCA | 1085 |
| Db | 1081 | GCGCGGCAGCTCACGAGCAGAGAGGACACGCTGAGCCTCGTCACTGCCGACCACTCCCA | 1140 |
| QY | 1086 | TGTTTTTCTTTTGGTGTTACACTTTGAGAGGTACTTCTATTTTGGTTTGGCTCCAGG | 1145 |
| Db | 1141 | CGTCTTCTCCTTCCGAGGCTACCCCTCGAGGAGCTTCATCTTGGGCTGGCCCTGG | 1200 |
| QY | 1146 | TAAGCTTTGATAGTAAGCTTACACTTCTATTTTGTATGCTAATGATCCAGGTATGC | 1205 |
| Db | 1201 | CAAGCCCCGGGACAGGAAGGCTTACCGGTCTCTTATACGGAACGATCCAGGCTATGT | 1260 |
| QY | 1206 | TTTGGGTGGTGTCTTAGACCAAGATGTTAATGCTAGTACTAGTAAGAACCATCTTACAG | 1265 |
| Db | 1261 | GCTCAAGACGGGCGCCCGGCGGATGTTAACGAGAGCGAGAGCGGGAGCCCGAGTATCG | 1320 |
| QY | 1266 | ACAACAAGCTGCTGTTCATTGGCTAGTGAAACTCATGGTGTGTAAGATGTTGCTGTTT | 1325 |
| Db | 1321 | GCAGCAGTCAGCAGTGCCCCCTGGACGAAGAACCCACGCGGAGAGACGTGGCGGTGTT | 1380 |
| QY | 1326 | TGCTAGAGTCCACAAGCTCATTTGGTTCATGTTTCAAGAAAGAACTTTTGTGCTCA | 1385 |
| Db | 1381 | CGCGCGGCGCCCGCAGCGCACTGTGTTCACGGCGTGACGAGACAGACCTTATAGCGCA | 1440 |
| QY | 1386 | TATTTATGGCTTTTGTGCTGTTGTGTTGAACATACACTGAATTGTAATTTGCCAGCTCAGC | 1445 |
| Db | 1441 | CGTCATGGCCTTCCGCCCTGCTCGAGCCCTACACCGGCTGCGCACTGGCGCCCCCGC | 1500 |

Search completed: October 19, 2004, 23:49:31
Job time : 758.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2004, 10:20:22 ; Search time 5049.5 Seconds
(without alignments)
10651.558 Million cell updates/sec

Title: US-09-911-132A-5
Perfect score: 1476
Sequence: 1 gaattcttgattccagctga.....gtattccagattaagttacc 1476

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

| | |
|----|-----------|
| 1: | gb_est1:* |
| 2: | gb_est2:* |
| 3: | gb_hlc:* |
| 4: | gb_est3:* |
| 5: | gb_est4:* |
| 6: | gb_est5:* |
| 7: | gb_est6:* |
| 8: | gb_gss1:* |
| 9: | gb_gss2:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 360.4 | 24.4 | 2459 | 3 AK076459 | AK076459 Mus muscu |
| 2 | 357.6 | 24.2 | 733 | 7 CK956273 | CK956273 4096346 B |
| 3 | 350.6 | 23.8 | 950 | 5 BX458398 | BX458398 BX458398 |
| 4 | 346.6 | 23.5 | 1027 | 5 BX439339 | BX439339 BX439339 |
| 5 | 343.6 | 23.3 | 991 | 5 BX379970 | BX379970 BX379970 |
| 6 | 334.6 | 22.7 | 1587 | 9 AY404255 | AY404255 Mus muscu |
| 7 | 330.4 | 22.4 | 984 | 1 AL552555 | AL552555 AL552555 |
| 8 | 308 | 20.9 | 888 | 7 CF591568 | CF591568 AGENCOURT |
| 9 | 303.6 | 20.6 | 1593 | 9 AY404253 | AY404253 Homo sapi |
| 10 | 303.2 | 20.5 | 936 | 5 BX417625 | BX417625 BX417625 |
| 11 | 301.6 | 20.4 | 902 | 1 AL553521 | AL553521 AL553521 |
| 12 | 298.4 | 20.2 | 1125 | 5 BX343739 | BX343739 BX343739 |
| 13 | 297 | 20.1 | 724 | 6 BY732148 | BY732148 BY732148 |
| 14 | 292 | 19.8 | 772 | 7 CK453205 | CK453205 908900 MA |
| 15 | 288.4 | 19.5 | 681 | 7 CK834465 | CK834465 4058791 B |
| 16 | 284.2 | 19.3 | 905 | 1 AL540746 | AL540746 AL540746 |
| 17 | 280.8 | 19.0 | 928 | 1 AL549703 | AL549703 AL549703 |
| 18 | 280 | 19.0 | 992 | 1 AL548705 | AL548705 AL548705 |
| 19 | 278.6 | 18.9 | 625 | 9 AY416261 | AY416261 Mus muscu |
| 20 | 276.4 | 18.7 | 929 | 1 AL551653 | AL551653 AL551653 |
| 21 | 275.8 | 18.7 | 625 | 9 AY416259 | AY416259 Homo sapi |
| 22 | 267.8 | 18.1 | 636 | 7 CN792609 | CN792609 4127499 B |
| 23 | 264.8 | 17.9 | 722 | 6 BY732151 | BY732151 BY732151 |
| 24 | 262 | 17.8 | 1083 | 1 AL545591 | AL545591 AL545591 |

| | | | | | |
|----|-------|------|------|------------|--------------------|
| 25 | 260.2 | 17.6 | 890 | 4 B1161220 | B1161220 602865678 |
| 26 | 253.6 | 17.2 | 550 | 9 AY416260 | AY416260 Pan trogl |
| 27 | 251.8 | 17.1 | 616 | 6 CF176922 | CF176922 805350 MA |
| 28 | 251.6 | 17.0 | 935 | 4 BG832086 | BG832086 602765105 |
| 29 | 251.6 | 17.0 | 1422 | 3 AK008000 | AK008000 Mus muscu |
| 30 | 251.2 | 17.0 | 2084 | 3 CR681888 | CR681888 Tetraodon |
| 31 | 250 | 16.9 | 1593 | 9 AY404254 | AY404254 Pan trogl |
| 32 | 249.6 | 16.9 | 782 | 6 CB989365 | CB989365 AGENCOURT |
| 33 | 243.8 | 16.5 | 650 | 7 CN723202 | CN723202 E0856C01- |
| 34 | 239.4 | 16.2 | 685 | 6 BY736065 | BY736065 BY736065 |
| 35 | 237 | 16.1 | 855 | 6 CB998271 | CB998271 AGENCOURT |
| 36 | 235.4 | 15.9 | 740 | 6 CB959579 | CB959579 AGENCOURT |
| 37 | 233.8 | 15.8 | 651 | 7 CN718332 | CN718332 E0763C04- |
| 38 | 233.2 | 15.8 | 544 | 7 CN719377 | CN719377 E0783E06- |
| 39 | 231 | 15.7 | 607 | 7 CN721228 | CN721228 E0818D06- |
| 40 | 229.2 | 15.5 | 653 | 7 CN788362 | CN788362 4122694 B |
| 41 | 227.2 | 15.4 | 630 | 7 CN705542 | CN705542 E0503D01- |
| 42 | 227 | 15.4 | 565 | 4 BG079784 | BG079784 H3045A08- |
| 43 | 221.2 | 15.0 | 799 | 4 BG480361 | BG480361 602529434 |
| 44 | 220.6 | 14.9 | 535 | 2 AW450908 | AW450908 UI-H-B13- |
| 45 | 220.6 | 14.9 | 597 | 7 CN720761 | CN720761 E0809E05- |

ALIGNMENTS

| | | | | | |
|------------|---|---|------|--------|-----------------|
| RESULT 1 | AK076459 | 2459 bp | mRNA | linear | HTC 03-APR-2004 |
| LOCUS | AK076459 | Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833407E05 product:alkaline phosphatase 2, liver, full insert sequence. | | | |
| DEFINITION | AK076459 | AK076459.1 GI:26096820 | | | |
| ACCESSION | AK076459 | HTC; CAP trapper. | | | |
| VERSION | AK076459.1 | Mus musculus (house mouse) | | | |
| KEYWORDS | | Mus musculus | | | |
| SOURCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| ORGANISM | | | | | |
| REFERENCE | | | | | |
| AUTHORS | Carninci, P. and Hayashizaki, Y. | | | | |
| TITLE | High-efficiency full-length cDNA cloning | | | | |
| JOURNAL | Meth. Enzymol. 303, 19-44 (1999) | | | | |
| MEDLINE | 99279253 | | | | |
| PUBMED | 10349636 | | | | |
| REFERENCE | | | | | |
| AUTHORS | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | | | | |
| TITLE | RIKEN integrated sequence analysis (RISA) system--384-format | | | | |
| JOURNAL | sequencing pipeline with 384 multicapillary sequencer | | | | |
| MEDLINE | Genome Res. 10 (11), 1757-1771 (2000) | | | | |
| PUBMED | 20530913 | | | | |
| REFERENCE | 11076861 | | | | |
| AUTHORS | 4 | | | | |
| TITLE | The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. | | | | |
| JOURNAL | Functional annotation of a full-length mouse cDNA collection | | | | |
| REFERENCE | Nature 409, 685-690 (2001) | | | | |
| AUTHORS | 5 | | | | |
| | The FANTOM Consortium and the RIKEN Genome Exploration Research | | | | |

| | | |
|----|---------------------------|--|
| | TITLE | Group Phase I & II Team. |
| | JOURNAL REFERENCE | Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) |
| | AUTHORS | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gscl.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/. Location/Qualifiers 1. .2459 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM,DB:4833407E05" /db_xref="taxon:10090" /clone="4833407E05" /tissue_type="head" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="0 day neonate" 179. .1754 /note="alkaline phosphatase 2, liver (MGD MG1:87983, GB NM_007431, evidence: BLASTN, 99%, match=2451) putative" polyA_signal 2430. .2435 /note="putative" 2459 /note="putative" |
| | ORIGIN | |
| Oy | Query Match | 24.4%; Score 360.4; DB 3; Length 2459; |
| Db | Best Local Similarity | 56.1%; Pred. No. 1.5e-78; |
| | Matches 809; Conservative | 0; Mismatches 611; Indels 22; Gaps 6; |
| Oy | 2 | AATCTTGATTCCAGCTGAAGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGTCAAG 61 |
| Db | 225 | ACTCTTTTGTGCAGAAAGAGAGAGACCCAGTACTGTGGACAGCAAAGCCCAAGAGA 284 |
| Oy | 62 | CTTGGATGTTGCTAAGAGATTGCCAACCATTC AAC--TGCTGCTAAGATGTTATT 118 |
| Db | 285 | CCTGAAAATGCCCCGTAACCTCCAAGCTCAACACCAATGTAGCCCAAGATGTCAATCA 344 |
| Oy | 119 | TGTTTTGGGTGATGTTATGGGTGTTCCAACCTGTTACTGCTACTAGAATTTGAAGGCTC 178 |
| Db | 345 | TGTTCTCGGAGATGTTATGGGCGTCTCCACAGTAACCGCTGCCGAATCTTAAAGGCC 404 |
| Oy | 179 | AAATGAATGTTAGTTGGGCTCCAGAACTCCATTGGCTATGATCAATTTCCATAACGTTG 238 |
| Db | 405 | AGCTACACCACAACGCGGAGAGAGACCCGCGCTGGAGATGACAAATTTCCCCTTTGTGG 464 |

| | | | |
|----|------|---|------|
| QY | 235 | CTTTGTCTAAGACTTACAAATGTTGATAGACAAAGTTCAGATTCTGCTGCTACTGCTACTG | 298 |
| Db | 465 | CCCTCTCCAAAGACATATTAACCAACGCTCAGGTTCCCTGACAGCGCGGGCACTGCCACTG | 524 |
| QY | 299 | CTTACTGTGTGGTGTAAAGGGTAATTACAGAACTATTGGTGTCTTGCTGCTGCTAGAT | 358 |
| Db | 525 | CCTACTGTGTGGCGTGAAGGCCAACGAGGGCAGTGGAGTGAGCGCAGCCACAGAGC | 584 |
| QY | 359 | ACAATCAATGTAACTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGAGTAAGA | 418 |
| Db | 585 | GCAAGCATGCAACACCACTCAGGGCAATGAGTTCATCCATCCTGCGCTGGGCCAAGG | 644 |
| QY | 419 | AGGCTGTAAGGCTGTTGGTGTGTTACTACTACTAGAGTTCAACATGCTTCCAGCTG | 478 |
| Db | 645 | ATGCTGGAGAGTCCGGTGGGCATTGTGACTACCACTCGGGTGAACCAAGCCACCAAGT | 704 |
| QY | 479 | GTCCTAACGCTCATCTGTATAGAAATTGGTACTCTGATGCTGATTTGGCAGCTGATG | 538 |
| Db | 705 | CAGCCTACGCACACTCGGCCGATCGGGACTGTGTACTCGGATTAACGAGATGCCACAGAG | 764 |
| QY | 539 | CTCAAAAGAATGTTGTCAAGATATTGCTGCTCAATTGGTTACAATAT--GGATATTG | 595 |
| Db | 765 | CTCTGAGCCAGGCTGCAAGGACATCGCATATCAAGTAATGACAAATATCAAGGATATCG | 824 |
| QY | 596 | ATGTTATTTGGGTGGTGTAGAAATGTACATGTTCCAGAAGTACTCCAGATCCAGAAT | 655 |
| Db | 825 | ACGTGATCATGGGTGGCGCGCCGAAATATCATGTAAACCGAAGAACAGAACTGATGTGAAT | 884 |
| QY | 656 | ACCAGATGATGCTTCTGTTAATGTGTGAAGAAAGTAAGCAAAATTTGGTTCAAGAAT | 715 |
| Db | 885 | ACGAATGATGAGAAAGCCAGGGTACAAAGGCTAGATGGCTGATCTCATCAGTATTT | 944 |
| QY | 716 | GG-----CAAGCTAAGCATCAAGGTCTCAATATGTTGGAATAGAACTGCTTTGT | 766 |
| Db | 945 | GGAAGAGCTTTAAACCCAGACACAGACATGCCACTATGTCTGGAACCGCACTGAACCTG | 1004 |
| QY | 767 | TGCAAGCTGCTGATGATTTCTAGTGTTACTCTCATTTGATGGGTTGTTGAAACCACTGATA | 826 |
| Db | 1005 | TG--GCCCTTGACCCCTCCAGGGGTGACTTACTTAAAGTCTCTTGAGCCCGGGGACA | 1061 |
| QY | 827 | TGAAGTATATGTTTCAACAAGATCATACTTAAGATCCAACTTTGGCTGAATGACTGAAG | 886 |
| Db | 1062 | TGCAGTATGAATGAATCGGAACAACCTGACTGACCCTTCGCTCTCGAGATGCTGAGG | 1121 |
| QY | 887 | CTGCTTTCGAAGTTTGTCTAGAAATCCAAAGGTTTTTACTTGTGTTGTAAGGTGTA | 946 |
| Db | 1122 | TGGCCCTCCGATCTCTGACCAAAAACCTCAAGGCTTCTTCTGCTGTGTGAAGAGGCA | 1181 |
| QY | 947 | GAATTGATCATGCTCATCATGATGTAAGGCTTATATGGCTTTGACTGAAGCTATATGT | 1006 |
| Db | 1182 | GGATTGACCAAGGACATCATGAGGTAAGGCCAAGCAGGCTCTGCATGAAGCAGTGAGA | 1241 |
| QY | 1007 | TTGATAATGCTATTGCTAAGGCTAATGAATTGACTTCTGAATTGGATTGACTTTTGG | 1066 |
| Db | 1242 | TGGACCAAGGCCATTGGCAAGGCAAGCGCCCATGACATCCAGAAAGACACCTTGACTGTG | 1301 |
| QY | 1067 | TTACTGCTGATCATAGTCATGTTTTTTCTTTGCTGTACACTTTGAAGGTAATTCTTA | 1126 |
| Db | 1302 | TTACTGCTGATCATTTCCACAGTTTTCACATTGGTGATACACCCCCGGGGCAACTCCA | 1361 |
| QY | 1127 | TTTTTGGTTGGCTCCA--GGTAAGGCTTTGGATAGTAAGTCTTACACTTTCTAATTTGT | 1183 |
| Db | 1362 | TCTTTGGTCTGGCTCCCATGTGTAGCGACACGGAAGAACCCCTTTCAGCGGCATCTTAT | 1421 |
| QY | 1184 | ATGTAATGCTCAGGTTATGCTTTGGGTGTGTTCTAGACCAGATGTTAATGTAGTA | 1243 |
| Db | 1422 | ATGTAACGGGCTGTGGCTACAAGGTGTGACGGTGAACGGAAATGTCTCATGTAG | 1481 |
| QY | 1244 | CTAGTAAGAACCATCTTACAGACACAAGGCTGCTGTTCCATTTGGCTAGTAACAATCATG | 1303 |
| Db | 1482 | ATTACGCTCACAAACAATAACGAGGCCAGTCCGCTGTTCCCTCGGCCATGAGACCCACG | 1541 |

| QY | 1304 | GTG | TGA | AGATG | TGCTG | TTT | TG | CTAG | AGG | TC | CA | CA | AG | CT | CA | TT | TG | -G | TC | AT | GG | TG | TT | 1362 | |
|--|------|-----|------|-------|-------|-----|----|------|-----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|------|------|
| Db | 1542 | GTG | A | A | G | A | A | G | A | C | G | T | G | G | C | G | G | T | T | G | C | C | A | A | 1601 |
| QY | 1363 | CA | A | G | A | A | A | C | T | T | T | G | T | T | G | T | C | A | T | A | T | A | T | 1422 | |
| Db | 1602 | C | A | T | G | A | G | A | C | A | C | A | T | A | C | A | T | T | C | C | C | A | T | 1661 | |
| QY | 1423 | GA | 1424 | | | | | | | | | | | | | | | | | | | | | | |
| Db | 1662 | GA | 1663 | | | | | | | | | | | | | | | | | | | | | | |
| <p>RESULT 2</p> <p>CK956273</p> <p>LOCUS</p> <p>DEFINITION</p> <p>CK956273 733 bp mRNA linear EST 15-MAR-2004</p> <p>4096346 BARC 10BOV Bos taurus CDNA clone 10BOV35_H01 5', mRNA</p> <p>sequence.</p> <p>ACCESSION</p> <p>CK956273</p> <p>VERSION</p> <p>CK956273.1 GI:45470653</p> <p>KEYWORDS</p> <p>EST.</p> <p>SOURCE</p> <p>Bos taurus (cow)</p> <p>ORGANISM</p> <p>Bos taurus</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.</p> <p>REFERENCE</p> <p>1 (bases 1 to 733)</p> <p>Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.</p> <p>Production of EST from cDNA libraries derived from immunologically activated bovine gut</p> <p>unpublished (2004)</p> <p>JOURNAL</p> <p>CONTACT: Tad S. Sonstegard</p> <p>Bovine Functional Genomics Laboratory</p> <p>Animal and Natural Resources Institute</p> <p>Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA</p> <p>Tel: 3015048416</p> <p>Fax: 3015048414</p> <p>Email: tads@anri.barc.usda.gov</p> <p>Single pass sequencing. Bases called and trimmed with phred</p> <p>0.000925 using options -trim_alt "-trim.fasta. Vector identified</p> <p>by cross_match using options -mismatch 12 -minscore 18</p> <p>Plate: 35 row: H column: 01</p> <p>Seq primer: CCCAGTCACGACGTTGTAAACG</p> <p>High quality sequence stop: 733.</p> <p>FEATURES</p> <p>Source</p> <p>1..733</p> <p>/organism="Bos taurus"</p> <p>/mol_type="mRNA"</p> <p>/strain="Holstein"</p> <p>/db_xref="taxon:9913"</p> <p>/clone="10BOV35_H01"</p> <p>/sex="Male"</p> <p>/tissue_type="Pooled"</p> <p>/dev_stage="Multiple"</p> <p>/lab_host="DH10B T1 phage resistant"</p> <p>/clone_lib="BARC 10BOV"</p> <p>/note="Organ: Small Intestine; Vector: pAgen-1; Site_1: EcorV; Site_2: NotI; Equimolar amounts of mRNA extracted from proximal jejunums of 18 and 21 wk old steers, and distal ileums of 14 day old calves. proximal jejunum exposed to C. oncophora for 3 and 6 weeks, and distal ileum exposed to C. parvum for 7 days"</p> | | | | | | | | | | | | | | | | | | | | | | | | | |
| <p>ORIGIN</p> <p>Query Match 24.2%; Score 357.6; DB 7; Length 733;</p> <p>Best Local Similarity 70.6%; Pred. No. 5.6e-78;</p> <p>Matches 477; Conservative 0; Mismatches 199; Indels 0; Gaps 0;</p> | | | | | | | | | | | | | | | | | | | | | | | | | |
| QY | 791 | TT | A | C | T | C | A | T | T | G | A | T | T | G | A | A | C | A | C | A | G | T | G | A | 850 |
| Db | 12 | T | A | A | C | A | C | C | T | C | A | T | G | G | C | C | T | T | T | G | A | C | C | G | 71 |

| | | | | |
|----|--|------|--|------|
| Oy | | 851 | ATACTAAGGATCCAACTTTGGCTGAATAGACTGAACTGCTTTGGCAAGTTTGCTAGAA | 910 |
| Db | | 72 | ACACCAGAAGGCCGACCTGCAGAAATGACAGAGTGGCCCTCGAGTGTAAAGCAGGA | 131 |
| Oy | | 911 | ATCCAAGAGGTTTTTAATTGTTGTTGGTAGAGGTGTAGAATTGATCATGTTCATGATG | 970 |
| Db | | 132 | ACCCGAGGGGCTTCTAACCTCTTTGTGAGGAGGCCGATTTGACCACGGTTCACCATGATG | 191 |
| Oy | | 971 | GTAAGCTTATATGCGTTGACTGAAGCTATATGTTTGATATGCTATTGCTAAGGCTA | 1030 |
| Db | | 192 | ACAAAGCTTATATGCGACTGACCGGAGGCGGTCAITGTTGACAATGCCATCGCCAAAGCTA | 251 |
| Oy | | 1031 | ATGAATTGACTTCTGAAATTGGATACCTTGATTTGGTTACTGCTGATCATAGTCATGTTT | 1090 |
| Db | | 252 | ATGAGCTCACTAGCGAACTGGACACGCTGATCTTGTCACTGACAGCACCTTCATGTCT | 311 |
| Oy | | 1091 | TTTCTTTTGGTGGTTAACACTTTGAGAGGTACTCTATTTTGGTTTGGCTCCAGSTAAGG | 1150 |
| Db | | 312 | TCTCTTTTGGTGGCTATACACTGCGTGGAGCTCCATTTTGTCTGGCCCCCAGCAAAGG | 371 |
| Oy | | 1151 | CTTTGATAGTAAGTCTTACACTTCTATTTTGTATGTAATGTAATGTCACAGTTATGCTTTGG | 1210 |
| Db | | 372 | CCTTAGACAGCAAGTCTTACACCTCCATCCTCTATGSCAATGGCCCTGGCTATGCGCTTG | 431 |
| Oy | | 1211 | GTGCTGTTCTAGACCAAGATGTTAATGTTAGTACTAGTGAAGAACCATTCTACAGACAAC | 1270 |
| Db | | 432 | GCGGGGCTCGAGGCCGATGTTAATGACAGACAAGCAGAGACCCCTCGTACAGCAGC | 491 |
| Oy | | 1271 | AAGCTGCTGTTCCATTGGCTAGTAGAACTCATGCTGCTGTAAGATGTTGCTGTTTGGCTA | 1330 |
| Db | | 492 | AGCGGGCGCTGCCCTCGGCTAGCGAGACCCACGSGGGCGAGAGCGTGGCGGTTCGCGC | 551 |
| Oy | | 1331 | GAGTCCACAAAGCTCATTTGCTTCATGCTGTGTCAAGAAGAAGACTTTGTTGCTCATATTA | 1390 |
| Db | | 552 | GCGGCGCGCAGGCGGCACTGTGTGACGCGCGTGCAGAGAGACCTTCGTGCGGCACATCA | 611 |
| Oy | | 1391 | TGGCTTTGCTGTTGTGTGAACCATACACTGATTTGTAATTTGCCAGCTCCAGCTACTG | 1450 |
| Db | | 612 | TGGCCTTTGGGGCTGCGTGGAGCCCTACACCGACTGCAATCTGCCAGCCCCCACCACCG | 671 |
| Oy | | 1451 | CTACTAGTATTCACGA | 1466 |
| Db | | 672 | CCACCAGCATCCCCGA | 687 |

RESULT 3
BX458398 LOCUS BX458398 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE002YN21 DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX458398
VERSION BX458398.2 GI:47053565
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31023009.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 1699.f
For more information about this cluster, see

```

FEATURES
  source      http://www.genoscope.cns.fr/cdna?s=CS0DE002CG11QP1&c=1699.f
              location/Qualifiers
              1. .950

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE002YN21"
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/clone_fib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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ORIGIN

| | | | | |
|---------------------------|--------|--------------------|-----------|-------------|
| Query Match | 23.8% | Score 350.6; | DB 5; | Length 950; |
| Best Local Similarity | 63.5%; | Pred. No. 3.3e-76; | | |
| Matches 533; Conservative | 1; | Mismatches 305; | Indels 0; | Gaps 0; |

| | | | | |
|----|-----|---|--|-----|
| OY | | 6 | CTTGATTCAGCTGAAAGAAGAAAATCCAGCTTTTGGAAATAGACCAAGCTGCTCAAAGCTTT | 65 |
| Db | 112 | CATCATCCAGTTGAGGAGAGAACCCGGAATTCTGAAACCGCAGGCAGCCGAGGCCCT | 171 | |
| OY | | 66 | GGATGTGCTAAGAAGTTGCAACCATAATCCAATGCTGCTAGAAATGTTATTTGTTTTT | 125 |
| Db | 172 | GGGTGCCGCAAGAAGCTGACGCTGCACAGACAGCCGCAAGAACCCTCATCTTCTCT | 231 | |
| OY | | 126 | GGGTGATGATGGGTGTTCCAACGTGTACTGTAAGAAATTTGAAGGTCAAATGAA | 185 |
| Db | 232 | GGGCGATGGGATGGGGGTGTCTACGGTGCACCTGCCAGGATCTTAAAGGGCAGAAGAA | 291 | |
| OY | | 186 | TGCTAAGTTGGGTCAGAAACTCCATTGGCTATGGATCAATTTCCATACGTTGCTTTGTC | 245 |
| Db | 292 | GGACAAACTGGGGCCTGAGTTACCCCTGGCCATGGACCGCTTCCATATGTGGCTGTCTC | 351 | |
| OY | | 246 | TAAGACTTACAATGTTGATAGACCAAGTTCAGATTTCTGCTGTACTGTCTACTGCTTACTT | 305 |
| Db | 352 | CAAGACATACATGTAGACAAACATGTGCCAGACAGTGAGCCACAGCCAGCGCTTACT | 411 | |
| OY | | 306 | GTGTGTTGTTAAGGTAATTAACAACATAATTGGTGTCTGCTGCTGCTAGATACAATCA | 365 |
| Db | 412 | GTGCGGGGTCAAGGGCACTTCCAGACCAATTGGCTTGAGTGACAGCCGCCGCTTTAAACA | 471 | |
| OY | | 366 | ATGTAATACTACTAGAGSTAATGAAGTTACTTCTGTTATTATAGAGCTAAGAAAGCTGG | 425 |
| Db | 472 | GTGCAACACGACACGCGGCAACGAGTCACTCCGTGATGAATCGGGCCAAGAAAGCAGG | 531 | |
| OY | | 426 | TAAGCGTGTGGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTGCTTA | 485 |
| Db | 532 | GAAGTCA GTGGAGTGTAAACCAACCAAGAGTGACAGCACGCTCGCCAGCGGCACTTA | 591 | |
| OY | | 486 | CGCTCATCTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAA | 545 |
| Db | 592 | CGCCACACGCGTGAACCGCACTGTACTCGGACGCCGACGTGCTCGGCGCCGCCA | 651 | |
| OY | | 546 | GAATGTTGTCAAGATATTGCTGCTCAATTGGTTTACAATATGATATTTGATGTTATTTT | 605 |
| Db | 652 | GGAGGGGTGCCAGGACATCGCTTACGCACTCATCTCCAACATGGACATTTGACGTGATCCT | 711 | |
| OY | | 606 | GGGTGTTGTTAGATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGA | 665 |
| Db | 712 | AGGTGAGGCCGAAAGTACATGTTTGCATGGGAAACCCAGACCCTGAGTACCAGATGA | 771 | |
| OY | | 666 | TGCTTCTGTTAATGATGTTAGAAAGSATAAGCAAAATTTGTTCAAGAAATGGCAAGCTAA | 725 |
| Db | 772 | CTACAGCCAAAGTGGGACCAAGCTGACGGGAAGAATCTGGTGCAAGAAATGGCTGGCGAM | 831 | |
| OY | | 726 | GCATCAAGSTGCTCAATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGATGATTC | 785 |
| Db | 832 | GGCCAGGGGTGCCCGGTACGTGTGGAACCGCACTGAGCTCATGCAAGGCTTCCCTGGACCC | 891 | |
| OY | | 786 | TAGTGTACTCATTTGATGGGTTTGTGTAACCAAGCTGATATGAAGTATTAATGTTCAAC | 844 |

Db 892 GTCTGTGARCACATCTCATGGGCTCTTTGAGCCTGGAGACATGAATAACGAGATCCACC 950

| | |
|------------|--|
| RESULT | 4 |
| BX439339 | |
| LOCUS | 1027 bp mRNA linear EST 05-MAY-2004 |
| DEFINITION | BX439339 Homo sapiens PLACENTA cDNA clone CS0DE009YD10 |
| | 5-PRIME, mRNA sequence. |
| ACCESSION | BX439339 |
| VERSION | BX439339.2 GI:47036618 |
| KEYWORDS | EST. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |

ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1027)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30789748.

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1699.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DE009DB05QP1&c=1699.f>.

<http://www.genoscope.cns.fr/cdna?S=CS0DE009DB05QP1&c=1699.f>

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...g: / ...g:und: 27  
FEATURES      Location/Qualifiers  
source        1. .1027
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE009YD10"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

```

ORIGIN

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|---------------------------|--------|--------------------|-----------|--------------|
| Query Match | 23.5%; | Score 346.6; | DB 5; | Length 1027; |
| Best Local Similarity | 62.6%; | Pred. No. 3.3e-75; | | |
| Matches 577; Conservative | 6; | Mismatches 335; | Indels 3; | Gaps 3; |

| | | | |
|----|-----|---|-----|
| QY | 6 | CTTGATTCAGCTGAAGAAGAAAATCCAGCTTTTGGATAGACAAGCTGCTCAAGCTTT | 65 |
| | | | |
| Db | 104 | CATCATCCCAAGTTGAGAGAGAACCCGGACTTCTGAAACCGGAGCGACCGAGCCCT | 163 |
| QY | 66 | GGATGTTGCTAAGAAGTTCACCAATTCAAACTGCTGCTAAGAAATGTTATTTTGT | 125 |
| | | | |
| Db | 164 | GGGTGCCGCCAAGAAGCTGTCAGCCTGCACAGACAGCCGCCAAGAACCCTCATCTTCCCT | 223 |
| QY | 126 | GGGTGATGGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGTCAAATGAA | 185 |
| | | | |
| Db | 224 | GGCGATGGATGGGGTGTTCTACGGTGACAGCTGCCAGATCTTAAAGGGCAGAAAGAA | 283 |
| QY | 186 | TGGTAAGTTGGGTCCAGAACTCCATTGGCTATGATCAATTTCCATAACGTTGCTTGTGTC | 245 |
| | | | |
| Db | 284 | GGACAAACTGGGGCCTGAGTTTACCCCTGGCCATGGACCGCTTCCCATATGTGGCTCTGTGTC | 343 |
| QY | 246 | TAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGGTACTGCTACTGCTTACTT | 305 |
| | | | |
| Db | 344 | CAAGACATACAATGTAGACAACAATGTGTCAGACAGCTGAGGCCACAGCCACGGCCTTACCT | 403 |
| QY | 306 | GTGTGTTGTTAAGGTAATTACAGAACATATTGTGTTTCTGCTGCTGCTAGATACAATCA | 365 |

Db 404 GTGCGGGGTCAAGGCACTTCCAGACCATGTGGCTTGAGTGACGCCGCCGCTTTAAACCA 463
QY 366 ATGTAATACTACTAGAGTAATGAAGTACTTCTGTATTATAGAGCTAAGAGGCTGG 425
Db 464 GTGCAACACGACACCGCGCAACGAGGTCACTCCGTGATGAATCGGGCCAGAAAGCAGG 523
QY 426 TAAGGCTGTGGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA 485
Db 524 GAAGTCAGTGGAGTGGTAACCAACACACAGAGTGACACGCCCTCGCCAGCGGCACTTA 583
QY 486 CGCTCATCTGTTAATAGAAATTGCTACTCTGATGCTGATTGGCCAGCTGATGCTCAAAA 545
Db 584 CGCCACACGGTGAACCGCAACTGTACTCGGACGCCGACGTGCTGCTCGGCCGCCCA 643
QY 546 GAATGTTGTCAAGATATGTCTGCTCAATTGTTTACAATATGATATGATGTTATTTT 605
Db 644 GGAGGGGTGCCAGACATCGCTACGACGCTCATCTCCAACATGACATTTGACGTGATCCT 703
QY 606 GGGTGTGTAGATATGATCATGTTTCCAGAGGTACTCCAGATCCAGAAATCCAGATGA 665
Db 704 AGGTGAGGCGCCGAAGTACATGTTT-CGCATGGGAACCCAGACCCTGAGTACCCAGATGA 762
QY 666 TGCTTCTGTTAATGCTGTTAGAAAGATAGCAAAATTGGTTCAGAGATGGCAAGCTAA 725
Db 763 CTACAGCCAAAGGTGG-GACAGGCTGACCGGAGAAATCTGTGACAGAAATGGCTGGCGAM 821
QY 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGATGATTG 785
Db 822 GCCCAGGGGTGCCCGGTACGTGTGAACCGCACTGAGCTCATGACAGGCTTCCCTGAGCCC 881
QY 786 TAGTGTACTCATTTGATGGGTTTGTGGAACAGCTGATATGAAGTATATGTTCA-AC 844
Db 882 GTCTGTGACCCATCTCATGGGTCTCTTGAAGCTGGAAGACATGAAMAMAGATCCACCC 941
QY 845 AAGATCATCTAAGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTGCAGTTTGT 904
Db 942 GAGACTCCMCACCTGRRCCCTCCYTGATGAGRTGACAGAGGCTGCCCTGCTGCTGA 1001
QY 905 CTAGAATCCAGAGGTTT 925
Db 1002 GCAGGAACCCCGCGCTTTT 1022

RESULT 5
BX379970 991 bp mRNA linear EST 26-APR-2004
LOCUS BX379970 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1042YG09 5-PRIME, mRNA sequence.
ACCESSION BX379970
VERSION BX379970.2 GI:46573405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 991)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30448840.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0D1042AD05QPl&c=1699.f.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1042YG09"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
primer="1st strand cDNA was primed with a NotI-oligo(dt)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 23.3%; Score 343.6; DB 5; Length 991;
Best Local Similarity 63.3%; Pred. No. 1.8e-74;
Matches 557; Conservative 1; Mismatches 320; Indels 2; Gaps 2;
QY 6 CTTGATTCAGCTGAAGAAGAAATCCAGCTTTTGAATAGACAAGCTGCTCAAGCTTT 65
Db 106 CATCATCCCAAGTTGAGAGAGAGAACCCGACTTCTGGAACCGGAGGACGCGGCCCT 165
QY 66 GGATGTTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGAATGTTATTTGTTT 125
Db 166 GGGTCCCGCCAGAAAGCTGCAGCCTGCACAGACAGCCGCAAGAACCTCATCTTCT 225
QY 126 GGGTATGTTATGGGTGTTCCACTGTTACTGCTACTAGATTTGAAGGTCAAATGAA 185
Db 226 GGGCGATGGATGGGGGTGTTCAAGCTGTTACTGCTGCTGCTGCTGCTGCTGCT 285
QY 186 TGTTAAGTTGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGT 245
Db 286 GGACAAACTGGGGCTGAGTTACCCCTGGCCATGGAACCGCTTCCATATGTGGCTGTC 345
QY 246 TAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGCTGCTGCTGCTGCTT 305
Db 346 CAAGACATACATGTAGACAAACATGTGCCAGACAGTGAGCCACAGCCAGCCTTACC 405
QY 306 GTGTGTTGTTAAGGTAATTACAGAACTATTGGTTTCTGCTGCTGCTGCTGCTGCT 365
Db 406 GTGCGGGGTCAAGGCAACTTCCAGACCATTTGGCTTGAAGTGAAGCCGCCGCTTAA 465
QY 366 ATGTAATACTACTAGAGTAATGAAGTACTTCTGTTATTAATAGAGCTAAGAGCTGG 425
Db 466 GTGCAACACGACACCGCGCAAGAGGTCACTCCGTGATGAATCGGGCCAGAAAGCAGG 525
QY 426 TAAGGCTGTTGGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGCTTA 485
Db 526 GAAGTCAGTGGAGTGTGAACCAACACAGAGTGACAGCAGCCTCGCCAGCCGACCTA 585
QY 486 CGCTCATCTGTTAATAGAAATTGCTACTGATGCTGATTTGCCAGCTGATGCTC-AA 544
Db 586 CGCCACACCGGTGAACCGCAACTGTACTCGAGCGGACGTGCTGCTGCGGCCGCA 645
QY 545 AGAATGTTGTCAGATATTTGCTGCTCAATTGTTTACAATATGATATGATGTTATT 604
Db 646 GGAGGGGTGCCAGAGACATCGCTACGACGCTCATCTCCAACATGACATGACGTATCC 705
QY 605 TGGTGTGTGTAAGATGATCATGTTTCCAGAGGTAAGTACTCCAGATCCAGATACCCAG 664
Db 706 TAGTGTGAGGCGCGAAGTACATGTTTCCGATGGGAACCCAGACCCCTGAGTACCCAG 765
QY 665 ATGCTTCTGTTAATGCTGTTAGAAAGATGAACCAAAATTGGTTCAAGATGCGCAAGCT 724
Db 766 ACTACAGCCAAAGTGGGACCAAGGCTGACGGGAAAGAAATCTGTGTCAGGAATGGCTGG 825
QY 725 AGCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGTCAGAGCTGCTGATGAT 784
Db 826 CGC-CAAGGGTCCCGTACGTGTGAACCGCACTGAGCTCATGACGCTTCCCTGAGCC 884
QY 785 CTAGTGTACTCATTTGATGGGTTGTTGAACCAAGCTGATATGAAGTATATGTTCAAC 844
Db 885 CGTCTGTGACCATCTCATGGGTCTCTTGAAGCTGAGAMATGAATAAGATCCACC 944


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QY      845 AAGATCATACTAAGATCCAACTTTGGCTGAATGACTGA 884
      |||  ||  |||  |||  ||  ||  |||  |||  :
DB      945 GAGACTCCACACTGAMCCCTCCCTGATGAGATGACARA 984

```

RESULT 6
AY404255

| | | | | | |
|------------|--|---------|-----|--------|-----------------|
| LOCUS | AY404255 | 1587 bp | DNA | linear | GSS 15-DEC-2003 |
| DEFINITION | Mus musculus ALPPL2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. | | | | |

ACCESSION AY404255
VERSION AY404255.1 GI:39760232

| | |
|----------|----------------------------|
| KEYWORDS | GSS. |
| SOURCE | Mus musculus (house mouse) |

REFERENCE
AUTHORS
Clark, A.G., GJanowski, S., Nielson, R., Thomas, P., Ketariwal, A.
1 (bases 1 to 1587)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1587)

| | |
|-----------|--|
| TITLE | Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios |
| JOURNAL | Science 302 (5652), 1960-1963 (2003) |
| PUBMED | 14671302 |
| REFERENCE | 2 (bases 1 to 1587) |
| AUTHORS | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., |

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

COMMENT
This sequence was made by sequencing genomic exons and ordering them based on alignment.

| source | location/Qualifiers |
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| 1. .1587 | |

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/organism="Mus musculus"
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/db_xref="taxon:10090"
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| Query Match | 22.7%; | Score 334.6; | DB 9; | Length 1587; |
| Best Local Similarity | 35.6%; | Pred. No. 3.6e-72; | | |
| Matches 512; Conservative | 0; | Mismatches 921; | Indels 6; | Gaps 1; |

Oy 8 TGATTCCAGCTGAGAAGAAATCCAGCTTTTGGAATAGACAAGCTGTCAAGCTTTGG 67
| | | | | | | | | | | | | | | | | | | |
Db 59 TCATTCCAGTGAGAGAGGAACCCGGCCTTCGTGGAACAAGAGGCAGCCGAGGCCCTGG 11

QY 68 ATGTTGCTAAGAGTTGCCAACCAATTCAAACCTGCTGCTAGAATGTATTTTGGTTTTGG 12
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 ATGCTGCCAAGAACTGCAGCCCATTCAGACATCAGCTAAGAACCTCATCATCTTCCCTGG 17

Oy 128 GTGATGTATGGCTGTCCAACTGTACTGTACTAGATTTTGAAGGTC AATGATG 18
| | | | | | | | | | | | | | | | | | | | |
Db 179 G-----GATGGGGTACCCACAGTAGACAGCACCAGGATCCTTAAGGGCGAGTTGGAAG 23

QY 188 GTAAGTTGGGTCAGAACCTCCATTGGCTATGGATCAATTCATACGTGCTTGTCTA 24
| | | | | | | | | | | | | | | | | | | | | |
Db 233 GCCATCTAGGACGGAGACACCCCCTAGCCATGGAACCTTCCCATACATGGCTTGTCCTCA 29

QY 248 AGACTTACAATGTTGATAGACAA GTTCAGA TTCTGCTGGTACTGTACTGTTACTTGT 30
DB 293 AGACATACAGTGTTGGACAGACAG GTTCCAGCA GTGCAGCAGCACGGGCCA CTGCTTACCCTGT 35

308 GTGGTGTAAAGGTAATTACAGACTATTGGTGTCTCTGCTGCTAGATACATCAAT 36

Db 353 GTGGGGTCAAGACCAACTACAAGACCATTGGCGGTAGCGCAGCCGCCGAGATTCCACCAGT 412

Qy 368 GTAATACTACTAGAGTAAATGAAGTTACTTCTGTTATTATATAGAGCTAAGAACGCTGTA 427

Db 413 GCAACACCCACATTGTGGCAATGAGGCTTCTTCAGTGATGTACCGGTGCCAAGAAAGACGGA 472

[illegible]

Oy 488 CTCATACCTGTTAATAGAAATTGGTACTGTGATGCTGATTGGCCAGCTGATGCTCAAAAAGA 547
| | | | | | | | | | | | | | | | | | | |
Db 533 CACACACCGTGTAACCGTAATTGTA CTAGATGCAGAGATGCCCTCTGCACTGCAGG 592

| | | |
|----|--|-----|
| QY | 548 ATGTTGTCAAGATATTGCTGCTCATTTGGTTACAATATGATATTGATTATTTCG | 607 |
| | | |
| Db | 593 ACGGCTGAAGACATCGCCACTTCAATCATCTTCCAACATGGACATTGATNNNNNNNNN | 652 |

| | | | |
|----|-----|--|-----|
| Qy | 608 | GTGCTGTAGATGTACATGTTCCAGAAGTACTCCAGATCCGAATACCAGATGATG | 667 |
| Db | 653 | NN | 712 |

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

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|----|------|--|-----|
| QY | 1148 | AGCCTTGATAGTCTTA CACTTCTATT TGTATGTAATGTCAGGTTATGCTT | 120 |
| Db | 1193 | NNNNNNNNNNNNNNNN NNNNNNNNNNNN NNNNNNNNNNNN NNNNNNNNNNNN NNNNNNNNNN | 125 |

| | | |
|----|--|-----|
| QY | 1208 TCGGTGTTCTAGACCAGATGTTAATGCTAGTACTGAAGAACAATTTCACAGAC | 126 |
| | | |
| Db | 1253 MNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCAACCCACGTACCAGC | 131 |

| | | | |
|----|--|--|------|
| QY | | 1268 AACAGCTGCTGTTCATTGGCTAGTGAACCTCATGTTGGTGTAAGATCTGCTGTTTTTG | 1332 |
| | | | |
| Db | | 1313 AGCAGGCTGCTGTACCCTGTTGTCAGAGAACCCACAGCGGGGAGGACTGGCAATATTCG | 1337 |

| | | | | | | |
|----|------|--------------------|------------------|-------------------|-----------------|------|
| QY | 1328 | CTAGAGTCCACAAGCTCA | TTGGTTCATG | TGTTCAAGAGAA | CTTTTGTTGCTCATA | 1338 |
| | | | | | | |
| Db | 1373 | CGCGTGCCACACAGGCG | CACTGTGTGCACGAGT | TCAGAGCAGAACTACAT | CGCCGACG | 1433 |
| | | | | | | |

QY 1388 TTATGGCTTTTGCTGGTGGTGTGAACCATACACTGATTTGTAATTGGCAGCTCCAGCT 1446

Db 1433 TCATGGCCTTCGACGCTGCTGGAGCCCTACACTGACTGCGCGCTGGCATCCCTGCT 1491

RESULT 7
AL552555
LOCUS
DEFINITION 984 bp mRNA linear EST 30-MAR-2004
AL552555 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI067YC24 5-PRIME, mRNA sequence.
ACCESSION
AL552555
VERSION
AL552555.3 GI:45857340
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 984)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On Feb 15, 2001 this sequence version replaced gi:31274370.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CSODI067BBI2QPI&c=1699.f.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI067YC24"
/issue_type="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 22.4%; Score 330.4; DB 1; Length 984;
Best Local Similarity 63.2%; Pred. No. 3.6e-71;
Matches 556; Conservative 0; Mismatches 321; Indels 3; Gaps 3;

OY 6 CTTGATTCACGCTGAGAAGAAATCCAGCTTTTGAATAGACAGCTGCTCAAGCTT 65
DB 106 CATCATCCCACTGAGAGAGAACCCGAGCTCTGGAACCGGACGCGAGCCCT 165
OY 66 GGATGTTGCTAAGAGTTGCAACCAATTCAAACTGCTGCTAAGAATGTTATTTT 125
DB 166 GGGTCCCGCAAGAGCTGCAGCTGCACAGACGCCCAAGAACTCATCTTCT 225
OY 126 GGGTATGATGGGTGTTCCAACTGTTACTGTAAGATTGGAAGGTCAAATGAA 185
DB 226 GGGGATGGATGGGGGTGTTCTACGGTGACAGCTGCAGATCTTAAAGGACAGAA 285
OY 186 TGGTAAGTGGGTCCAGAACTCCATGGCTGATGATCAATTCATAGCTTGTGTC 245
DB 286 GGACAACTGGGCTGAGTTACCCCTGGCCATGACCGCTTCCATATGTGGCTCTGC 345
OY 246 TAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTAAGTCTTACTT 305
DB 346 CAAGACATACATGTAGACAACATGTGCCAGACAGTGAAGCCACAGCCGCTACCT 405
OY 306 GTGTGTTTAAAGGTAATTACAGACTATGTGTTTCTGCTGCTGCTAGATACATCA 365
DB 406 GTGGGGGTCAAGGCACTTCCAGACCATGTGCTGAGTGCAAGCCGCGCTTTAACCA 465

OY 366 ATGTAACTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGACTAAGAGGCTGG 425
DB 466 GTGCAACACGACACCGCGCAACGAGGTCACTCCGTGATGAATCGGCGCAAGAAAGCAGG 525
OY 426 TAAGGCTGTTGTTGTTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGTGCTTA 485
DB 526 GAAGTCAGTGGAGTGTAAACCAACACGAGTGACAGCAGCCTGCGCCGCGCACCTA 585
OY 486 CGCTCATCTGTTAATAGAATTTGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 544
DB 586 CGCCCAACGCGTGAACCGCAACTGTTACTTGGACCGCCGACGCTGCTCGGCGCCCA 645
OY 545 AGAATGTTGTCAGATATTTGCTGCTCAATTGCTTTACAATATGATATGATGTTATT 604
DB 646 GGAGGGGTGCCAGGACATCGCTACGCACTCATCTCAACATGACATTTGACGTGATCS 705
OY 605 TGGTGGTGTAGAAATGTACATGTTCCAGAAAGTACTCCAGATCCAGAAATACCCAGATG 664
DB 706 TAGTGAGGCGGAAAGTACATGTTTGGCATGGAAACCCAGACCTGAGTACCAGATG 765
OY 665 ATGCTTCTGTTAATGCTGTTAGAAAGGTAAGCAAAATTTGTTCAAGAAATGCAAGCTA 724
DB 766 ACTACAGCCAAAGTGGGACCAAGCTGACGGGAAAGATCTGTTGACGAATGCTGGCGA 825
OY 725 AGCATCAAGTGTCTCATATGTTTGAATAGAACTGCTTGTGCAAGCTGCTGATGATT 784
DB 826 CGC-CAGGGGTGCGCGGTACGTGTGGAACCGCACTGAGCTCATGCAAGCTTCCCTGACC 884
OY 785 CTAGTGT-TACTCATTTGATGGGTTTGTGAACCAAGCTGATATGATATGTTCAA 843
DB 885 CGTCTGTGAACCATCTCATGCGTCTTTTGAGCCTTGAGACATGAATAACGATCCAC 944
OY 844 CAAGATCATACTAAGATCCAACTTTGCTGAATGACTG 883
DB 945 CGAGACTTCACACTGACCCCTCCTGATGAGATGACAG 984

RESULT 8
CF591568
LOCUS
DEFINITION 888 bp mRNA linear EST 26-SEP-2003
AGENCOURT 15681730 NICHD_XGC_Swb1N Xenopus tropicalis cDNA clone
IMAGE:7023090 5', mRNA sequence.
CF591568
CF591568.1 GI:36343216
EST.
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE
1 (bases 1 to 888)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Rob Granger, University of Virginia
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM14750 row: f column: 16
High quality sequence stop: 621.

FEATURES
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1. .888
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/clone="IMAGE:7023090"
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/clone_lib="NICHX XGC Swb1n"
/note="Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the F6 strain. 1st strand cDNA was primed with a Not
I - oligo(dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cots with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHX XGC Swb1). Library
was constructed by Open Biosystems (Huntsville, AL).
PLEASE NOTE: This library contains high level of
contamination by tubifex"

ORIGIN

Query Match 20.9%; Score 308; DB 7; Length 888;
Best Local Similarity 63.2%; Pred. No. 1.3e-65;
Matches 473; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

QY 10 ATTCAGCTGAGAAGAAATCCAGCTTTTGGATAGACAAGCTCTCAAGCTTGGAT 69
Db 61 ATTCAGCGGAGAAGAGCCAGCCTGATTTTGGACACAAATAATATCCAGATTAT 120
QY 70 GTTGCTAAGAAGTTGCAACCAATTCAAAGTCTGCTAAGAATGTTATTTGTTGGGT 129
Db 121 GAAGCCCTAAAGCTAAAGCCCATTCAGCACAGAGCTAAAAAAGCTGATCTCTTAGGT 180
QY 130 GATGATAGGGTGTTCCAACTGTACTGCTACTAGAAATTTGAAGGCTCAATGAATGCT 189
Db 181 GATGGATGGAGATTCACACAGTCACTGCCACAGAGATCTTAAGTGGGAGATGAAGAGA 240
QY 190 AAGTGGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGTCTAAG 249
Db 241 ATGCTGGAGAGAAGAAATGAGCTGGCAATGGAAGAAGTTCCCTACACGGCACTCTTAAG 300
QY 250 ACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTAAGTCTGCTTACTTGTGT 309
Db 301 ACATACAATGTGATCGCCAGTCTCTGACAGCGCGGTACTGCACTGCTTATATTTGT 360
QY 310 GGTGTTAAGGATATTACAGAACTATGTGTTTCTGCTGCTGCTAGATACAATCAATGT 369
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QY 370 AATTAATAAGGTAATGAAGTACTTCTGTTATTAATAGAGCTAAGAAAGGCTGTAAG 429
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QY 430 GCTGTGGTGTGTTACTACTAGTCAAGTTCACATGCTTCTCAGCTGTGCTTACGCT 489
Db 481 TCGGTAGAATGTTACTACAACAGAGTCCAGCATGCTTCCCTCTGGCACTTACGCT 540
QY 490 CATACTGTTAATAGAAATGCTACTGATGCTGATTTGCCAGCTGATGCTCAAAAGAA 549
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QY 550 GGTGTCAAGATATGCTGCTCAATGTTTACATATGATATGATGTTATTTGGGT 609
Db 601 GGGGTGAAGATATTTGCCAGCAGCTGATTTCAATGTGACATAGATGCTATCTTGGT 660
QY 610 GGTGTAGAATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGATGCT 669
Db 661 GGGGGGGGAAGTATATGACACCAAGTGGAACTTCTGATCTGAGTACCCCTGAGATAAG 720
QY 670 TCTGTTAATGTTAGAAAGGATAGCAAAATTTGTTCAAGAAATGGCAAGCTAAGCAT 729
Db 721 AAGCAAAATGGCATAGAAAAGATGAAAAGAACCTTATAGATGAATGGCTTTGAAAAC 780
QY 730 CAAAGTCTCAATATGTTTGAATAGAA 757
Db 781 AGGGGGCTCAGTATGTGTGAATAAA 808

RESULT 9
AY404253
LOCUS
DEFINITION Homo sapiens ALPPL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY404253
VERSION AY404253.1
KEYWORDS GI:39760230
SOURCE GSS.
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
PUBMED Science 302 (5652), 1960-1963 (2003)
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="ALPPL2"
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ORIGIN

Query Match 20.6%; Score 303.6; DB 9; Length 1593;
Best Local Similarity 34.2%; Pred. No. 1.9e-64;
Matches 493; Conservative 0; Mismatches 941; Indels 6; Gaps 1;

QY 6 CTTGATTCAGCTGAAGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTT 65
Db 57 CATCATCCAGTTGAGAGAGAAGAACCCGAGCTTCTGGAACCGCAGCAGCCGAGCCCT 116
QY 66 GGATGTTGCTAAGAAGTTCACCAATTCAAACCTGCTGCTAAGAATGTTATTTGTTT 125
Db 117 GGGTGCCGCCAAGAAGCTGACGCTGCACAGACAGAGCGGCCAAGAACTCATCTTCT 176
QY 126 GGGTATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGTCAAATGAA 185
Db 177 G-----GGATGGGGGTGTCTACGGTGACAGCTGCGCAGGATCCTAAAGGCGAGAA 230
QY 186 TGGTAAGTTGGGTCCAGAACTCCATTGGCTATGATCAATTTCCATAGCTTGTGTC 245
Db 231 GGACAAACTGGGGCTGAGACCTTCCCTGGCAGTGAACCGCTTCCGTAAGTGGCTGTC 290
QY 246 TAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTAAGTCTGCTTACTT 305
Db 291 CAAGACATACAGTGTAGACAAGCATGTGCCAGACAGTGGAGCCACAGCCAGGCTA 350
QY 306 GTGTGCTTTAAGGTAATTAACAAGTATTTGGTCTTCTGCTGCTGCTAGATCAATCA 365
Db 351 GTGCGGGGTCAAGGGCACTTCCAGACCATTTGGCTTGAAGTGCAAGCCGCGCTTTA 410
QY 366 ATGTAATACTACTAGAGTAATGAAGTACTTCTGTTATTAATAGAGCTAAGAGGCTGG 425
Db 411 GTGCAACAGCACAGCGCGCAAGAGGTATCTCGTATGAATCGGGCCAGAAAGCAGG 470

| | | | |
|----|------|--|------|
| Qy | 426 | TAAGCGTGTGGTGTGTTGTTACTACTACTAGAGTTCAATGCTTCTCCAGCTGGTGCTTA | 485 |
| Db | 471 | AAAGTCAGTGGAGTGTGAACCAACACAGGGGTGCAGCATGCTCTGCCAGCCGGCGCCTA | 530 |
| Qy | 486 | CGCTCATACTGTTAATAGAAATGGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAAA | 545 |
| Db | 531 | CGCCACACAGGTGAACCGCAACTGGTACTCGATGCGACGTGCTGCTCGGCCGCCA | 590 |
| Qy | 546 | GAATGCTGTCAAGATAATGCTGCTCAATTTGTTTACAATATGATATGATGTTATTTT | 605 |
| Db | 591 | GGAGGGGTGCCAGACATCGCCACGCACTCATCTCCACATGACATTGATNNNNNNNN | 650 |
| Qy | 606 | GGGTGTGTAGATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACCAGATGA | 665 |
| Db | 651 | NN | 710 |
| Qy | 666 | TGCTTCTGTTAATGCTGTAGAAAGATAAGCAAAATTTGTTCAAGAATGGCAAGCTAA | 725 |
| Db | 711 | NN | 770 |
| Qy | 726 | GCATCAAGGTGCTCAATATGTTTGGAAATGAACCTGCTTTGTTGCCAAGCTGCTGATGATTC | 785 |
| Db | 771 | NN | 830 |
| Qy | 786 | TAGTGTACTCATTTGATGGGTTTGTGTAACCACTGATATGAAGTATATATGTTCAACA | 845 |
| Db | 831 | NN | 890 |
| Qy | 846 | AGATCATACTAAGATCCAATTGGCTGAATGACTGAAGCTGCTTTGCCAAGTTTGTCTC | 905 |
| Db | 891 | NN | 950 |
| Qy | 906 | TAGAAATCCAAGAGTTTCTTACTTGTGTTGAAGGTGTAGAATTGATCATGTGATCA | 965 |
| Db | 951 | NN | 1010 |
| Qy | 966 | TGATGCTAAGCTTATATGGCTTTGACTGAAGCTATATGTTGATAATGCTATTTGCTAA | 1025 |
| Db | 1011 | NN | 1070 |
| Qy | 1026 | GGCTAATGAATTGACTTCTGAATTGGATACTTTGATTTTGGTTACTGCTGATCATAGTCA | 1085 |
| Db | 1071 | NN | 1130 |
| Qy | 1086 | TGTTTTTCTTTGGTGTTCACACTTGAGAGGTACTTCTAATTTTGGTTGGCTCCAGG | 1145 |
| Db | 1131 | NN | 1190 |
| Qy | 1146 | TAAGCCTTGGATAGTAACTCTACACTTCTAATTTGTATGTATGTGTCAGGTTATGC | 1205 |
| Db | 1191 | NN | 1250 |
| Qy | 1206 | TTTGGGTGTGTTCTAGACCAAGATGTTAATGTAGTACTAGTGAAGAACCATCTTACAG | 1265 |
| Db | 1251 | NN | 1310 |
| Qy | 1266 | ACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTCATGCTGTGAAGATGTTGCTGTTT | 1325 |
| Db | 1311 | GCAGCAGTCAGCAGTGCCTCTGACGAGAGACCCACGACGCGAGACGTCGCGGTGTT | 1370 |
| Qy | 1326 | TGCTAGAGGTCCACAAGCTCATTTGGCTTCATGCTGTTTCAAGAAGAACTTTTGTGCTCA | 1385 |
| Db | 1371 | CGCGCGCGGCCCGCAGCGCCCACTGCTTACGCGCGTGCAGAGACGACCTTCATAGCGCA | 1430 |
| Qy | 1386 | TATTAATGCTTTTGTGCTGTGTGTTGAACCATACCTGATTTGTAATTTGCCAGCTCCAGC | 1445 |
| Db | 1431 | CGTCATGGCCTTGCCTGCTGCTGAGCCCTACACCGCTGCGACCTGCGCGCCCGCCG | 1490 |

| | |
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| RESULT 10 | |
| BX417625 | |
| LOCUS | BX417625 |
| | 936 bp |
| | mRNA |
| | linear |
| | EST 03-MAY-2004 |

| | |
|------------|---|
| DEFINITION | BX417625 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YC17 |
| ACCESSION | 5-PRIME, mRNA sequence. |
| VERSION | BX417625 |
| KEYWORDS | BX417625.2 GI:46955936 |
| SOURCE | EST. |
| ORGANISM | Homo sapiens (human) |
| | Homo sapiens |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| REFERENCE | 1 (bases 1 to 936) |
| AUTHORS | Li,W.B., Gruber,C., Jesse,J. and Polayes,D. |
| TITLE | Full-length cDNA libraries and normalization |
| JOURNAL | Unpublished (2001) |
| COMMENT | On May15, 2003 this sequence replaced gi:30767760. |

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1699.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0DE011AB09QP1&c=1699.f>.

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .936 |

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/tissue_type="PLACENTA"
/clone_id="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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ORIGIN

| | Query Match | 20.5%; | Score 303.2; | DB 5; | Length 936; | |
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| | Best Local Similarity | 63.4%; | Pred. No. 2.1e-64; | | | |
| | Matches 458; | Conservative 3; | Mismatches 261; | Indels 0; | Gaps 0; | |
| QY | 6 | CTTGATTCAGCTGAGAGAAATAATCCAGCTTTTGGAAATGACACAAGCTGCTCAAAGCTTT | 65 | | | |
| Db | 142 | CATCATCCAGTTGAGAGAGAGAAACCCGACTTCTGAAACCGGAGGCAGCCGAGGCCCT | 201 | | | |
| QY | 66 | GGATGTTGCTAAGAGAGTTGCCAACCAATTCAAACTGCTCTAAGAAATGTTATTTGTTTTT | 125 | | | |
| Db | 202 | GGGTGCCGCCAAGAGAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCTTCT | 261 | | | |
| QY | 126 | GGGTGATGATGGGTGTTCCAACTGTTACTGCTACTAGAATTTTGAAGGGTCAAAATGAA | 185 | | | |
| Db | 262 | GGGCGATGGATGGGGGTGTTACGTTGACAGCTGCCAGATCTAAAGGGCAGAGAA | 321 | | | |
| QY | 186 | TGTTAGTTGGTCCAGAAACTCCATTGGCTATGATCAATTTCCATACGTGCTTTGTC | 245 | | | |
| Db | 322 | GGACAAACTGGGGCTGAGTTACCCCTGGCCATGACCGCTTCCCATATTTGGCTCTCTC | 381 | | | |
| QY | 246 | TAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGTAAGTCTACTGCTTACTT | 305 | | | |
| Db | 382 | CAAAACATACAATGTAGACAACAACATGTGCCAGACAGTGAACCAAGCCACGGGCTTACT | 441 | | | |
| QY | 306 | GTTGTGTTAAGGTAATTAACAAGCTATTGGTGTCTGCTGCTGCTAGATATACAATCA | 365 | | | |
| Db | 442 | TTKCGGGGTCAAGGCCAATTCAGACCATTTGGCTTATTTCAGCCGCCCTTTAACCA | 501 | | | |
| QY | 366 | ATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAAATAGAGCTAAGAGGCTGG | 425 | | | |
| Db | 502 | GTGCAACACGACACGGGCCAAGAGTCAATCTCCGTGATGAATCGGGCCAAGAAAGCAGG | 561 | | | |

| | | | |
|----|-----|--|-----|
| QY | 426 | TAAGCGTGTGGTGTGTTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTGCTTA | 485 |
| | | | |
| Db | 562 | GAAGTCA GTGGAGTGGTAAACCACCA CACGAGTGCAGCACGCTCGCTAGCCGGCACCTTA | 621 |
| QY | 486 | CGCTCATACTGTTAATAGAAA TTGGTACTCTGTAGTGTGATTTGCCAGCTGATGCTCAAAA | 545 |
| | | | |
| Db | 622 | CGCCACACAGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCTGCTCGGCCGCCA | 681 |
| QY | 546 | GAATGGTTGTCAGATATTTGCTGCTCAATTGGTTTACAAATATGATATTTGATGTTATTTT | 605 |
| | | | |
| Db | 682 | GGAGGGGTGCCAGACATCGCTACGACAGTCATCTCCAAATGACATTTGACGTGATCCT | 741 |
| QY | 606 | GGGTGGTGTAGATGTACATGTTTCCAGAAGTACTCCAGATCCAGAATACCAGATGA | 665 |
| | | | |
| Db | 742 | AGGTGAGGCCGAAAGTACATGTTTCGCATGGGAACCCASACCCTGAGTACCAGATGA | 801 |
| QY | 666 | TGCTTCTGTTAATGCGTGTAGAAAGATAAGCAAAATTTGGTTCAAGAATGGCAAGCTAA | 725 |
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| Db | 802 | CTACAGCCCAAGTGGGACCAAGCTGGA CCGGAAGAATCTGGTGCAGGAATGGCTGGCGAC | 861 |
| QY | 726 | GC 727 | |
| | | | |
| Db | 862 | GC 863 | |

| | | | | | |
|------------|---|--------|------|--------|-----------------|
| RESULT | 11 | | | | |
| AL553521 | | | | | |
| LOCUS | AL553521 | 902 bp | mrna | linear | EST 30-MAR-2000 |
| DEFINITION | AL553521 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1076YD24 5-PRIME, mRNA sequence. | | | | |

| | |
|-----------|---|
| ACCESSION | AL553521 |
| VERSION | AL553521.3 |
| KEYWORDS | GI:45858290 |
| SOURCE | EST. |
| ORGANISM | Homo sapiens (human) |
| | Homo sapiens |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| REFERENCE | 1 (bases 1 to 902) |
| AUTHORS | Li,W.B., Gruber,C., Jesse,J. and Polayes,D. |
| TITLE | Full-length cDNA libraries and normalization |
| JOURNAL | Unpublished (2001) |
| COMMENT | On Feb 15, 2001 this sequence version replaced gi:31275335. |

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primed
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?S=CS0DI076DB12QPI&c=1699.f>.

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FEATURES
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            /note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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| Query Match | 20.4% | Score 301.6; | DB 1, | Length 902; |
| Best Local Similarity | 63.6%; | Pred. No. 5.2e-64; | | |
| Matches 476; | Conservative | 8; | Mismatches 262; | Indels 2; |
| Gaps | | | | |
| 6 | CTTGATTCAGCTGAAGAGAAAATCCAGCTTTTGGATATAGACAAGCTGCTCAAGCTTT | 65 | | |

| | | | |
|----|-----|---|-----|
| Db | 106 | CATCATCCCAAGTTGAGAGAGAAACCGGACTTCTGGAACCGGAGGCGAGCCGAGGCCCT | 165 |
| QY | 66 | GGATGTTGCTAAGAGTTGCAACCAATTCAACTGCTGTGAAGATGTTATTTGTTTT | 125 |
| Db | 166 | GGGTGCCCGCAAGAAGCTGCAAGCTGCACAGACAGACGCCGCCAAGAACCCTCATCTTCT | 225 |
| QY | 126 | GGGTGATGTTATGGGTGTTCCACTGTACTGCTACTAGATTTTGAAGGTCGAATGA | 185 |
| Db | 226 | GGGCGATGGGATGGGGGTGTCTACGCTGACAGACTGCCAGATCTTAAAGGCGAGAAGA | 285 |
| QY | 186 | TGGTAAGTTGGGTCAGAAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGTGTC | 245 |
| Db | 286 | GGACAACTGGGGCTTGAGATACCTCTGGCCATGAGCCGCTTCCATATGTGGCTCTGTGTC | 345 |
| QY | 246 | TAAGACTTACAATGTTGATAGACAAGTTCAGATTCTGCTGCTACTGCTTACTT | 305 |
| Db | 346 | CAAGACATACAATGTAGACAAACATGTGCCAGACAGTGAAGCCACAGCCAGCCTACTCT | 405 |
| QY | 306 | GTGTGTTGTTAAGGGTAATTACAGAACTATTGGTGTTCCTGCTGCTAGATACAATCA | 365 |
| Db | 406 | GTGCGGGGTCAAGGGCACTTCCAGAACCATTTGGCTTGATGACAGCCGCCCTTTAACCA | 465 |
| QY | 366 | ATGTAATACTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGAGCTAAGAAGCGTGG | 425 |
| Db | 466 | GTGCACACGACACGCGGCAACGAGGTCTATCTCCGTGATGAATCGGGCCAGAAGAAGCAGG | 525 |
| QY | 426 | TAAGGCTGTTGGTGTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTGCTTA | 485 |
| Db | 526 | GAAGTCAGTGGGAGTGGTAACCAACACAGAGTGCAGCAGCCTCGCCAGCCGGCACTTA | 585 |
| QY | 486 | CGCTCACTACTGTTAATAGAAATTTGGTACTCTGATGCTGAATTTGCCAGCTGATGCTC-AAA | 544 |
| Db | 586 | CGCCACACGGTGAAACCGCACTGGTACTCGGACGCCGACGTGCTCGCCGCCGCCCA | 645 |
| QY | 545 | AGAATGGTGTCAAGATATGCTGCTCAATTGGTTTACAATATGATATGATGTTATT | 604 |
| Db | 646 | GGAGGGGTGCCARGACATCGCTACGACGCTCATCTCCAACATGACATTGACGTGATCC | 705 |
| QY | 605 | TGGGTGTTGTTAGAAATGTACATGTTTCCAGAAGGTACTCCAGATCCAGAATACCAGATG | 664 |
| Db | 706 | TAGGTGAGAGCCGAAAGTACATGTTTCCGATGGGAAMCCARACCTGAGTACCABATG | 765 |
| QY | 665 | ATGCTTCTGTTAATGCTGTAGAAAGATAAGCAAAATTTGGTTCAAGAATGGCAAGCTA | 724 |
| Db | 766 | AATMAAGCCCAAGGTGGGACCAACGCTGAGCGGAAGAATCTKGTGACAGAATKGTGGCGA | 825 |
| QY | 725 | AGCATCAAGGTGCTCAATATGTTGGAA | 752 |
| Db | 826 | CGC-CARGGGTGCCCCGGTATGTGGA | 852 |

| | | | | |
|------------|--|--|--|--|
| RESULT 12 | | | | |
| BX343739 | | | | |
| LOCUS | | | | |
| DEFINITION | | | | |
| ACCESSION | | | | |
| VERSION | | | | |
| KEYWORDS | | | | |
| SOURCE | | | | |
| ORGANISM | | | | |
| REFERENCE | | | | |
| AUTHORS | | | | |
| TITLE | | | | |
| JOURNAL | | | | |
| COMMENT | | | | |

BX343739 1125 bp mRNA linear EST 07-APR-2000
 BX343739 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1017YB14 5-PRIME, mRNA sequence.
 BX343739
 BX343739.2 GI:46270510
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1125)
 Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 2, 2003 this sequence version replaced gi:30336211.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1699.f

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?cs=CS1A1005ZB08QPl&c=1699.f>.

FEATURES

source

Location/Qualifiers

1..1125

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI017YB14"

/issue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was

digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 20.2%; Score 298.4; DB 5; Length 1125;
Best Local Similarity 63.5%; Pred. No. 3.5e-63;
Matches 517; Conservative 1; Mismatches 292; Indels 4; Gaps 4;

OY 6 CTTGATTCAGCTGAGAAGAAATCCAGCTTTTGAATAGACAGCTGCTCAAGCTTT 65
DB 211 CATCATCCAGTTGAGAGAGAGAACCCGAGCTTCTGGAACCGCGAGCGAGCCGACCT 270
OY 66 GGATGTTGCTAAGAGTTGCAACCAATTCAACTGCTGCTAAGATGTTATTTTGT 125
DB 271 GGGTCCGCCAAGAGAGCTGACGCTGCACAGACAGCCGCCAAGAACTCATCTTCT 330
OY 126 GGGTATGTTGGGTGTTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAATGAA 185
DB 331 GGGGATGGATGGGGGTGTCTACGGTGACAGCTGCCAGATCTTAAAGGCGAGAGAA 390
OY 186 TGGTAAGTTGGTCCAGAACTCCATGGCTATGATCAATTTCCATAGCTTGTGCT 245
DB 391 GGACAACTGGGGCTGAGTACCCTGGCCATGACCGCTTCCCATATGTGCTGTG 450
OY 246 TAAGACTTACATGTTGATAGACAAAGTTCCAGATTCTGCTGCTACTGCTTACTT 305
DB 451 CAAGACATACATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCAGCCCTACT 510
OY 306 GTGTGTTGTAAGGTAATTACAGAACTTGTGTTTCTGCTGCTGCTAGTACAATCA 365
DB 511 GTGCGGGGTCAAGGCACTTCCAGACCAATTGGCTTGAAGTCCAGCCGCCCTTAA 570
OY 366 ATGTAATCTACTAGAGGTAATGAAGTTACTTCTGTTATTAATAGAGTAAGAGGCT 425
DB 571 GTGCAACGACACGCGGCAAGGCTATCTCGTATGAATCGGGCCAAGAAAGCAGG 630
OY 426 TAAGGCTGTTGTTGTTTACTACTACTAGAGTTCAACATGCTTCCAGCTGCTGCTTA 485
DB 631 GAAGTCAAGTGGAGTGTAAACCAACAGAGTGCAGACAGCCTCGCACGCCGACCTA 690
OY 486 CGCTCATCTGTTAATAGAAATGTTCTGATGCTGATTTGCCAGCTGATGCTC-AAA 544
DB 691 CGCCACACGGTGAACCGCACTGTTCTGAGACGCCGAGCTGCTTCCGCCGCCCA 750
OY 545 AGAATGTTGTTCAAGATATTGCTGCTCAATTGTTTACAATATGATATTGATGTTATT 604
DB 751 GGAGGGGGTCCAGGACATCGCTACGCACTCATCTCCAACATGACATTGACGTGATCC 810
OY 605 TGGGTGGTGTAGATGTACATGTTTCCAGAGAGGTACTCCAGATCCAGATACCAGATG 664
DB 811 TAGGTGAGGCCGAAAGTACATGTT-CCGATGGGAACCCAGACCTGAGTACCCAGATG 869
OY 665 ATGCTTCTGTTAATGTTAGAAAGGTAAGCAAAATTTGTTCAAGATGGCAAGC-T 723
DB 870 ACTACAGCCAGGTGGAGCAGGCTGGACGGGAAGATCTGTTGCAGAATGCTGGCGG 929

OY 724 AAGCATCAGGTGCTCATATATGTTTGAATAGAACTGCTTGTGTCAGAGCTGTGATGAT 783
DB 930 ACGCCAGGGGTGCCCCGGTACGTGTGGRACCCGCACTGAGCTCATGACGCTTCCCTGAC 989
OY 784 TCTAGTCTTACTCATTTGATGCGTTTGTGTAAC 817
DB 990 CCGTCTGTGAC-CATCTCATAGGTTCTTTTGAGC 1022

RESULT 13

BY732148

LOCUS

DEFINITION

BY732148 RIKEN full-length enriched, 8 cells embryo Mus musculus

CDNA clone E860129L22 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

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Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

JOURNAL

PUBMED

COMMENT

TITLE

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,

Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Horii, F.,

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Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,

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Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)


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OY 987 TTGACTGAAGCTATATGTTTGTATGTAATGCTATGCTTAAGGCTAATGATGACTTCTGA 1046
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OY 1047 ATTGATACCTTGTATTTGGTACTGCTGATCATAGTCATGTTTCTTTGGTGCTTA 1106
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RESULT 15
LOCUS CK834465 681 bp mRNA linear EST 04-MAR-2004
DEFINITION 4058791 BARC 8BOV Bos taurus cDNA clone 8BOV_6J03 5', mRNA
sequence.
ACCESSION CK834465
VERSION CK834465.1 GI:45064951
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 681)
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and
Matukumalli,L.K.
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.umd.edu
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '-' -trim_fasta. Vector identified
by cross_match using options -mismatch 12 -minscore 18
Plate: 6_row: J column: 03
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High quality sequence stop: 681.
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FEATURES

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/dev_stage="Lactating, Neonatal"
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/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pcwvSport6.1; Site_1:
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library in pcwvSport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
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ORIGIN

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Query Match 19.5%; Score 288.4; DB 7; Length 681;
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OY 1049 TGGATACCTTGTATTTGTTACTGCTGATCATAGTCATGTTTCTTTGGTGCTTACA 1108
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OY 1109 CTTTGAAGGTACTTCTATTTTGGTTGGCTCCAGTAAGCTTTGGATAGTAAGTCTT 1168
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DB 182 CACTGCGTGGAGCTCCATTTTGGTCTGGCCCCCAGCAAGGCTTAGACAGCAAGTCTCT 241
OY 1169 ACACTTCTATTTGTATGTAATGCTCCAGGTATATGCTTTGGGTGGTCTAGACCAG 1228
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OY 1349 TGGTTCATGCTGTTCAAGAGAACTTTGTTGCTCATATATGCTTTGCTGCTGTTGGT 1408
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OY 1409 TTGAACCATACACTGATGTAATTTGGCAGCTCCAGCTACTGCTACTAGTATTCAGA 1466
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DB 482 TGAAGCCTACACGAGCTGCAATCTGCCAGCCCCCACCACCGCCACAGCATCCCCGA 539
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Job time : 5053.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2004, 07:43:22 ; Search time 6521 Seconds
(without alignments)
10703.818 Million cell updates/sec

Title: US-09-911-132A-1
Perfect score: 1476
Sequence: 1 gaattcctcatccacagctga.....gcattcccgactagsggtacc 1476

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 2 | 1476 | 100.0 | 1476 | 6 | AX356645 | AX356645 Sequence |
| 3 | 1464 | 99.2 | 1464 | 6 | AX840884 | AX840884 Sequence |
| 4 | 1462 | 99.1 | 1798 | 6 | E59950 | E59950 Highly acti |
| 5 | 1462 | 99.1 | 1798 | 6 | AR214214 | AR214214 Sequence |
| 6 | 1462 | 99.1 | 1798 | 6 | AX012341 | AX012341 Sequence |
| 7 | 1454.2 | 98.5 | 1650 | 6 | AX741748 | AX741748 Sequence |
| 8 | 1338.2 | 90.7 | 2460 | 4 | AF052226 | AF052226 Bos tauru |
| 9 | 1338.2 | 90.7 | 2460 | 6 | E59951 | E59951 Highly acti |
| 10 | 1338.2 | 90.7 | 2460 | 6 | AR214215 | AR214215 Sequence |
| 11 | 1338.2 | 90.7 | 2460 | 6 | AX012343 | AX012343 Sequence |
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| 14 | 1327 | 89.9 | 2542 | 6 | AR214216 | AR214216 Sequence |
| 15 | 1327 | 89.9 | 2542 | 6 | AX012345 | AX012345 Sequence |
| 16 | 1035.8 | 70.2 | 1587 | 6 | CQ725798 | CQ725798 Sequence |
| 17 | 1032.6 | 70.0 | 1587 | 6 | E08258 | E08258 CDNA encod1 |
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| 19 | 1032.6 | 70.0 | 1587 | 9 | HUMALPHB | M15694 Human adult |

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|----|--------|------|------|----|-----------|--------------------|
| 20 | 1028.2 | 69.7 | 1813 | 9 | HUMALP11 | M31008 Human intes |
| 21 | 1018.2 | 69.0 | 3076 | 6 | E10977 | E10977 Intron and |
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| 25 | 1008.8 | 68.3 | 3022 | 6 | E10976 | E10976 Intron and |
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| 28 | 1002.2 | 67.9 | 1728 | 6 | AX378141 | AX378141 Sequence |
| 29 | 1002 | 67.9 | 1779 | 6 | AX451462 | AX451462 Sequence |
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| 34 | 1000.8 | 67.8 | 1560 | 6 | AX407017 | AX407017 Sequence |
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| 36 | 1000.8 | 67.8 | 4869 | 12 | CV089940 | U89940 Cloning vec |
| 37 | 1000.8 | 67.8 | 4922 | 12 | CV089939 | U89939 Cloning vec |
| 38 | 1000.8 | 67.8 | 4989 | 6 | AR409601 | AR409601 Sequence |
| 39 | 1000.8 | 67.8 | 5083 | 6 | AR409600 | AR409600 Sequence |
| 40 | 1000.8 | 67.8 | 5115 | 12 | CV089938 | U89938 Cloning vec |
| 41 | 1000.8 | 67.8 | 5799 | 12 | CVU09660 | U09660 Cloning vec |
| 42 | 1000.8 | 67.8 | 5928 | 6 | AR455897 | AR455897 Sequence |
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| 44 | 1000.8 | 67.8 | 6056 | 12 | CVU09662 | U09662 Cloning vec |
| 45 | 1000.8 | 67.8 | 6248 | 12 | CVU09661 | U09661 Cloning vec |

ALIGNMENTS

RESULT 1
BD175591 1476 bp DNA linear PAT 18-MAR-2003
LOCUS Expression of alkaline phosphatase in yeast.
DEFINITION BD175591
ACCESSION BD175591.1 GI:29121289
VERSION BD175591.1
KEYWORDS JP 2002253269-A/1.
SOURCE Bos sp.
ORGANISM Bos sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 1476)
AUTHORS Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W., Glaser,S., Eckstein,H., Kirschbaum,T. and Riebel,B.B.N.
TITLE Expression of alkaline phosphatase in yeast
JOURNAL Patent: JP 2002253269-A 1 10-SEP-2002;
F HOFMANN LA ROCHE AG

COMMENT

OS Bos sp. (bovine)
PN JP 2002253269-A/1
PD 10-SEP-2002
PF 23-JUL-2001 JP 2001222153
PR 25-JUL-2000 DE 10036491.8
PI RAINER MUELLER, JOHANN PETER THALHOFER, FRANK GEIPEL, WERNER PI HOELKE,
PI STEPHAN GLASER, HELMUT ECKSTEIN, THOMAS KIRSCHBAUM, PI BETTINA BOMMARIUS NEE RIEBEL
PC C12N15/09, C12N1/19, C12N9/16// (C12N1/19, C12R1:645), (C12N1/19, PC C12R1:78),
PC (C12N9/16, C12R1:645), (C12N9/16, C12R1:78), C12N15/00 CC
Expression of alkaline phosphatase in yeast
FH Key Location/Qualifiers
FT source 1. 1476 /organism='Bos sp. (bovine)'.
FT location/Qualifiers 1. 1476 /organism='Bos sp. (bovine)'.
FT /mol_type='genomic DNA' /db_xref='taxon:29061'

FEATURES

source

Query Match

100.0%; Score 1476; DB 6; Length 1476;

ORIGIN

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| Db | 61 | GCCCTTGATGTAGCCCAAGAGTTGACAGCCGATCCAGACAGCTGCCAAGATGTATCTCTC | 120 | |
| QY | 121 | TTCTTGGGGATGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCCTTAAAGGGGCGAG | 180 | |
| Db | 121 | TTCTTGGGGATGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCCTTAAAGGGGCGAG | 180 | |
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| Db | 901 | CTGAGCAGGAACCCCGGGCTTCTTACTTCTTGTGAGGGAGGCGCATTGACCAAGGT | 960 | |
| QY | 961 | CACCATGACGGCAAGCTTATATGCACTGAGGCGCATGTGTTGACAATGCCATC | 1020 | |
| Db | 961 | CACCATGACGGCAAGCTTATATGCACTGAGGCGCATGTGTTGACAATGCCATC | 1020 | |
| QY | 1021 | GCCAAGGCTAACGAGCTCACTAGCGAACTGGAACGCTGATCCTTGTCACTGCAGACCAAC | 1080 | |
| Db | 1021 | GCCAAGGCTAACGAGCTCACTAGCGAACTGGAACGCTGATCCTTGTCACTGCAGACCAAC | 1080 | |

| | | | | |
|----|------|---|------|--|
| Db | 1021 | GCCAAAGGCTAACGAGCTCACTAGCGAACTGGAACGCTGATCCTTGTCACTGCAGACCAAC | 1080 | |
| QY | 1081 | TCCCATGTCTTCTTTTGGTGCTACACACTGCGTGGACCTCCATTTTCGCTGGCC | 1140 | |
| Db | 1081 | TCCCATGTCTTCTTTTGGTGCTACACACTGCGTGGACCTCCATTTTCGCTGGCC | 1140 | |
| QY | 1141 | CCCGCAAGGCTTGAACAGCAAGTCTTACACTCCATCCTCTATGGCAAATGGCCAGGC | 1200 | |
| Db | 1141 | CCCGCAAGGCTTGAACAGCAAGTCTTACACTCCATCCTCTATGGCAAATGGCCAGGC | 1200 | |
| QY | 1201 | TATGCGCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGACACAAGCGAAGAACCTTCA | 1260 | |
| Db | 1201 | TATGCGCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGACACAAGCGAAGAACCTTCA | 1260 | |
| QY | 1261 | TACCGGACAGGCGGCGGTGCCCTTGCTTAGCGAGACCCACGCGGGCGAAGACGTGGCG | 1320 | |
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| QY | 1321 | GTGTTGCGCGAGGCGCGGACGCGCACCTGTGTGACAGGCGGTGACAGAGACCTTCTGTG | 1380 | |
| Db | 1321 | GTGTTGCGCGAGGCGCGGACGCGCACCTGTGTGACAGGCGGTGACAGAGACCTTCTGTG | 1380 | |
| QY | 1381 | GCGCACATCATGCGCTTTCGCGGTGCGGTGAGAGCCCTTACACCGACTGCAATGCGACGC | 1440 | |
| Db | 1381 | GCGCACATCATGCGCTTTCGCGGTGCGGTGAGAGCCCTTACACCGACTGCAATGCGACGC | 1440 | |
| QY | 1441 | CCCGCCACCGCCACGACATCCCGACTAGGGTACC | 1476 | |
| Db | 1441 | CCCGCCACCGCCACGACATCCCGACTAGGGTACC | 1476 | |

RESULT 2

AX356645

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .1476

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/db_xref="taxon:9913"

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 9.1e-270;

Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

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Db

1

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60

QY

61

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120

Db

61

GCCCTTGATGTAGCCAGAAGTTGACAGCCGATCCAGACAGCTGCCAAGAATGTATCTCTC

120

QY

121

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180

Db

121

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180

QY

181

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240

Db

181

ATGAATGGCAAACTGGGACCTTGAGACACCCCTGGCCATGACCACTTCCCATACGTGGCT

240

Db 181 ATGAATGGCAAACTGGGACCTGAGACACCCCTGGCCATGGAACCAAGTTCCTCATACGTGGCT 240

Qy 241 CTGTCCAAAGACATACAACGTGGACAGACAGGTGCCAGACAGCGCAGCACTGCCACTGCC 300

Db 241 CTGTCCAAAGACATACAACGTGGACAGACAGGTGCCAGACAGCGCAGCACTGCCACTGCC 300

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Db 301 TACCTGTGTGGGGTCAAGGGCACTACGAACCATCGGTGTAAAGTGAGCCCGCGCTAC 360

Qy 361 AATCAGTGCACACGACACGTGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAGAAA 420

Db 361 AATCAGTGCACACGACACGTGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAGAAA 420

Qy 421 GCAGGGAAAGCCGTGGGAGTGTGACCAACCAAGGGTGCAAGCATGCCCTCCCAAGCCGG 480

Db 421 GCAGGGAAAGCCGTGGGAGTGTGACCAACCAAGGGTGCAAGCATGCCCTCCCAAGCCGG 480

Qy 481 GCCTACGCGCACACGGTGAAACCGAACTGGTACTCAGACGCCGACCTGCTGTGATGCA 540

Db 481 GCCTACGCGCACACGGTGAAACCGAACTGGTACTCAGACGCCGACCTGCTGTGATGCA 540

Qy 541 CAGAAAGATGCGCTGCCAGACATCGCCGACACAGCTGTGTACAAATGATATTGACGTG 600

Db 541 CAGAAAGATGCGCTGCCAGACATCGCCGACACAGCTGTGTACAAATGATATTGACGTG 600

Qy 601 ATCCTGGGTGAGGCCGAATGTACATGTTCTTGAGGGGAGCCCAACCTGATATACCA 660

Db 601 ATCCTGGGTGAGGCCGAATGTACATGTTCTTGAGGGGAGCCCAACCTGATATACCA 660

Qy 661 GATGATGCCACTGTGAATGAGTCCGGAAAGACAAGCAAGCAACCTGTGTGAGGAATGGCAG 720

Db 661 GATGATGCCACTGTGAATGAGTCCGGAAAGACAAGCAAGCAACCTGTGTGAGGAATGGCAG 720

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Qy 781 GACTCCAGTGTAAACACACCTCATGCGCTCTTGAGCCGGCAGACATGAATATATGTT 840

Db 781 GACTCCAGTGTAAACACACCTCATGCGCTCTTGAGCCGGCAGACATGAATATATGTT 840

Qy 841 CAGCAAGACCAACCAAGGACCCGACCTGCGGAGATGACGAGCGCGCCCTGCAAGTG 900

Db 841 CAGCAAGACCAACCAAGGACCCGACCTGCGGAGATGACGAGCGCGCCCTGCAAGTG 900

Qy 901 CTGAGCAGGAACCCCGGGCTTCTACTCTTCTGAGGGAGCGCCCATTTGACCACGGT 960

Db 901 CTGAGCAGGAACCCCGGGCTTCTACTCTTCTGAGGGAGCGCCCATTTGACCACGGT 960

Qy 961 CACCATGACGGCAAGCTTATATGCACTGAGCGGATCATGTTTGAACAATGCCATC 1020

Db 961 CACCATGACGGCAAGCTTATATGCACTGAGCGGATCATGTTTGAACAATGCCATC 1020

Qy 1021 GCCAAGCTAACGAGCTCACTAGCAACTGACACGCTGATCCTTGCTCACTGCAGACCAC 1080

Db 1021 GCCAAGCTAACGAGCTCACTAGCAACTGACACGCTGATCCTTGCTCACTGCAGACCAC 1080

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Qy 1141 CCGGGAAGGCTTAGACAGCAAGTCTTACCTCCATCTCTATGGAATGGCCAGGC 1200

Db 1141 CCGGGAAGGCTTAGACAGCAAGTCTTACCTCCATCTCTATGGAATGGCCAGGC 1200

Qy 1201 TATGCGCTTGGCGGGGCTCGAGGCGCCGATGTTAATGGCAGACAAAGGAAACCTTCA 1260

Db 1201 TATGCGCTTGGCGGGGCTCGAGGCGCCGATGTTAATGGCAGACAAAGGAAACCTTCA 1260

Qy 1261 TACCGGCAAGGCGCGCTGCGCTGCTAGCGAGACCCACGGGGCGAAGACGTGGCG 1320

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Db 1321 GTGTCGCGGAGGCGCCGACGCGCACTGTGACAGCGCGTGAGAGAGACCTTGTG 1380

Qy 1381 GCGCAATCATGCGCTTTCGGGCTCGGTGAGACCCCTACACCGAATGCAATCTGCCAGCC 1440

Db 1381 GCGCAATCATGCGCTTTCGGGCTCGGTGAGACCCCTACACCGAATGCAATCTGCCAGCC 1440

Qy 1441 CCGGCAAGGCGCGCAAGCATCCCGAAGTACGAGTACC 1476

Db 1441 CCGGCAAGGCGCGCAAGCATCCCGAAGTACGAGTACC 1476

RESULT 3

AX840884 1464 bp DNA linear PAT 16-DEC-2003

LOCUS Sequence 1 from Patent EP1348760.

DEFINITION AX840884

ACCESSION AX840884

VERSION AX840884.1 GI:39979031

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE

1 Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W. and Kirschbaum,T. Production of inactive mutants or mutants with a low activity of an alkaline phosphatase and their expression in yeast

JOURNAL Patent: EP 1348760-A 1 01-OCT-2003;

FEATURES

Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)

location/Qualifiers

1..1464

/organism="Bos taurus"

/mol_type="unassigned DNA"

/db_xref="taxon:9913"

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CDS

ORIGIN

Query Match 99.2%; Score 1464; DB 6; Length 1464;

Best Local Similarity 100.0%; Pred.No. 1.7e-267;

Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTGATCCAGCTGAGGAGGAAACCCCGCTTCTGGAACCGCGCAGGAGCCGCTT 60

Qy 67 GATGTAGCAAGAAGTTGACGCGATCCAGACAGCTGCCAAGAATGTCATCTTCTTG 126

Db 61 GATGTAGCAAGAAGTTGACGCGATCCAGACAGCTGCCAAGAATGTCATCTTCTTG 120

Qy 127 GGGATGGATGGGGGCTTACCGGTGACAGCCACTCGGATCCTTAAAGGGCAGATGAAT 186

Db 121 GGGATGGATGGGGGCTTACCGGTGACAGCCACTCGGATCCTTAAAGGGCAGATGAAT 180

Qy 187 GGCAACTGGGACCTGAGACACCCCTGGCCATGAGCAGATTCCCATACGTGCTGTCC 246

Db 181 GGCAACTGGGACCTGAGACACCCCTGGCCATGAGCAGATTCCCATACGTGCTGTCC 240

| | | | |
|----|------|---|------|
| QY | 247 | AAGACATACAACGTGGACAGACAGTGCACAGCGCAGGCACTGCGCACTGCTTACCTG | 306 |
| Db | 241 | AAAGCATACAACGTGGACAGACAGTGCACAGCGCAGGCACTGCGCACTGCTTACCTG | 300 |
| QY | 307 | TGTGGGGTCAAGGGCACTACAGAACCATCGGTGTAAAGTGCAGCCCGCTTACATCAG | 366 |
| Db | 301 | TGTGGGGTCAAGGGCACTACAGAACCATCGGTGTAAAGTGCAGCCCGCTTACATCAG | 360 |
| QY | 367 | TGCACACGACACGTGGGAATGAGGTCACTGTGTATCAACCGGGCCAAAGAACAGAGG | 426 |
| Db | 361 | TGCACACGACACGTGGGAATGAGGTCACTGTGTATCAACCGGGCCAAAGAACAGAGG | 420 |
| QY | 427 | AAGCCGTGGGAGTGTGACCAACAGGGGTGCAGCATGCTCCCAAGCCGGGCTTAC | 486 |
| Db | 421 | AAGCCGTGGGAGTGTGACCAACAGGGGTGCAGCATGCTCCCAAGCCGGGCTTAC | 480 |
| QY | 487 | GCGCACACGGTGAACCGAACTGGTACTCAGACGCCGACCTGCTGCTGATGCACAGAA | 546 |
| Db | 481 | GCGCACACGGTGAACCGAACTGGTACTCAGACGCCGACCTGCTGCTGATGCACAGAA | 540 |
| QY | 547 | AATGGTGCACAGACATCGCCGCACAGCTGCTTACAACATGATATTGACGTGATCCTG | 606 |
| Db | 541 | AATGGTGCACAGACATCGCCGCACAGCTGCTTACAACATGATATTGACGTGATCCTG | 600 |
| QY | 607 | GGTGAGGCCGAATGTACATGTTTCTTGAAGGGGAGCCCAAGACCTTGAATACCAAGATG | 666 |
| Db | 601 | GGTGAGGCCGAATGTACATGTTTCTTGAAGGGGAGCCCAAGACCTTGAATACCAAGATG | 660 |
| QY | 667 | GCCAGTGTGAATGAGTCCGGAAGACAGCAAGAACCTGCTGTCAGGAATGGCAGGCCAA | 726 |
| Db | 661 | GCCAGTGTGAATGAGTCCGGAAGACAGCAAGAACCTGCTGTCAGGAATGGCAGGCCAA | 720 |
| QY | 727 | CACCAAGGAGCCAGTATGTGTGAACCGCACTGCGCTCCTTCAAGCGCGCGATGACTCC | 786 |
| Db | 721 | CACCAAGGAGCCAGTATGTGTGAACCGCACTGCGCTCCTTCAAGCGCGCGATGACTCC | 780 |
| QY | 787 | AGTGTACACACCTCATGCGCTCTTGAACCGCGCAGACATGAAGTATATGTTCAAGAA | 846 |
| Db | 781 | AGTGTACACACCTCATGCGCTCTTGAACCGCGCAGACATGAAGTATATGTTCAAGAA | 840 |
| QY | 847 | GACCAACCAAGGAGCCGACCCCTGGCGGAGATGACGGAGCGCGCTTCAAGTGTGAGC | 906 |
| Db | 841 | GACCAACCAAGGAGCCGACCCCTGGCGGAGATGACGGAGCGCGCTTCAAGTGTGAGC | 900 |
| QY | 907 | AGGAACCCCGGGCTTCTACCTCTTGTGAGGAGGCGCGCATTTGACCAAGGTCAACAT | 966 |
| Db | 901 | AGGAACCCCGGGCTTCTACCTCTTGTGAGGAGGCGCGCATTTGACCAAGGTCAACAT | 960 |
| QY | 967 | GACGGCAAAGCTTATATGCACTGACGAGCGATCATGTTTGAATGCCATCGCCAAG | 1026 |
| Db | 961 | GACGGCAAAGCTTATATGCACTGACGAGCGATCATGTTTGAATGCCATCGCCAAG | 1020 |
| QY | 1027 | GCTAACGAGCTCACTAGCGAACTGACAAGCTGATCCTTGTCACTGACAGCACTCCAT | 1086 |
| Db | 1021 | GCTAACGAGCTCACTAGCGAACTGACAAGCTGATCCTTGTCACTGACAGCACTCCAT | 1080 |
| QY | 1087 | GTCCTCTCTTTTGTGCTACACACTGCGTGGGACCTCCATTTCGGTCTGGCCCCGGC | 1146 |
| Db | 1081 | GTCCTCTCTTTTGTGCTACACACTGCGTGGGACCTCCATTTCGGTCTGGCCCCGGC | 1140 |
| QY | 1147 | AAGGCTTTAGACAGCAAGTCTTACACTTCATCCTTATGGCAATGGCCAGGCTATGCG | 1206 |
| Db | 1141 | AAGGCTTTAGACAGCAAGTCTTACACTTCATCCTTATGGCAATGGCCAGGCTATGCG | 1200 |
| QY | 1207 | CTTGCGGGGCTCGAGGCCGATGTTAATGGCAGCAACAAGCGAGGAACCTCATACCGG | 1266 |
| Db | 1201 | CTTGCGGGGCTCGAGGCCGATGTTAATGGCAGCAACAAGCGAGGAACCTCATACCGG | 1260 |
| QY | 1267 | CAGCAGCGGGCCGTGCCCCCTGGCTAGCGAGACCCACGGGGCGAAGAGTGGCGGTGTC | 1326 |
| Db | 1261 | CAGCAGCGGGCCGTGCCCCCTGGCTAGCGAGACCCACGGGGCGAAGAGTGGCGGTGTC | 1320 |

| | | | |
|----------------------------|------|--|------|
| QY | 1327 | GCGCGAGGCCCGCAGCGCCGACCTGTGTACCGGCGGTGCAGAGAGACCTTCTGTGGCGAC | 1386 |
| Db | 1321 | GCGCGAGGCCCGCAGCGCCGACCTGTGTACCGGCGGTGCAGAGAGACCTTCTGTGGCGAC | 1380 |
| QY | 1387 | ATCATGGCCTTTGCGGGCTGCGTGGAGCCCTTACACCGACTGCAATCTGGCAGCCCGCC | 1446 |
| Db | 1381 | ATCATGGCCTTTGCGGGCTGCGTGGAGCCCTTACACCGACTGCAATCTGGCAGCCCGCC | 1440 |
| QY | 1447 | ACCGCACACGATCCCCGACTAG 1470 | |
| Db | 1441 | ACCGCACACGATCCCCGACTAG 1464 | |
| RESULT 4 | | | |
| E59950 | | | |
| LOCUS | | | |
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| ORGANISM | | | |
| REFERENCE | | | |
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| PF | | | |
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| PI | | | |
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| CC | | | |
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| FT | | | |
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| Best Local Similarity | | | |
| Matches 1462; Conservative | | | |
| QY | 6 | CCTCATCCAGCTGAGAGGAAAAACCCGCTTGTGAAACCGCCAGGAGCCCGCCCT | 65 |
| Db | 107 | CTCATCCAGCTGAGAGGAAAAACCCGCTTGTGAAACCGCCAGGAGCCCGCCCT | 166 |
| QY | 66 | TGATGTAGCCAAGAGTTGACCCGATCCAGACAGCTGCCAAGATGTATCTTCTT | 125 |
| Db | 167 | TGATGTAGCCAAGAGTTGACCCGATCCAGACAGCTGCCAAGATGTATCTTCTT | 226 |
| QY | 126 | GCGGATGGGATGGGGTGCTACGGTGAACAGCCACTCGGATCCTAAAGGGGAGATGAA | 185 |
| Db | 227 | GCGGATGGGATGGGGTGCTACGGTGAACAGCCACTCGGATCCTAAAGGGGAGATGAA | 286 |
| QY | 186 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGACCAAGTTCCATACGTGCTGTC | 245 |
| Db | 287 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGACCAAGTTCCATACGTGCTGTC | 346 |
| QY | 246 | CAAGACATACAACGTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTTACT | 305 |
| Db | 347 | CAAGACATACAACGTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTTACT | 406 |

QY 306 GTGTGGGTCAAGGGCAACTACAGAACCATCGGTGTAGTGACAGCCGGCCCTACAATCA 365
Db 407 GTGTGGGTCAAGGGCAACTACAGAACCATCGGTGTAGTGACAGCCGGCCCTACAATCA 466
QY 366 GTGCAACACGACAGTGGGAATGAGGTACGCTCTGTGATCAACCGGGCCAAGAACGAG 425
Db 467 GTGCAACACGACAGTGGGAATGAGGTACGCTCTGTGATCAACCGGGCCAAGAACGAG 526
QY 426 GAAGCCCTGGAGTGTGTGACCAACCACAGGGGTGCAGCATGCTCCCAAGCCGGGGCTTA 485
Db 527 GAAGCCCTGGAGTGTGTGACCAACCACAGGGGTGCAGCATGCTCCCAAGCCGGGGCTTA 586
QY 486 CGCGCACACGGTGAACCGAACTGGTACTCAGACGGCCGACCTGCTGTATGCACAGAA 545
Db 587 CGCGCACACGGTGAACCGAACTGGTACTCAGACGGCCGACCTGCTGTATGCACAGAA 646
QY 546 GAATGCTGCCAGGACATCGCCGACAGCTGTCTACAACATGATGATTAATGACGTGATCCT 605
Db 647 GAATGCTGCCAGGACATCGCCGACAGCTGTCTACAACATGATGATTAATGACGTGATCCT 706
QY 606 GGGTGAAGCCGAATGTACATGTTTCTGTAGGGGACCCAGACCCCTGAATACCCAGATGA 665
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QY 666 TGCCAGTGTGAATGGAATCCGGAAAGACAGCAGAACCTGGTGCAGGAAATGGCAGGCCAA 725
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QY 726 GCACCAAGGAGCCCAATATGTGTGAACCGCACTGCGCTCCTTCAGGGCGCCGATGACTC 785
Db 827 GCACCAAGGAGCCCAATATGTGTGAACCGCACTGCGCTCCTTCAGGGCGCCGATGACTC 886
QY 786 CAGTGTAAACAACCTCATGGGCTCTTTGAGCCGGCAGACATGAATGATTAATGTTTCAGCA 845
Db 887 CAGTGTAAACAACCTCATGGGCTCTTTGAGCCGGCAGACATGAATGATTAATGTTTCAGCA 946
QY 846 AGACCACACCAAGAGACCCGACCTGGCGGAGATGACGAGGCGGCCCTGCAGTGTGAG 905
Db 947 AGACCACACCAAGAGACCCGACCTGGCGGAGATGACGAGGCGGCCCTGCAGTGTGAG 1006
QY 906 CAGGAACCCCGGGGCTTCTACCTCTTCTGTGAGGAGGAGCGCCGATGACCAAGGTACCA 965
Db 1007 CAGGAACCCCGGGGCTTCTACCTCTTCTGTGAGGAGGAGCGCCGATGACCAAGGTACCA 1066
QY 966 TGACGGGCAAAAGCTTATATGGCACTGATGAGGCGATCATGTTTGACATGCCATCGCCAA 1025
Db 1067 TGACGGGCAAAAGCTTATATGGCACTGATGAGGCGATCATGTTTGACATGCCATCGCCAA 1126
QY 1026 GAGTAAAGAGCTCACTAGCGAAGTGAACGCTGATCCTTGTCACTGCAGACCACTCCCA 1085
Db 1127 GAGTAAAGAGCTCACTAGCGAAGTGAACGCTGATCCTTGTCACTGCAGACCACTCCCA 1186
QY 1086 TGTCTTCTTTTGGTGTACACACTGGGTGGGACCTCCATTTTCGGTCTGCCCCCGG 1145
Db 1187 TGTCTTCTTTTGGTGTGTACACACTGGGTGGGACCTCCATTTTCGGTCTGCCCCCGG 1246
QY 1146 CAAGGCTTGAACAGCAAGTCTTACCTTCATCTCTATGGCAATGGCCCAAGGCTATGC 1205
Db 1247 CAAGGCTTGAACAGCAAGTCTTACCTTCATCTCTATGGCAATGGCCCAAGGCTATGC 1306
QY 1206 GCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCACAAGCGAGAAACCTCATACCG 1265
Db 1307 GCTTGGCGGGGCTCGAGGCCCGATGTTAATGGCAGCACAAGCGAGAAACCTCATACCG 1366
QY 1266 GCAGCAGGCGGCGGTGCCCTGGCTAGCAGAACCCAGGGGCGAAGAGCTGGCGGTGT 1325
Db 1367 GCAGCAGGCGGCGGTGCCCTGGCTAGCAGAACCCAGGGGCGAAGAGCTGGCGGTGT 1426
QY 1326 CGCGCAGGCGCGCAGGCGCACCTGTGCAAGCGGTGCAGAGAGAGACCTTCGTGCGCA 1385
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QY 1386 CATCATGGCTTTGCGGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCCAGCCCCCGC 1445
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QY 1446 CACCGCCACCGACATCCCCGAC 1467
Db 1547 CACCGCCACCGACATCCCCGAC 1568
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AR214214 1798 bp DNA linear PAT 25-SEP-2002
LOCUS AR214214
DEFINITION Sequence 1 from patent US 6406899.
ACCESSION AR214214
VERSION AR214214.1 GI:23311768
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1798)
AUTHORS Hoelke,W., Muller,R., Burtscher,H. and Millan,J.L.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: US 6406899-A 1 18-JUN-2002;
FEATURES location/Qualifiers
source 1..1798
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ORIGIN
Query Match 99.1%; Score 1462; DB 6; Length 1798;
Best Local Similarity 100.0%; Pred. No. 4e-267;
Matches 1462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 107 CCTCATCCAGCTGAGAGAGAAACCCGCTTCTGGAACGCCAGCAGCCAGGCCCT 166
QY 66 TGATGTACCAAGAAGTTGCAAGCCGATCCAGACAGCTGCCAAGAATGTCATCCTTCTT 125
Db 167 TGATGTACCAAGAAGTTGCAAGCCGATCCAGACAGCTGCCAAGAATGTCATCCTTCTT 226
QY 126 GGGGATGGGATGGGGTGCCCTACGCTGACAGCACTCCGATCTTAAAGGGGAGATGAA 185
Db 227 GGGGATGGGATGGGGTGCCCTACGCTGACAGCACTCCGATCTTAAAGGGGAGATGAA 286
QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCAAGTCCATACGTGCTGTGC 245
Db 287 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCAAGTCCATACGTGCTGTGC 346
QY 246 CAAGCATACAACGTGAGACAGAGGTGCCAGACAGCGGCACTGCCACTGCTTACCT 305
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QY 366 GTGCAACACGACAGCTGGGAATGAGGTACGCTGTGTATCAACGGGGCCAAGAAAGCAGG 425
Db 467 GTGCAACACGACAGCTGGGAATGAGGTACGCTGTGTATCAACGGGGCCAAGAAAGCAGG 526
QY 426 GAAGGCGTGGGAGTGTGACCAACCAGGGGTGCAGCATGCTCCCAAGCCGGGGCTTA 485
Db 527 GAAGGCGTGGGAGTGTGACCAACCAGGGGTGCAGCATGCTCCCAAGCCGGGGCTTA 586
QY 486 CGCGCACACGGTGAACCGAACTGGTACTCAGACGGCCGACCTGCTGTATGCACAGAA 545
Db 587 CGCGCACACGGTGAACCGAACTGGTACTCAGACGGCCGACCTGCTGTATGCACAGAA 646
QY 546 GAATGCTGCCAGGACATCGCCGACAGCTGTCTACAACATGATTAATGACGTGATCCT 605
Db 647 GAATGCTGCCAGGACATCGCCGACAGCTGTGTACAACATGATTAATGACGTGATCCT 706

| | | | |
|----|------|---|------|
| QY | 606 | GGGTGAGAGCCGGAATGTACATGTTTCTGAGGGAGCCCGACAGCCCTGAATACCCAGATGA | 665 |
| Db | 707 | GGGTGAGAGCCGGAATGTACATGTTTCTGAGGGAGCCCGACAGCCCTGAATACCCAGATGA | 766 |
| QY | 666 | TGCCAGTGTGAATGAGTCCCGAAGACAAGCAGAACCTGTGTGAGGAATGGCAGGCCAA | 725 |
| Db | 767 | TGCCAGTGTGAATGAGTCCCGAAGACAAGCAGAACCTGTGTGAGGAATGGCAGGCCAA | 826 |
| QY | 726 | GCACCAAGGAGGCCAGATGTGTGGAACCCGACTGCGCTCCTTCAGGGCGCGATGACTC | 785 |
| Db | 827 | GCACCAAGGAGGCCAGATGTGTGGAACCCGACTGCGCTCCTTCAGGGCGCGATGACTC | 886 |
| QY | 786 | CAGTGTAAACACACCTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTACGA | 845 |
| Db | 887 | CAGTGTAAACACACCTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTACGA | 946 |
| QY | 846 | AGACCACACCAAGAGACCCGACCCTGGCGGAGATGACGAGGCGCGCCTGCAAGTGTAG | 905 |
| Db | 947 | AGACCACACCAAGAGACCCGACCCTGGCGGAGATGACGAGGCGCGCCTGCAAGTGTAG | 1006 |
| QY | 906 | CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGAGCGCGCATTTGACCACGCTACCA | 965 |
| Db | 1007 | CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGAGCGCGCATTTGACCACGCTACCA | 1066 |
| QY | 966 | TGACGGCAAAAGCTTATATGGCACTGACTGAGGGCATCATGTTTGACAATGCCATCGCAA | 1025 |
| Db | 1067 | TGACGGCAAAAGCTTATATGGCACTGACTGAGGGCATCATGTTTGACAATGCCATCGCAA | 1126 |
| QY | 1026 | GGCTAAGAGCTCACTAGCGAACTGGACACGCTGATCCTTGTCTACTGCAGACCACTCCCA | 1085 |
| Db | 1127 | GGCTAAGAGCTCACTAGCGAACTGGACACGCTGATCCTTGTCTACTGCAGACCACTCCCA | 1186 |
| QY | 1086 | TGTCTTCTTTTGGTGTACACACTGCGTGGGACCTCCATTTTCGGTCTGGCCCCCGG | 1145 |
| Db | 1187 | TGTCTTCTTTTGGTGTACACACTGCGTGGGACCTCCATTTTCGGTCTGGCCCCCGG | 1246 |
| QY | 1146 | CAAGGCTTGAACAGCAAGTCTTACACTTCATCCTTATGGCAATGGCCAGGCTATGC | 1205 |
| Db | 1247 | CAAGGCTTGAACAGCAAGTCTTACACTTCATCCTTATGGCAATGGCCAGGCTATGC | 1306 |
| QY | 1206 | GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGACAAAGCGAGAAACCTCATACCG | 1265 |
| Db | 1307 | GCTTGGCGGGGCTCGAGGCCGATGTTAATGGCAGACAAAGCGAGAAACCTCATACCG | 1366 |
| QY | 1266 | GCAGCAGGCGGCGCTGCCCCGTGCTAGCGAGAACCCACGGGGCGAAGACGTGGCGTGT | 1325 |
| Db | 1367 | GCAGCAGGCGGCGCTGCCCCGTGCTAGCGAGAACCCACGGGGCGAAGACGTGGCGTGT | 1426 |
| QY | 1326 | CGCGCGAGGCGCGCAGGCGCACTGTGTGACGGCGTGACAGGAGAGACCTTCGTGGCGCA | 1385 |
| Db | 1427 | CGCGCGAGGCGCGCAGGCGCACTGTGTGACGGCGTGACAGGAGAGACCTTCGTGGCGCA | 1486 |
| QY | 1386 | CATCATGGCTTTTGGGGCTGCGTGAGGCCCTACACCGACTGCAATCTGCCAGCCCCCGC | 1445 |
| Db | 1487 | CATCATGGCTTTTGGGGCTGCGTGAGGCCCTACACCGACTGCAATCTGCCAGCCCCCGC | 1546 |
| QY | 1446 | CACCGCCACAGCATCCCCGAC 1467 | |
| Db | 1547 | CACCGCCACAGCATCCCCGAC 1568 | |

RESULT 6
AX012341
LOCUS AX012341 1798 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent EP0955369.
ACCESSION AX012341
VERSION AX012341.1 GI:9998390
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

| | | | |
|----------------------------|-----|---|---|
| REFERENCE | | 1 | Burtscher, H.D., Mueller, R.D., Hoelke, W.D. and Millan, J.L. |
| AUTHORS | | | High active alkaline phosphatase |
| TITLE | | | Patent: EP 0955369-A 1 10-NOV-1999; |
| JOURNAL | | | ROCHE DIAGNOSTICS GMBH (DE) |
| FEATURES | | | Location/Qualifiers |
| source | | 1. .1798 | /organism="Bos taurus" |
| | | | /mol_type="unassigned DNA" |
| | | | /db_xref="taxon:9913" |
| ORIGIN | | | |
| Query Match | | 99.1%; Score 1462; DB 6; Length 1798; | |
| Best Local Similarity | | 100.0%; Pred. No. 4e-267; | |
| Matches 1462; Conservative | | 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY | 6 | CCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTGGAACCGCCAGGAGCCGCT | 65 |
| Db | 107 | CCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTGGAACCGCCAGGAGCCGCT | 166 |
| QY | 66 | TGATGTAGCCAAAGTTGACGCCGATCCAGACAGCTGCCAAGATGTATCTTCTT | 125 |
| Db | 167 | TGATGTAGCCAAAGTTGACGCCGATCCAGACAGCTGCCAAGATGTATCTTCTT | 226 |
| QY | 126 | GGGGATGGATGGGGGTGCTTACGCTGACAGCCACTCGGATCCTAAAGGGCAGATGA | 185 |
| Db | 227 | GGGGATGGATGGGGGTGCTTACGCTGACAGCCACTCGGATCCTAAAGGGCAGATGA | 286 |
| QY | 186 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGACCACTTCCCATACGTGGCTGTG | 245 |
| Db | 287 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGACCACTTCCCATACGTGGCTGTG | 346 |
| QY | 246 | CAAGACATACAACTGTGACAGACAGGTGCCAGACACCGCAGGCACTGCCACTGCTTACCT | 305 |
| Db | 347 | CAAGACATACAACTGTGACAGACAGGTGCCAGACACCGCAGGCACTGCCACTGCTTACCT | 406 |
| QY | 306 | GTTGGGGTCAAGGGCACTACAGAACCATCGGTGTAAAGTGACAGCCGCGCTCAATCA | 365 |
| Db | 407 | GTTGGGGTCAAGGGCACTACAGAACCATCGGTGTAAAGTGACAGCCGCGCTCAATCA | 466 |
| QY | 366 | GTCGAACACGACACGTGGGAATGAGTCACTGTGATCAACCGGGCCAAAGCAGG | 425 |
| Db | 467 | GTCGAACACGACACGTGGGAATGAGTCACTGTGATCAACCGGGCCAAAGCAGG | 526 |
| QY | 426 | GAAAGCCGTGGAGTGTGACCAACCAAGGCTGACATGCTCCCAAGCCGAGCCTA | 485 |
| Db | 527 | GAAAGCCGTGGAGTGTGACCAACCAAGGCTGACATGCTCCCAAGCCGAGCCTA | 586 |
| QY | 486 | CGCGCACACGGTGAACCGGAACTGTACTCAGACGCGGACCTGCTGTATGACAGAA | 545 |
| Db | 587 | CGCGCACACGGTGAACCGGAACTGTACTCAGACGCGGACCTGCTGTATGACAGAA | 646 |
| QY | 546 | GAATGGCTGCCAGGACATCGCCGACAGCTGGTCTTACAACATGGATATTGACGTGATCCT | 605 |
| Db | 647 | GAATGGCTGCCAGGACATCGCCGACAGCTGGTCTTACAACATGGATATTGACGTGATCCT | 706 |
| QY | 606 | GGGTGAGGCGCGAATGTACATGTTTCTGAGGGGAGCCCGACAGCCCTGAATACCCAGATGA | 665 |
| Db | 707 | GGGTGAGGCGCGAATGTACATGTTTCTGAGGGGAGCCCGACAGCCCTGAATACCCAGATGA | 766 |
| QY | 666 | TGCCAGTGTGAATGAGTCCCGAAGAGACAAAGCAACTGTGACGAAGATGGCAGGCCAA | 725 |
| Db | 767 | TGCCAGTGTGAATGAGTCCCGAAGAGACAAAGCAACTGTGACGAAGATGGCAGGCCAA | 826 |
| QY | 726 | GCACCAAGGAGGCCAGTATGTGTGGAACCGCACTGCGCTCCTTCAGGGCGCGATGACTC | 785 |
| Db | 827 | GCACCAAGGAGGCCAGTATGTGTGGAACCGCACTGCGCTCCTTCAGGGCGCGATGACTC | 886 |
| QY | 786 | CAGTGTAAACACACCTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTACGA | 845 |
| Db | 887 | CAGTGTAAACACACCTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATGTTACGA | 946 |
| QY | 846 | AGACCACACCAAGAGACCCGACCCTGGCGGAGATGACGGAAGCGCGCCTGCAAGTGTGAG | 905 |

Db 947 AGACCAACACCAAGACACCCGACCCCTGGCCGAGATGACGGAGCGGCCCTTGCAGAGTGTAG 1006
Qy 906 CAGGAACCCCCGGGGCTTCTACCTTTCGTGAGGGAGGCCGATTTGACCAAGGTACCA 965
Db 1007 CAGGAACCCCCGGGGCTTCTACCTTTCGTGAGGGAGGCCGATTTGACCAAGGTACCA 1066
Qy 966 TGACGGCAAAAGCTTATATGACACTGAGCGGATCATGTTTGACAAATGCCATGCGCAA 1025
Db 1067 TGACGGCAAAAGCTTATATGACACTGAGCGGATCATGTTTGACAAATGCCATGCGCAA 1126
Qy 1026 GGCTAACGAGCTCACTAGCGAAGTGAACAGCTGATCCTTGTCACTGACAGCACTCCCA 1085
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Qy 1086 TGTCTTCTCTTTTGGTGCTACACACTGCGTGGAACCTCCATTTTCGCTGCCCCCGG 1145
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Qy 1146 CAAGGCTTACAGACGAAGTCTTACACCTTCTCTATGGAATGAGCCAGGCTATGC 1205
Db 1247 CAAGGCTTACAGACGAAGTCTTACACCTTCTCTATGGAATGAGCCAGGCTATGC 1306
Qy 1206 GCTTGGCGGGGCTCGAGGCCGATGTTAAATGGACACAAAGCGAAGACCTCATACCG 1265
Db 1307 GCTTGGCGGGGCTCGAGGCCGATGTTAAATGGACACAAAGCGAAGACCTCATACCG 1366
Qy 1266 GCAGCAGGCGCGGTGCCCCCTGCTAGCGAGACCCACGGGGCGAAGAGTGGCGGT 1325
Db 1367 GCAGCAGGCGCGGTGCCCCCTGCTAGCGAGACCCACGGGGCGAAGAGTGGCGGT 1426
Qy 1326 CGCGCAGGCGCGCGAGGCCACCTGTGCAAGCGCTGACAGAGAGACCTTCTGGCGCA 1385
Db 1427 CGCGCAGGCGCGCGAGGCCACCTGTGCAAGCGCTGACAGAGAGACCTTCTGGCGCA 1486
Qy 1386 CATCATGGCTTTGGGGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCCAGCCCCGC 1445
Db 1487 CATCATGGCTTTGGGGGCTGCGTGAAGCCCTACACCGACTGCAATCTGCCAGCCCCGC 1546
Qy 1446 CACCGCCACGATCCCGGAC 1467
Db 1547 CACCGCCACGATCCCGGAC 1568

RESULT 7
AX741748 1650 bp DNA linear PAT 10-MAY-2003
LOCUS AX741748
DEFINITION Sequence 26 from Patent WO03002736.
ACCESSION AX741748
VERSION AX741748.1 GI:30524393
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1
AUTHORS Shao,Z., Kratzsch,P., Schmuck,R., von der Eltz,H. and Kenklies,J.
TITLE A walk-through technique for in vitro recombination of
polynucleotide sequences
JOURNAL Patent: WO 03002736-A 26 09-JAN-2003;
FEATURES Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
Location/Qualifiers
source 1.1650
/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"

ORIGIN
Query Match 98.5%; Score 1454.2; DB 6; Length 1650;
Best local Similarity 99.8%; Pred. No. 1.2e-265;
Matches 1456; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 ATCCAGCTGAGGAGGAAAAACCCGCTTCTGGAACCGCCAGGAGCCGACCCCTTGAT 69
Db 159 ATCCAGCTGAGGAGGAAAAACCCGCTTCTGGAACCGCCAGGAGCCGACCCCTTGAT 218
Qy 70 GTAGCAAGAAATTGACAGCCGATCCAGACAGCTGCGCAAGAAATGATCTTCTTGAGG 129
Db 219 GTAGCAAGAAATTGACAGCCGATCCAGACAGCTGCGCAAGAAATGATCTTCTTGAGG 278
Qy 130 GATGGATGGGGGTGCTACGCTGACAGCCACTCGGATCCTAAAGGGGAGATGATGGC 189
Db 279 GATGGATGGGGGTGCTACGCTGACAGCCACTCGGATCCTAAAGGGGAGATGATGGC 338
Qy 190 AAATGGGACCTGAGACACCCCTGGCCATGGAACAGTTCCCATACGTGGCTCTGTCCAAG 249
Db 339 AAATGGGACCTGAGACACCCCTGGCCATGGAACAGTTCCCATACGTGGCTCTGTCCAAG 398
Qy 250 ACATACAGCTGAGACAGAGGTGCGACAGCGCAGGACCTGCACTGCTTACCTGTGT 309
Db 399 ACATACAGCTGAGACAGAGGTGCGACAGCGCAGGACCTGCACTGCTTACCTGTGT 458
Qy 310 GGGTCAAGGGCAACTACAGAACCAATCGGTGAAGTGACAGCCGCGCTACAATCAGTGC 369
Db 459 GGGTCAAGGGCAACTACAGAACCAATCGGTGAAGTGACAGCCGCGCTACAATCAGTGC 518
Qy 370 AACACGACACGTGGGAATGAGGTCACTGTGTATCAACCGGGGCAAGAAAGCAGGAAG 429
Db 519 AACACGACACGTGGGAATGAGGTCACTGTGTATCAACCGGGGCAAGAAAGCAGGAAG 578
Qy 430 GCCGTGGAGTGTGTACCAACCAAGGTGACAGATGCTCCCGAGCCGCGCTACGCG 489
Db 579 GCCGTGGAGTGTGTACCAACCAAGGTGACAGATGCTCCCGAGCCGCGCTACGCG 638
Qy 490 CACACGGTGAACCGAAACTGTGTACTCAGACCGGACCTGCTGTATGACAGAAAGAT 549
Db 639 CACACGGTGAACCGAAACTGTGTACTCAGACCGGACCTGCTGTATGACAGAAAGAT 698
Qy 550 GGCTGCCAGACATCGCCGACAGCTGTCTCAACATGATATGACGTATCTTGGGT 609
Db 699 GGCTGCCAGACATCGCCGACAGCTGTCTCAACATGATATGACGTATCTTGGGT 758
Qy 610 GGAGGCCGAATGTACATGTTTCTGAGGGGAGCCCGACACCTGATATCCAGATGATGCC 669
Db 759 GGAGGCCGAATGTACATGTTTCTGAGGGGAGCCCGACACCTGATATCCAGATGATGCC 818
Qy 670 AGTGTGAATGAGTCCGGAAGGACAGAACTGTGTGAGGAATGGCAGGCCAAGCAC 729
Db 819 AGTGTGAATGAGTCCGGAAGGACAGAACTGTGTGAGGAATGGCAGGCCAAGCAC 878
Qy 730 CAGGAGCCAGTATGTGTGAACCGCACTGCGCTCTTCAAGGCGCGATGACTCCAGT 789
Db 879 CAGGAGCCAGTATGTGTGAACCGCACTGCGCTCTTCAAGGCGCGATGACTCCAGT 938
Qy 790 GTAACACCTCATGAGGCTCTTGAAGCCGACAGACATGAAGTAATGTTCAAGAACAG 849
Db 939 GTAACACCTCATGAGGCTCTTGAAGCCGACAGACATGAAGTAATGTTCAAGAACAG 998
Qy 850 CACACCAAGGACCCGACCTGGCGGAGATGACGAGGCGGCGCTGAAGTGTGAGCAGG 909
Db 999 CACACCAAGGACCCGACCTGGCGGAGATGACGAGGCGGCGCTGAAGTGTGAGCAGG 1058
Qy 910 AACCCCCGGGCTTCTACCTTTCGTGAGGGAGGGCCGCAATGACCAAGGTACCATGAC 969
Db 1059 AACCCCCGGGCTTCTACCTTTCGTGAGGGAGGGCCGCAATGACCAAGGTACCATGAC 1118
Qy 970 GGCAAGCTTATATGACACTGAGGCGGATCATGTTTGACAAATGCCATGCCAAGGCT 1029
Db 1119 GGCAAGCTTATATGACACTGAGGCGGATCATGTTTGACAAATGCCATGCCAAGGCT 1178
Qy 1030 AACGAGCTCACTAGCAAGTGAACAGCTGATCCTGTCTACTGAGACCACTCCCATGTC 1089
Db 1179 AACGAGCTCACTAGCAAGTGAACAGCTGATCCTGTCTACTGAGACCACTCCCATGTC 1238
Qy 1090 TTCTCTTTTGGTGCTACACACTGCGTGGGACCTCCATTTTCGCTGCGCCCGGCAAG 1149

Db 1239 TTCTCCTTTGGTGCTACACACTGCGTGGAGCTCCATTTCGGTCTGGCCCCCGCAAG 1298

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Db 1299 GCCTTAGACAGCAAGTCTTACACCTCCATCTCTATGGCAATGGCCAGGCTATGCGCTT 1358

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Db 1359 GGGGGGGGCTGAGCGCCCGATGTTAATGGCAGACAAGCGAGAACCTTCGTAACGGCAG 1418

QY 1270 CAGGCGGCGCTGCGCCCTGCGTACGAGACCAAGGGGCGAAGACGTGGCGGTTCGCG 1329

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QY 1330 CGAGCGCCGCGAGCGCACCTGTGACAGCGGCTGACAGAGAGACCTTCGTGGCGACATC 1389

Db 1479 CGAGCGCCGCGAGCGCACCTGTGACAGCGGCTGACAGAGAGACCTTCGTGGCGACATC 1538

QY 1390 ATGGCCTTTGCGGGCTGCGTGGAGCGCCCTACACCGACTGCAATCTGCCAGCCCCGCCACC 1449

Db 1539 ATGGCCTTTGCGGGCTGCGTGGAGCGCCCTACACCGACTGCAATCTGCCAGCCCCCTCCACC 1598

QY 1450 GCCACCGACATCCCCGACT 1468

Db 1599 GCCACCGACATCCCCGACT 1617

RESULT 8
AF052226 2460 bp mRNA linear MAM 03-SEP-1998
LOCUS AF052226 Bos taurus intestinal alkaline phosphatase III mRNA, complete cds.
DEFINITION AF052226
ACCESSION AF052226
VERSION AF052226.1 GI:3510650
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 2460)
AUTHORS Manes,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and Millan,J.L.
TITLE Bovine alkaline phosphatases
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2460)
AUTHORS Manes,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and Millan,J.L.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-1998) Medical Genetics, Umea University, S-901 85 Umea, Sweden
FEATURES
source Location/Qualifiers
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/mol_type="mRNA"
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66..1658
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LGGRKYMPEGETPDEYPHDASVNGVRKDKNLVQEMQAKHQAOYVNRTELLQAA
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CDS

ORIGIN

Query Match 90.7%; Score 1338.2; DB 4; Length 2460;
Best Local Similarity 94.4%; Pred. No. 1.1e-243;
Matches 1388; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGGAGGAAAAACCCGCTTCTTGAAACCGCCAGGCGAGCCGCT 65

Db 122 CTTATCCAGTTGAGGAGAAAGACCCCGCTTCTTGAAACCGCCAGGCGAGCCGCT 181

QY 66 TGATGTAGCCAAAGATTGCAAGCCGATCCAGACAGCTGCCAAGATGTCATCTTCTT 125

Db 182 TGATGTGCTAAGAAAGCTGCAAGCCCATCCAGAAAGCCGCAAGATGTCATCTTCTT 241

QY 126 GGGGATGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCTTAAAGGGCAGATGAA 185

Db 242 GGGAGATGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCTTAAAGGGCAGATGAA 301

QY 186 TGCAAACTGGACCTGAGACACCCCTGGCCATGACCAAGTTCCCATACGTGGCTGTG 245

Db 302 TGACAAAGCTGGGACCTGAGACACCCCTGGCCATGACCAAGTTCCCATACGTGGCTGTG 361

QY 246 CAAGACATACACGTGACAGACAGAGGTGCCAGACGCCAGGCACTGCCACTGCTTACCT 305

Db 362 CAAGACATACACGTGACAGACAGAGGTGCCAGACGCCAGGCACTGCCACTGCTTACCT 421

QY 306 GTGTGGGCTCAAGGGCACTACAGAACCATGGTGTAAAGTGACAGCCGCGCTACAATCA 365

Db 422 GTGTGGGCTCAAGGGCACTACAGAACCATGGTGTAAAGTGACAGCCGCGCTACAATCA 481

QY 366 GTGCAACACGACACGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAGAAAGCAGG 425

Db 482 GTGCAACACGACACGTGGGAATGAGTCAAGTCTGTGATCAACCGGGCCAAGAAAGCAGG 541

QY 426 GAAAGCCGTGGAGTGTGTGACCAACCAAGGTGACAGCATGCTCCCAAGCCGGGCTTA 485

Db 542 GAAGTCAGTGGAGTGTGTGACCAACCAAGGTGACAGCATGCTCCCAAGCCGGGCTTA 601

QY 486 CGCGCACACGCTGAACCGAAATGTGACTGAGACGCCGACCTGCTGTATGCACAGAA 545

Db 602 TGACACACACGCTGAACCGTGAAGTCAAGTCTGTGATGAACCGGGCCAAGAAAGCAGG 661

QY 546 GAATGGCTGCCAGGACATCGCCGACACAGCTGGTCTACACATGAGATATTGACGTGATCCT 605

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QY 606 GGGTGAAGCCGGAATGTACATGTTTCTTGAGGGGGAACCCAGACCTGTAATACCCAGATGA 665

Db 722 GGGTGAAGCCGGAATGTACATGTTTCTTGAGGGGGAACCCAGACCTGTAATACCCAGATGA 781

QY 666 TGCCAGTGTGAATGAGTCCGGAAGACAGCAAGAACTGGTGCAGGATGGCAGGCCAA 725

Db 782 TGCCAGTGTGAATGAGTCCGGAAGACAGCAAGAACTGGTGCAGGATGGCAGGCCAA 841

QY 726 GCACCAAGGAGCCAGTATGTGTGAAACGCACTGCGCTCCTTACGGCGGCGGATGACTTC 785

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QY 786 CAGTGTAAACACCTCATGGGCTCTTTGAGCCGGCAGACATGAGATTAATGTTTCAGCA 845

Db 902 CAGTGTAAACACCTCATGGGCTCTTTGAGCCGGCAGACATGAGATTAATGTTTCAGCA 961

QY 846 AGACCAACCAAGAACCCGACCTGGCGGAGATGACGAGGCGGCGCTGCAAGTGTGAG 905

Db 962 AGACCAACCAAGAACCCGACCTGGCGGAGATGACGAGGCGGCGCTGCAAGTGTGAG 1021

QY 906 CAGGAACCCCGGGGCTTCTACCTCTTCTGTGAGGAGGCGCGCATTTGACCAAGGTACCA 965

Db 1022 CAGGAACCCCGGGGCTTCTACCTCTTCTGTGAGGAGGCGCGCATTTGACCAAGGTACCA 1081

QY 966 TGACGGCAAAAGCTTATATGGCACTGACGTAGGCGGATCATGTTTGACAAATGCCATCGCCAA 1025

Db 1082 TGATAGCAAAAGCTTATATGGCGCTGACTGAGCGGCTCATGTTTGACAAATGCCATCGCCAA 1141

QY 1026 GGCTAACGAGCTCACTAGCGAACTGGACACGCTGATCCTTGTCTACTGACAGCACTCCCA 1085
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Db 1322 GCTTGGTGGGGCTCAAGGCCCGATGTTAATGACAGCATAAGCGAGAACCCCTCATACCG 1381
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Db 1382 GCAGCAGCGCGCGGTGGCCCTGGCTAGCGAGACCCACGGGGCGAAGACGTGGCGGT 1441
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Db 1562 TGGCCTCTCCGACGCGCGCACCTGGCGGCC 1592

RESULT 9
E59951
LOCUS Highly active alkaline phosphatase. 2460 bp DNA linear PAT 13-AUG-2002
DEFINITION E59951
ACCESSION E59951
VERSION E59951.1 GI:13017721
KEYWORDS JP 1999332586-A/2.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 2460)
AUTHORS Werner,H., Reina,M., Herumutto,B. and Jose,L.M.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: JP 1999332586-A 2 07-DEC-1999;
ROCHE DIAGNOSTICS GMBH
COMMENT OS Bovidae
PN JP 1999332586-A/2
PD 07-DEC-1999
PF 06-MAY-1999 JP 1999126494
PR 05-MAY-1998 DE 19819962:7
PI WERNER HOERUKU,REINA MÜLLER,HERUMUTTO BURUTOSHA, PI JOSE LOUIS MILAN
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/16, PC C12N15/00,C12N5/00
CC

FEATURES
FH Key Location/Qualifiers
FT source 1..2460
FT /organism='Bovidae'.
LOCATION/Qualifiers
1..2460
/organism="Bos taurus"
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ORIGIN
Query Match 90.7%; Score 1338.2; DB 6; Length 2460;
Best Local Similarity 94.4%; Pred. No. 1.1e-243;

Matches 1388; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 6 CCTCATCCAGCTGAGAGGAAAAACCCGCTTCTGMAACCGCAGGACCCAGGCCCT 65
Db 122 CTTCACTCCAGTTGAGAGGAAAGACCCGCTTCTGMAACCGCAGGACCCAGGCCCT 181
QY 66 TGATGTAGCAAGAGTTGACGCCGATCCAGACAGCTGCGCAAGATGTATCTCTT 125
Db 182 TGATGTAGCAAGAGTTGACGCCGATCCAGAGAGCCGCAAGATGTATCTCTT 241
QY 126 GGGGATGGGATGGGGGTGCGCTTACGCTGACAGCCACTCGGATCTTAAAGGGCAGATGAA 185
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QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGACCACTTCCATACGTGCTGTG 245
Db 302 TGACAAAGCTGGGACCTGAGACACCCCTGGCCATGAGACCACTTCCATACGTGCTGTG 361
QY 246 CAAGACATCAACGCTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTACCT 305
Db 362 CAAGACATCAACGCTGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTACCT 421
QY 306 GTGTGGGCTCAAGGGCACTACAGAACCATCGGTGTAAGTGACGCCGCCCTACATCA 365
Db 422 GTGTGGGCTCAAGGGCACTACAGAACCATCGGTGTAAGTGACGCCGCCCTACATCA 481
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Db 482 GTGCAACACGACAGCTGGGATGAGTCAAGTCTGTGATCAACCGGGCCAAAGAACAGG 541
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Db 542 GAAGTCAAGTGGGAGTGTGACCAACCAAGGGTGACGATGCTTCCCAAGCCGGGTGCTTA 601
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| ORGANISM | Bos taurus |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. |
| AUTHORS | Manes,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and Millan,J.L. |
| TITLE | Bovine alkaline phosphatases |
| JOURNAL | Unpublished |
| REFERENCE | 2 (bases 1 to 2536) |
| AUTHORS | Manes,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and Millan,J.L. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (05-MAR-1998) Medical Genetics, Umea University, S-901 85 Umea, Sweden |
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| ORIGIN | |
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| QY | 126 GGGGGATGGATGGGGGTGCTTACGGGTGACAGCCACTCGGATCCTTAAAGGGGACATGAA |
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| QY | 666 TGCCAGTGTGAATGAGTCCGGAAAGACAAAGCAGAACTGTGACAGGAATGCGAGGCCAA |
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| E59952 | |

LOCUS E59952 2542 bp DNA linear PAT 13-AUG-2002
DEFINITION Highly active alkaline phosphatase.
ACCESSION E59952
VERSION E59952.1 GI:13017722
KEYWORDS JP 1999332586-A/3.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 2542)
AUTHORS Werner,H., Reina,M., Herumulto,B. and Jose,L.M.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: JP 1999332586-A 3 07-DEC-1999;
ROCHE DIAGNOSTICS GMBH
COMMENT OS Bovidae
PN JP 1999332586-A/3
PD 07-DEC-1999
PF 06-MAY-1999 JP 1999126494
PR 05-MAY-1998 DE 19819962:7
PI WERNER HOBRUKU,REINA MULLER,HERUMUTTO BURUTOSHA, PI JOSE
LOUIS MILAN
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/16, PC
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LOCUS AR214216
DEFINITION Sequence 5 from patent US 6406899.
ACCESSION AR214216
VERSION AR214216.1 GI:23311770

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2542)
AUTHORS Hoelke,W., Muller,R., Burtseher,H. and Millan,J.L.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: US 6406899-A 5 18-JUN-2002;
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AX012345 2542 bp DNA linear PAT 06-SEP-2000
LOCUS AX012345
DEFINITION Sequence 5 from Patent EP0955369.
ACCESSION AX012345
VERSION AX012345.1 GI:9998392
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
REFERENCE 1 Burtseher,H.D., Mueller,R.D., Hoelke,W.D. and Millan,J.L.
AUTHORS
TITLE High active alkaline phosphatase
JOURNAL Patent: EP 0955369-A 5 10-NOV-1999;
FEATURES
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QY 6 CCTCATCCAGCTGAGAGAGAAACCCGCTTCTGGAACCCGACAGCCCAAGCCCT 65
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QY 606 GGGTGGAGCCGAATGTACATGTTTCTGAGGGGACCCGACACCTGATTAACCATGTA 665
DB 721 GGGTGGAGCCGAATGTACATGTTTCTGAGGGGACCCGACACCTGATTAACCATGTA 780
QY 666 TGCCAGTGTGAATGAGTCCGGAAGACAGAACTGTGTGAGGAATGGCAGGCCAA 725
DB 781 TGTCAATCAGACTGGAATCCGGAAGACAGAACTGTGTGAGGAATGGCAGGCCAA 840
QY 726 GCACCAAGGAGCCAGTATGTGGAACCGCACTGCGCTCCTTCAGCGCGCGATGACTC 785
DB 841 GCACCAAGGAGCCAGTATGTGGAACCGCACTGCGCTCCTTCAGCGCGCGATGACTC 900
QY 786 CAGTGTAAACACCTCATGGGCTCTTGAAGCCGCAACATGAATGAATGAATGTTCAACA 845
DB 901 CAGTGTAAACACCTCATGGGCTCTTGAAGCCGCAACATGAATGAATGAATGTTCAACA 960
QY 846 AGACCAACCAAGGAGCCGACCTGCGGAGATGACGGAAGCGGCGCTGCAAGTGTGAG 905
DB 961 AGACCAACCAAGGAGCCGACCTGCGGAGATGACGGAAGCGGCGCTGCAAGTGTGAG 1020
QY 906 CAGGAACCCCGGGGCTTCTACCTCTTCTGAGAGGAGCGCGEATGACCAAGTCAACA 965
DB 1021 CAGGAACCCCGGGGCTTCTACCTCTTCTGAGAGGAGCGCGEATGACCAAGTCAACA 1080
QY 966 TGAAGGCAAGCTTATATGCACTGACATGAGCGATCATGTTTGAATGCCATCGCCAA 1025
DB 1081 TGAAGGCAAGCTTATATGCACTGACATGAGCGATCATGTTTGAATGCCATCGCCAA 1140
QY 1026 GGCTAACGAGCTCACTAGCGAATGACACGCTGATCTTGTCACTGACAGCACTCCCA 1085
DB 1141 GGCTAACGAGCTCACTAGCGAATGACACGCTGATCTTGTCCACTGACAGCACTCCCA 1200

QY 1086 TGTCTTCTTTTGGTGCTACACACTGCGTGGGACCTCCATTTTGGTCTGGCCCCCG 1145
DB 1201 TGTCTTCTTTTGGTGCTACACACTGCGTGGGACCTCCATTTTGGTCTGGCCCCCG 1260
QY 1146 CAAGCCTTAGACAGCAAGTCTTACCTCATCTCTATGCAATGAGCCCAAGCTATGC 1205
DB 1261 CAAGCCTTAGACAGCAAGTCTTACCTCATCTCTATGCAATGAGCCCAAGCTATGC 1320
QY 1206 GCTTGGCGGGCTCGAGGCCGATGTTAATGGACACAGCGAGAACCTCATACCG 1265
DB 1321 GCTTGGCGGGCTTAAAGGCCGATGTTAATGACAGCATTAAGCGAGACCTCGTACCG 1380
QY 1266 GCAGCAGCGCGCGTGCCTGCTGAGGAGACCCACGCGGCGAAGAGTGGCGGTGTT 1325
DB 1381 GCAGCAGCGCGCGTGCCTGCTGAGGAGTCCACAGGCGCGAGAGAGTGGCGGTGTT 1440
QY 1326 CGCGCAGCGCGCGAGCGGACCTGTGACAGCGGTGACAGGAGAGACCTTGTGGCGCA 1385
DB 1441 CGCGCAGCGCGCGAGCGGACCTGTGACAGCGGTGACAGGAGAGACCTTGTGGCGCA 1500
QY 1386 CATCATGGCTTTGCGGGCTGCGTGAAGCCCTACACGACTGCAATCTGCAAGCCCCGC 1445
DB 1501 CATCATGGCTTTGCGGGCTGCGTGAAGCCCTACACGACTGCAATCTGCAAGCCCCGC 1560
QY 1446 CACCGCACACATCCCGACTAGGTTACC 1476
DB 1561 TGGCTCTCCAGCGCGCGCACCTGCGGCC 1591

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